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OM nucleic - nucleic search, using sw model

Run on: May 16, 2005, 06:18:14 ; Search time 17058 Seconds
(Without alignments)
17512.393 Million cell updates/sec

Title: US-10-791-666-1

Perfect score: 6165
Sequence: 1 acgtcgaagtcacaaatg.....gggaccagcttcagataa 6165

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
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13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6165	100.0	6165	6 ARS34558	Sequence
2	6165	100.0	6165	6 AX574425	Sequence
3	6161.8	99.9	6298	6 AX504254	Sequence
4	6160.2	99.9	6165	6 AX671105	Sequence
5	6160.2	99.9	8603	6 AX671108	Sequence
6	6142.2	99.6	6156	6 AX671112	Sequence
7	6126	99.4	6159	6 AX166510	Sequence
8	6121.8	99.3	6189	6 AX503780	Sequence
9	6105.4	99.0	6201	6 AX503778	Sequence
10	5843.2	94.8	8576	9 AY257469	Homo sapi
11	5837	94.7	5877	6 ARS34559	Sequence
12	5837	94.7	5877	6 ARS34559	Sequence
13	5661.4	91.8	6159	6 AX429514	Sequence
14	5661.4	91.8	6574	6 AX429512	Sequence
15	5105.2	82.8	6954	10 AF086824	Mus muscu
16	4909.6	79.6	5920	6 CQ723254	Sequence
17	4021.2	65.2	4967	10 AF070066	Mus muscu
18	4018.2	65.2	5019	10 MMU39904	Mus muscu
19	3906.6	63.4	5952	10 AF039218	Rattus no

20	2818.2	45.7	5261	6 AX671110	Sequence
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22	2808.2	45.6	5251	6 AX925604	Sequence
23	2682.8	43.5	2896	6 CQ498283	Sequence
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26	1436.2	23.3	1799	9 AY209000	Homo sapi
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45	311.2	5.0	136436	9 AC002563	Human PAC

ALIGNMENTS

RESULT 1
LOCUS ARS34558 6165 bp. DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1 from patent US 6734009.
ACCESSION ARS34558
VERSION ARS34558.1 GI:53924885
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 6165)
AUTHORS Yu,X.S., Miranda,M. and Fridde,C.J.
TITLE Human kinases and polynucleotides encoding the same
JOURNAL Patent: US 6734009-A 1 11-MAY-2004;
FEATURES
source location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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DB	1	ATGTTGAAGTTCAATATGAGCGCGGAATCCTTGGATGCTGCTGAACCAT	60	
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DB	61	GCGAGCGGCGCTTCAGGCTGAATCTGTTCTTCAGGGGAAACCACTTATGACTCA	120	
QY	121	CAGCAGATGTCCTCTCTTCCGAGAGGAGATTTAATGCGCCCTTGTCTTTGAA	180	
DB	121	CAGCAGATGTCCTCTCTTCCGAGAGGAGATTTAATGCGCCCTTGTCTTTGAA	180	
QY	181	GAATGACGACGCTGCTGATGAAGATTAAAGCACTGACACTTGTCCGAGATAT	240	
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QY	241	TCCGACCATTAAGTGAATTACAGAGAGCTCCAGCTTCCGAAAGACTTGAAGTCA	300	

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LOCUS      AX574425
DEFINITION      Sequence 1 from Patent WO02059325.
ACCESSION      AX574425
VERSION      AX574425.1 GI:27551751
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SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1. Yu, X., Miranda, M. and Friedle, C.J.
AUTHORS      Human kinases and polynucleotides encoding the same
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JOURNAL      Lexicon Genetics Incorporated (US)
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 ORGANISM
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Gururajan, R., Baughn, M.R., Walla, N.K., Elliott, V.S., Xu, Y.,
 Arvizu, C., Yao, M.G., Ramkumar, J., Ding, L., Tang, Y.T., Hafalia, A.J.,
 Nguyen, D.B., Gandhi, A.R., Lu, Y., Ye, H., Burford, N., Bandman, O.,
 Tribouley, C.M., Lal, P.G., Reclon, S.A., Lu, D.A., Botowsky, M.L.,
 Thornton, M., Swarnaker, A., Thangavelu, K., Khan, F.A. and Ison, C.H.
 Human kinases
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DEFINITION Sequence 1 from Patent WO03004523.
ACCESSION AX671105
VERSION AX671105.1 GI:29329569
KEYWORDS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1. Zhu, Z.
Regulation of human cItron rho/rac-interacting kinase
Patent: WO 03004523-A.1 16-JAN-2003;
Bayer Aktiengesellschaft (DE)
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Db 61 GCCAGCGGGCTCCAGGCTGAATCTGTTCTTCAAGGGGAAACCAACCTTTAAGCTCAA 120

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QY	4621	GCAAAATACAGCAAAAGCAGATGATCCCATACATCTGAAAGATGAAATCTCACCCGACACC	4680
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Qy	5761	AGGGTCATTTTGTCTGCAAGGAAACCTCTGTGAAGAGTCCGCACTGAACACACCCGGGCG	5820	
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SOURCE				
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REFERENCE				
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TITLE	Plowman, G.D., Whyte, D., Manning, G.S., Sudarshanam, S.S., Martinez, R., Flanagan, P., and Clardy, D.S.			
JOURNAL	Novel human protein kinases and protein kinase-like enzymes Patent: WO 0138503-A 1 31-MAY-2001; Sugen, Inc. (US)			
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Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 6145;	Conservative	0;	Mismatches	10;
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				3;
				Gaps
				1;

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Db 1 ATGTTGAAGTTCAAATATNGAGGCGGGAATCCTTTGATGCTGGTCTGTAACCAT 60
QY 61 GCCAGCGGGGCTTCCAGCTGGAATCTGTTCTTCCAGGGGAAACCACTTATGACTCAA 120
Db 61 GCCAGCGGGGCTTCCAGCTGGAATCTGTTCTTCCAGGGGAAACCACTTATGACTCAA 120
QY 121 CAGCAATGTTCTCTCTTTTCCCGAAGGGAATTAATAGTCCCTTTGTTCTTTGAA 180
Db 121 CAGCAATGTTCTCTCTTTTCCCGAAGGGAATTAATAGTCCCTTTGTTCTTTGAA 180
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Db 181 GAATGCACTGAGCTGCTGATGAAGATTAAAGCACTGAGCACTTTGCCGAAAGTG 240
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Db 241 TATTCGACACCAATAGCTGATTACAGAGCTCCAGCTTCGCGAAGAAGCTTGAAGTC 300
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QY 418 TCATTTTGTGAGAAAGCGGAACATTTATCTGAAAGCACAAGCCGCTGATCCCCAA 477
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AUTHORS
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 REFERENCE
 AUTHORS
 1 Gerlach,V.L., Macdougall,J.R., Smithson,G., Milliet,I., Stone,D.,
 Gunther,E., Ellerman,K., Grose,W.M., Alsbrook,J.P., Lepley,D.M.,
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 JOURNAL
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 Patent: WO 0226826-A 8 04-APR-2002;
 Curagen Corporation (US)
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 Location/Qualifiers


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RESULT 10
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DEFINITION Homo sapiens rho/rac-interacting citron kinase (CIT) mRNA, complete
cde.
ACCESSION AY257469
VERSION AY257469.1 GI:3088969
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
Homo; Homo sapiens; Homo sapiens; Homo sapiens; Homo sapiens;
Huang, C.Q., Wu, S.L., Shan, Y.X., Liu, S. and Xiao, P.J.
REFERENCE 1 (bases 1 to 8576)
AUTHORS
TITLE Direct Submission

JOURNAL

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Biology, Basic Medicine, Suzhou University, Renming Road 48,
Suzhou, Jiangsu 215007, China

FEATURES

source

Location/Qualifiers

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ORIGIN

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DEFINITION	Sequence 3 from patent US 6734009.		
ACCESSION	ARS34559		
VERSION	ARS34559.1	GI:53924886	
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 5877)		
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Qy	2101	GAGAAACAAGGTAAAGAGACTAGAGACCATGAGCGGTAGAGAAACAGACTGAAGATGAC	2160
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VERSION AX574427.1 GI:27551752
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Yu, X., Miranda, M. and Fridde, C.J.
TITLE Human kinases and polynucleotides encoding the same
JOURNAL Patent: WO 02059325-A 3 01-AUG-2002;
Lexicon Genetics Incorporated (US)
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ORIGIN

Query Match 94.7%; Score 5837; DB 6; Length 5877;
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ORGANISM Homo sapiens
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AUTHORS Kapeller-Liebermann, R.
TITLE 13245, a novel human myotonic dystrophy type protein kinase and
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MILLENNIUM PHARM INC (US)
FEATURES
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ORGANISM
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Di Cunto,F., Calautti,E., Heiao,J., Ong,L., Topley,G., Turco,E. and
Dotto,G.P.
TITLE Citron rho-interacting kinase, a novel tissue-specific ser/thr
kinase encompassing the Rho-Rac-binding protein Citron
J. Biol. Chem. 273 (45), 29706-29711 (1998)
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2 (bases 1 to 6954)
Di Cunto,F., Calautti,E., Heiao,J., Ong,L., Topley,G., Turco,E. and
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TITLE Direct Submision
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ORIGIN

Query Match 82.8%; Score 5105.2; DB 10; Length 6954;
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Job time : 17095 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2005, 09:14:34 ; Search time 653 Seconds
(without alignments)
1548.156 Million cell updates/sec

Title: US-10-791-666-1

Perfect score: 6165
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Scoring table: IDENTITY NUC
Gapop 10'-0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6165	100.0	6165	US-10-028-946-1	Sequence 1, Appli
2	5837	94.7	5877	US-10-028-946-3	Sequence 3, Appli
3	1398.2	22.7	1515	US-09-804-471A-1	Sequence 1, Appli
4	1398.2	22.7	1515	US-10-238-709-1	Sequence 1, Appli
5	958.8	15.6	2162	US-09-774-528-419	Sequence 419, App
6	756.4	12.3	1133	US-09-916-204-1	Sequence 1, Appli
7	756.4	12.3	1133	US-10-282-048-1	Sequence 1, Appli
8	258	4.2	2358	US-09-016-434-513	Sequence 513, App
9	233	3.8	2423	US-09-949-016-2640	Sequence 2640, Ap
10	227.2	3.7	2726	US-08-422-699A-12	Sequence 12, Appli
11	227.2	3.7	2726	US-08-422-706B-12	Sequence 12, Appli
12	220.4	3.6	2511	US-08-422-699A-8	Sequence 8, Appli
13	220.4	3.6	2511	US-08-422-706B-8	Sequence 8, Appli
14	220	3.6	3182	US-08-484-044-11	Sequence 11, Appli
15	205	3.3	174493	US-09-804-471A-3	Sequence 3, Appli
16	205	3.3	174493	US-10-238-709-3	Sequence 3, Appli
17	195.6	3.2	2706	US-08-630-832A-61	Sequence 61, Appli
18	195.6	3.2	2706	US-09-005-069-61	Sequence 61, Appli
19	195.6	3.2	2706	US-09-171-156A-20	Sequence 20, Appli
20	195.6	3.2	2706	US-09-004-730A-20	Sequence 20, Appli
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22	186	3.0	4363	US-08-685-576-5	Sequence 5, Appli
23	184.4	3.0	4848	US-09-976-594-295	Sequence 295, App
24	178.8	2.9	48763	US-09-916-204-3	Sequence 3, Appli
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36	125.4	2.0	1961	3	US-09-509-902A-15	Sequence 15, Appli
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38	121	2.0	3018	2	US-08-860-150-6	Sequence 6, Appli
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40	114.6	1.9	1935	2	US-08-878-989-11	Sequence 11, Appli
41	114.6	1.9	1935	3	US-09-272-796-11	Sequence 11, Appli
42	113	1.8	3213	3	US-09-442-100-5	Sequence 5, Appli
43	113	1.8	3213	4	US-08-939-106-5	Sequence 5, Appli
44	113	1.8	3213	4	US-09-442-102-5	Sequence 5, Appli
45	110.4	1.8	1251	4	US-09-248-796A-4400	Sequence 4400, Ap

ALIGNMENTS

RESULT 1
US-10-028-946-1
Sequence 1, Application US/10028946
Patent No. 6734009
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Fridlie, Carl Johan
TITLE OF INVENTION: No. 6734009e1 Human Kinases and Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6165
TYPE: DNA
ORGANISM: homo sapiens
US-10-028-946-1

Query Match 100.0%; Score 6165; DB 4; Length 6165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-10-946-3
; Sequence 3, Application US/10028946
; Patent No. 673409
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanhuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fiddie, Carl Johan
; TITLE OF INVENTION: No. 673409el Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028, 946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258, 335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-946-3

Query Match 94.7%; Score 5837; DB 4; Length 5877;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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3001 GACAAGCTGTAATCTCAACCAACCAAAATTTCTACTTGTCCAAACAACCTGCATGAGGCTTCT 3060
3001 GACAAGCTGTAATCTCAACCAACCAAAATTTCTACTTGTCCAAACAACCTGCATGAGGCTTCT 3060
3061 GGGCCCAACGACGAGATTGTACAACCTGCAAGTGAAGTGAACCATCTCGGCGGGAGATC 3120
3061 GGGCCCAACGACGAGATTGTACAACCTGCAAGTGAAGTGAACCATCTCGGCGGGAGATC 3120
3061 GGGCCCAACGACGAGATTGTACAACCTGCAAGTGAAGTGAACCATCTCGGCGGGAGATC 3120
3121 ACGGAAACGAGAGATGACGCTTACCAAGCAGAGCAAAACGATGAGGCTTGAAGACCAAG 3180
3121 ACGGAAACGAGAGATGACGCTTACCAAGCAGAGCAAAACGATGAGGCTTGAAGACCAAG 3180
3121 ACGGAAACGAGAGATGACGCTTACCAAGCAGAGCAAAACGATGAGGCTTGAAGACCAAG 3180
3181 TGCACCATGCTGGAGAAACAGGTCATGATTTGAGAGCCCTTAAACGATGAGCTGTAGAA 3240
3181 TGCACCATGCTGGAGAAACAGGTCATGATTTGAGAGCCCTTAAACGATGAGCTGTAGAA 3240
3181 TGCACCATGCTGGAGAAACAGGTCATGATTTGAGAGCCCTTAAACGATGAGCTGTAGAA 3240
3241 AAAGACGCGACAGTGGAGGCTGTGAGAGGCTCTGGGTGATGAGAAATCCAGTTTGAAG 3300
3241 AAAGACGCGACAGTGGAGGCTGTGAGAGGCTCTGGGTGATGAGAAATCCAGTTTGAAG 3300
3241 AAAGACGCGACAGTGGAGGCTGTGAGAGGCTCTGGGTGATGAGAAATCCAGTTTGAAG 3300
3301 TGTGGGTTTGAAGAGTGCAGAGATGCTGACACCGAAGAACAGACAGAGGCGAGAGCC 3360
3301 TGTGGGTTTGAAGAGTGCAGAGATGCTGACACCGAAGAACAGACAGAGGCGAGAGCC 3360
3301 TGTGGGTTTGAAGAGTGCAGAGATGCTGACACCGAAGAACAGACAGAGGCGAGAGCC 3360
3361 GATCAGCGGATCACCCAGTCTCGCCAGGTGTGAGACTGACAGTGAAGAGCAAGAGCT 3420
3361 GATCAGCGGATCACCCAGTCTCGCCAGGTGTGAGACTGACAGTGAAGAGCAAGAGCT 3420
3421 GAGATTCTGCTCTGAGAGAGGCTCTCAAGAGCAGAACTGAAGGCCCGAGAGCCCTCTCT 3480
3421 GAGATTCTGCTCTGAGAGAGGCTCTCAAGAGCAGAACTGAAGGCCCGAGAGCCCTCTCT 3480
3421 GAGATTCTGCTCTGAGAGAGGCTCTCAAGAGCAGAACTGAAGGCCCGAGAGCCCTCTCT 3480
3481 GACAAGCTCAATGACTCTGAGAGAAAGACATGCTATCTTGAATGAATCCCGAGACTTA 3540
3481 GACAAGCTCAATGACTCTGAGAGAAAGACATGCTATCTTGAATGAATCCCGAGACTTA 3540
3481 GACAAGCTCAATGACTCTGAGAGAAAGACATGCTATCTTGAATGAATCCCGAGACTTA 3540
3541 CAGCAGAAAGCTGAGACTGAACAGAGCTCAAAACAGAGGCTTCTGGAAAGAGCAAGCAAA 3600
3541 CAGCAGAAAGCTGAGACTGAACAGAGCTCAAAACAGAGGCTTCTGGAAAGAGCAAGCAAA 3600
3601 TTACAGCAGCAGATGAGCTTGCAGAAATTCATTTTCCGTCTGATCTCAAGACTGCA 3660
3601 TTACAGCAGCAGATGAGCTTGCAGAAATTCATTTTCCGTCTGATCTCAAGACTGCA 3660

3601 TTACAGCAGCAGATGAGCTTGCAGAAATTCATTTTCCGTCTGATCTCAAGACTGCA 3660
3661 GAAGCTCTAGATCGGCTGATCTTACTGAGACAGAAAGAGTGAATCTGAGATCAAGCTG 3720
3661 GAAGCTCTAGATCGGCTGATCTTACTGAGACAGAAAGAGTGAATCTGAGATCAAGCTG 3720
3721 GAAAACATTCAAGTTCTCTATTCTCATGAAAGGTGAAAATGGAAGCATTATTTCTCAA 3780
3721 GAAAACATTCAAGTTCTCTATTCTCATGAAAGGTGAAAATGGAAGCATTATTTCTCAA 3780
3781 CAAACCAATCTCATTTGATTTTCTGCAAGCCCAAAATGGAACCACTGCTAAAAAGAAAG 3840
3781 CAAACCAATCTCATTTGATTTTCTGCAAGCCCAAAATGGAACCACTGCTAAAAAGAAAG 3840
3841 GTTCTCTGAGTACATGAGCTGAAGCTGGCCCTGGAGAGAGAAAGCTCGCTGTGCA 3900
3841 GTTCTCTGAGTACATGAGCTGAAGCTGGCCCTGGAGAGAGAAAGCTCGCTGTGCA 3900
3901 GAGCTGAGGAGAGCCCTTCAAGAAACCCGATGAGCTCCGTTCCGCGGAGAGAAAGCT 3960
3901 GAGCTGAGGAGAGCCCTTCAAGAAACCCGATGAGCTCCGTTCCGCGGAGAGAAAGCT 3960
3901 GAGCTGAGGAGAGCCCTTCAAGAAACCCGATGAGCTCCGTTCCGCGGAGAGAAAGCT 3960
3961 GCCCACCAGAAACCAACGACCAACCCATCCACACGCAAGCCAGCCAGCCGAGAGAGAG 4020
3961 GCCCACCAGAAACCAACGACCAACCCATCCACACGCAAGCCAGCCAGCCGAGAGAGAG 4020
4021 ATGCGCATGCTCCGCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 4080
4021 ATGCGCATGCTCCGCACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 4080
4081 GCGCCGCAATCCAGCCGCAAGAAAGAGTCTTCAACTCCAGAGAAATTTAGTCGGCTCTT 4140
4081 GCGCCGCAATCCAGCCGCAAGAAAGAGTCTTCAACTCCAGAGAAATTTAGTCGGCTCTT 4140
4141 AAGGAACGATGACCAACCAATTTCTCAACCAATTAAGTGAAGTGAACATGCGAGCC 4200
4141 AAGGAACGATGACCAACCAATTTCTCAACCAATTAAGTGAAGTGAACATGCGAGCC 4200
4201 ACAAGTGTCTGTGTCTGTGATACCTGTCATCTTGAACGCGCAGCATCTCAATGTCTC 4260
4201 ACAAGT 4260
4201 ACAAGT 4260
4261 GAATGTCAAGTATGTGTCAACCCCAAGTCTCAAGTCTTGCACGACCTTGCAGGCTTG 4320
4261 GAATGTCAAGTATGTGTCAACCCCAAGTCTCAAGTCTTGCACGACCTTGCAGGCTTG 4320
4261 GAATGTCAAGTATGTGTCAACCCCAAGTCTCAAGTCTTGCACGACCTTGCAGGCTTG 4320
4321 CCGTGTGAATATGCAACACTTCAACGAGGCTTCTGCGGTGACAAATGAAATCTCCCA 4380
4321 CCGTGTGAATATGCAACACTTCAACGAGGCTTCTGCGGTGACAAATGAAATCTCCCA 4380
4321 CCGTGTGAATATGCAACACTTCAACGAGGCTTCTGCGGTGACAAATGAAATCTCCCA 4380
4381 GGTCTTCAGACCAAGAGCCCGACAGAGCTTGCACCTTGAAGAGGTGATGAAGTGC 4440
4381 GGTCTTCAGACCAAGAGCCCGACAGAGCTTGCACCTTGAAGAGGTGATGAAGTGC 4440
4381 GGTCTTCAGACCAAGAGCCCGACAGAGCTTGCACCTTGAAGAGGTGATGAAGTGC 4440
4441 AAGAAATTAACAAACGAGACAGAGAGCTGGAGCAGAAAGTACATTTGCTGGAGGATCA 4500
4441 AAGAAATTAACAAACGAGACAGAGAGCTGGAGCAGAAAGTACATTTGCTGGAGGATCA 4500
4441 AAGAAATTAACAAACGAGACAGAGAGCTGGAGCAGAAAGTACATTTGCTGGAGGATCA 4500
4501 AAGATCTCATTTTATGACAAATGAACCAAGAGCTTGAACAGAGCCGATGAAATTTT 4560
4501 AAGATCTCATTTTATGACAAATGAACCAAGAGCTTGAACAGAGCCGATGAAATTTT 4560
4561 GAGCTGTGCTTCCGAGCGGAGATGATCTATCTATGATGATGATGATGATGATGATGATG 4620
4561 GAGCTGTGCTTCCGAGCGGAGATGATCTATCTATGATGATGATGATGATGATGATGATG 4620
4621 GAAATTAACAGCCAAAGAGATGCTCCATATCACTGAAAGATGAAATTCACCCGACACC 4680
4621 GAAATTAACAGCCAAAGAGATGCTCCATATCACTGAAAGATGAAATTCACCCGACACC 4680
4621 GAAATTAACAGCCAAAGAGATGCTCCATATCACTGAAAGATGAAATTCACCCGACACC 4680
4681 AACTGTGTGCTGCGGAGAAACCTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4740
4681 AACTGTGTGCTGCGGAGAAACCTTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4740

QY 4741 TGGGTACCCCTTAGAATAGTTGTGCAAGTGGAGAGTTTCTAGGGAAAAAGCAGAA 4800
DB 4741 TGGGTACCCCTTAGAATAGTTGTGCAAGTGGAGAGTTTCTAGGGAAAAAGCAGAA 4800
QY 4801 GCTGATGCTAACTGCTTGGAAAACCTCCCTCTGAAAACCTGGAAGGTGATGACCCCTAGAC 4860
DB 4801 GCTGATGCTAACTGCTTGGAAAACCTCCCTCTGAAAACCTGGAAGGTGATGACCCCTAGAC 4860
QY 4861 ATGAATGCAAGCTGCTTCAAGTACCAAGTGGTGGTGGGCAACGAGAAAGGCTC 4920
DB 4861 ATGAATGCAAGCTGCTTCAAGTACCAAGTGGTGGTGGGCAACGAGAAAGGCTC 4920
QY 4921 TACGCTGTAATGCTTGAAGAACTCCCTAACCCATGCTCCAGAAATGGAAGCTTTC 4980
DB 4921 TACGCTGTAATGCTTGAAGAACTCCCTAACCCATGCTCCAGAAATGGAAGCTTTC 4980
QY 4981 CAAATTTATTTATCAAGAGACTGGAGAGACTACTGATAGAGAGAGAGAGGAGCA 5040
DB 4981 CAAATTTATTTATTTCAAGAGACTGGAGAGACTACTGATAGAGAGAGAGAGGAGCA 5040
QY 5041 CTGTGCTTGTGAGCTGAGAGAAAGTGAACAGTCCCTGGCCAGTCCCACTGCTGCC 5100
DB 5041 CTGTGCTTGTGAGCTGAGAGAAAGTGAACAGTCCCTGGCCAGTCCCACTGCTGCC 5100
QY 5101 CAGCCGCAATCTCACCACCAATTTTGAAGCTGTCAAGGCTGCACTTGTGTTGGGCA 5160
DB 5101 CAGCCGCAATCTCACCACCAATTTTGAAGCTGTCAAGGCTGCACTTGTGTTGGGCA 5160
QY 5161 GCGAAGATTGAGAAAGGCTGCTGATCTGTGACAGCTGCTCCAGCAAAAGTGTCTTC 5220
DB 5161 GCGAAGATTGAGAAAGGCTGCTGATCTGTGACAGCTGCTCCAGCAAAAGTGTCTTC 5220
QY 5221 CGCTACAGAGAAACCTCAGAAATATCTGATCCGGAAGAGATAGAGACTCAGAGCCC 5280
DB 5221 CGCTACAGAGAAACCTCAGAAATATCTGATCCGGAAGAGATAGAGACTCAGAGCCC 5280
QY 5281 TGGAGCTGATTCACATTCACCAATTAAGTATCTCAATGGAACCAATTAATTTACGAA 5340
DB 5281 TGGAGCTGATTCACATTCACCAATTAAGTATCTCAATGGAACCAATTAATTTACGAA 5340
QY 5341 ATGACATGTAAGAGTACAGCTGCTGAGAAATCTGATGAAGTACATTTCTTGGCA 5400
DB 5341 ATGACATGTAAGAGTACAGCTGCTGAGAAATCTGATGAAGTACATTTCTTGGCA 5400
QY 5401 CCGCTGTGTTTGGCGCTCTTCCACAGCTTCCCTGCTCAATCGAGCTGAGAGAGC 5460
DB 5401 CCGCTGTGTTTGGCGCTCTTCCACAGCTTCCCTGCTCAATCGAGCTGAGAGAGC 5460
QY 5461 GCAAGGAGAGAGAGAGTACTGCTGTGTTTCCAGAAATTTGAGTGTCTGATTTCT 5520
DB 5461 GCAAGGAGAGAGAGAGTACTGCTGTGTTTCCAGAAATTTGAGTGTCTGATTTCT 5520
QY 5521 TACGGAAGAGTACCGCAGACGATCTCAAGTGAAGTGCCTTACCTTTGGCTTTGCC 5580
DB 5521 TACGGAAGAGTACCGCAGACGATCTCAAGTGAAGTGCCTTACCTTTGGCTTTGCC 5580
QY 5581 TACGAGAAACCTTATCTGTTTGTGACCACTTCAATCACTCGAAGTAAATGAGATCCAG 5640
DB 5581 TACGAGAAACCTTATCTGTTTGTGACCACTTCAATCACTCGAAGTAAATGAGATCCAG 5640
QY 5641 GCAAGCTCTCAG 5700
DB 5641 GCAAGCTCTCAG 5700
QY 5701 CTGGGCTCTGCAATTTCTCAGAGAGAGATTTACTTGGCTGCTCATACAGATTAATTA 5760
DB 5701 CTGGGCTCTGCAATTTCTCAGAGAGAGATTTACTTGGCTGCTCATACAGATTAATTA 5760
QY 5761 AGGTTCAATTTGCTCAAG 5820
DB 5761 AGGTTCAATTTGCTCAAG 5820

QY 5821 CCGTCCACCTCCGAG 5837
DB 5821 CCGTCCACCTCCGAG 5837

RESULT 3
US-09-804-471A-1
; Sequence 1, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ. ID NOS.: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO. 1
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Human
US-09-804-471A-1

Query Match 22.7%; Score 1398.2; DB 4; Length 1515;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTGAAGTTCAAATATGAGAGCGCGAATCTTTGATGCTGTGCTGTAACCAT 60
DB 7 ATGTGAAGTTCAAATATGAGAGCGCGAATCTTTGATGCTGTGCTGTAACCAT 66
QY 61 GCCAGCGGCGCTCCAGGCTGTAATCTGTCTTCCAGAGGAGAAACCACTTATGACTCA 120
DB 67 GCCAGCGGCGCTCCAGGCTGTAATCTGTCTTCCAGAGGAGAAACCACTTATGACTCA 126
QY 121 CAGAGATGCTCTCTCTTCCGAGAGAGATTTAGATCCCTCTTGTCTTTGAA 180
DB 127 CAGAGATGCTCTCTCTTCCGAGAGAGATTTAGATCCCTCTTGTCTTTGAA 186
QY 181 GAATGCACTGAGCTGCTGATGAGATTAAGCACTGAGCACTTGTCCGAGATAT 240
DB 187 GAATGCACTGAGCTGCTGATGAGATTAAGCACTGAGCACTTGTCCGAGATAT 246
QY 241 TCCGACACATAGCTGATTAAGAGAGCTCAGGCTCCGCAAGAGACTTGAAGTCA 300
DB 247 TCCGACACATAGCTGATTAAGAGAGCTCAGGCTCCGCAAGAGACTTGAAGTCA 306
QY 301 AGCTTGTAGTGTGCTCACTTGTGCTGAAGTGCAGGTGGTAAAGAGAAACCGGG 360
DB 307 AGCTTGTAGTGTGCTCACTTGTGCTGAAGTGCAGGTGGTAAAGAGAAACCGGG 366
QY 361 GACATCTATCTATGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 367 GACATCTATCTATGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 426
QY 421 TTTTGAAG 480
DB 427 TTTTGAAG 486
QY 481 CAGTATGCTTTCAG 540
DB 487 CAGTATGCTTTCAG 546
QY 541 GACTTGTGCTCACTTTGAATTAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 547 GACTTGTGCTCACTTTGAATTAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 606
QY 601 TACTTACTGAGCTGATTTTGGCTGCTCAGAGGTTGATGAGAGAGATAGTGCATGCA 660
DB 607 TACTTACTGAGCTGATTTTGGCTGCTCAGAGGTTGATGAGAGAGATAGTGCATGCA 666

QY 661 GACATCAAGCCTGAGAACTTCTGTTGACCGGACAGGACACATCAAGTCGTGATTTT 720
 Db 667 GACATCAAGCCTGAGAACTTCTGTTGACCGGACAGGACACATCAAGTCGTGATTTT 726
 QY 721 GGAATCTGCGGAAATGAAATTCACACAGATGCTGATGCAAACTCCGATGGAGAC 780
 Db 727 GGAATCTGCGGAAATGAAATTCACACAGATGCTGATGCAAACTCCGATGGAGAC 786
 QY 781 CCAGATTACATGCTGCTGAAAGTCTGATGATGAAACGGGGATGGAAGGACCTTAC 840
 Db 787 CCAGATTACATGCTGCTGAAAGTCTGATGATGAAACGGGGATGGAAGGACCTTAC 846
 QY 841 GGCGCTGACCTGATCTGAGTGTGATGAGGCGGTGATGCTATGATGATTTATGGGAGA 900
 Db 847 GGCGCTGACCTGATCTGAGTGTGATGAGGCGGTGATGCTATGATGATTTATGGGAGA 906
 QY 901 TCCCGCTTCCGAGAGGGAACCTTGCCAGAACCTTCAATTAATTAATTAATTAATTAAT 966
 Db 907 TCCCGCTTCCGAGAGGGAACCTTGCCAGAACCTTCAATTAATTAATTAATTAATTAAT 966
 QY 961 TTTTGGAAATTTTCCAGATGACCCCAAGTGAAGTGAATTTCTTGAATTCGAAAGC 1020
 Db 967 TTTTGGAAATTTTCCAGATGACCCCAAGTGAAGTGAATTTCTTGAATTCGAAAGC 1026
 QY 1021 TTGTTGGGCGGCGAGAAAGAGAGCTGAAGTTGAAGTCTTGGCGCATCCCTTCTTC 1080
 Db 1027 TTGTTGGGCGGCGAGAAAGAGAGCTGAAGTTGAAGTCTTGGCGCATCCCTTCTTC 1086
 QY 1081 TCTAAATTTGACTGGAACCAATTCGTAACTCTCTCCCTCCCTCCCTCCCTCCCTCCAG 1140
 Db 1087 TCTAAATTTGACTGGAACCAATTCGTAACTCTCTCCCTCCCTCCCTCCCTCCCTCCAG 1146
 QY 1141 TCTGAAGATGACCTTCCATTTTGAATGAACAGAGAAAGATTCGTGGTTTCAATCTCT 1200
 Db 1147 TCTGAAGATGACCTTCCATTTTGAATGAACAGAGAAAGATTCGTGGTTTCAATCTCT 1206
 QY 1201 CCGTGCAGCTGAGCCCTCAGGCTCTCGGGTGAAGAACTGCGTTTGGGGTTTTCG 1260
 Db 1207 CCGTGCAGCTGAGCCCTCAGGCTCTCGGGTGAAGAACTGCGTTTGGGGTTTTCG 1266
 QY 1261 TACAGCAAGGCACTGGGGATTTCTGTGATGATCTGAGTCTGTGTGTGCGGCTGCACTCC 1320
 Db 1267 TACAGCAAGGCACTGGGGATTTCTGTGATGATCTGAGTCTGTGTGTGCGGCTGCACTCC 1326
 QY 1321 CCTGCCAAGACTGCTTCATGAAAGAACTTCTCATCAAAAGCAAGAGCTTACAAGAC 1380
 Db 1327 CCTGCCAAGACTGCTTCATGAAAGAACTTCTCATCAAAAGCAAGAGCTTACAAGAC 1386
 QY 1381 TCTCAGGACAGGTGTCACAAAGAT 1403
 Db 1387 TCTCAGGACAGGTGTCACAAAGAT 1409

RESULT 4
 US-10-238-709-1
 ; Sequence 1, Application US/10238709
 ; Patent No. 6680188
 ; GENERAL INFORMATION:
 ; APPLICANT: WEBSTER, Marion et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: CL001164DIV
 ; CURRENT APPLICATION NUMBER: US/10/238, 709
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1515
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-238-709-1

Query Match 22.7%; Score 1398.2; DB 4; Length 1515;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1400; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ATGTGAAGTTCAAAATATGAGAGCGGAAATCTTTGGAATGCTGTGCTGGAACCAT 60
 Db 7 ATGTGAAGTTCAAAATATGAGAGCGGAAATCTTTGGAATGCTGTGCTGGAACCAT 66
 QY 61 GCCAGCGGCGCTCCAGGCTGAAATCTGTTCTTCAAGGGAACCACTTTATGACTCAA 120
 Db 67 GCCAGCGGCGCTCCAGGCTGAAATCTGTTCTTCAAGGGAACCACTTTATGACTCAA 126
 QY 121 CACGAGATGCTGCTCTTTCCCGAAGAGGATATTAATGATCCCTCTTGTCTTTGAA 180
 Db 127 CACGAGATGCTGCTCTTTCCCGAAGAGGATATTAATGATCCCTCTTGTCTTTGAA 186
 QY 181 GAATGACATGACGCTGCTGATGAAGATTAAGACGTAAGCACTTTGTCGGGAAGTAT 240
 Db 187 GAATGACATGACGCTGCTGATGAAGATTAAGACGTAAGCACTTTGTCGGGAAGTAT 246
 QY 241 TCCGACACCATAGCTGATGATTAAGAGCTTCAGGCTTCCGCAAGGACCTTGAAGTCA 300
 Db 247 TCCGACACCATAGCTGATGATTAAGAGCTTCAGGCTTCCGCAAGGACCTTGAAGTCA 306
 QY 301 AGCTTGTAGTGTGTGTGCTCACTTGTGATGATGATGATGATGATGATGATGATGAT 360
 Db 307 AGCTTGTAGTGTGTGTGCTCACTTGTGATGATGATGATGATGATGATGATGATGAT 366
 QY 361 GACATCTAATGCTAATGAAGATGAAGAAAGGCTTTATTTGGCCGAGAGGAGTTTCA 420
 Db 367 GACATCTAATGCTAATGAAGATGAAGAAAGGCTTTATTTGGCCGAGAGGAGTTTCA 426
 QY 421 TTTTGGAGAAAGCGGAAATATTTATCTGAAAGCAAGCCGTTGATCCCGCAATTA 480
 Db 427 TTTTGGAGAAAGCGGAAATATTTATCTGAAAGCAAGCCGTTGATCCCGCAATTA 486
 QY 481 CAGTATGCTTTTCAGGACAAATATCATCTTTATCTGTGATGATGATGATGATGATGAT 540
 Db 487 CAGTATGCTTTTCAGGACAAATATCATCTTTATCTGTGATGATGATGATGATGATGAT 546
 QY 541 GACTGCTGCTCTTTTGAATGATATGAGACCACTTATGATGAAACCTGATACAGTTT 600
 Db 547 GACTGCTGCTCTTTTGAATGATATGAGACCACTTATGATGAAACCTGATACAGTTT 606
 QY 601 TACCTAGCTGACGCTGATTTTGGCTGTTCAACAGCTTCATCTGATGGATACGTCATCA 660
 Db 607 TACCTAGCTGACGCTGATTTTGGCTGTTCAACAGCTTCATCTGATGGATACGTCATCA 666
 QY 661 GACATCAAGCCTGAGAACATTTCTGTTGACCGGACAGACATCAAGCTGTGATTTT 720
 Db 667 GACATCAAGCCTGAGAACATTTCTGTTGACCGGACAGACATCAAGCTGTGATTTT 726
 QY 721 GGAATCTGCGGAAATGAAATTCACACAGATGCTGATGCAAACTCCGATGGAGAC 780
 Db 727 GGAATCTGCGGAAATGAAATTCACACAGATGCTGATGCAAACTCCGATGGAGAC 786
 QY 781 CCAGATTACATGCTGCTGAAAGTCTGATGATGAAACGGGGATGGAAGGACCTTAC 840
 Db 787 CCAGATTACATGCTGCTGAAAGTCTGATGATGAAACGGGGATGGAAGGACCTTAC 846
 QY 841 GGCGCTGACCTGATCTGAGTGTGATGAGGCGGTGATGCTATGATGATTTATGGGAGA 900
 Db 847 GGCGCTGACCTGATCTGAGTGTGATGAGGCGGTGATGCTATGATGATTTATGGGAGA 906
 QY 901 TCCCGCTTCCGAGAGGGAACCTTGCCAGAACCTTCAATTAATTAATTAATTAATTAAT 960
 Db 907 TCCCGCTTCCGAGAGGGAACCTTGCCAGAACCTTCAATTAATTAATTAATTAATTAAT 966
 QY 961 TTTTGGAAATTTTCCAGATGACCCCAAGTGAAGTGAATTTCTTGAATTCGAAAGC 1020
 Db 967 TTTTGGAAATTTTCCAGATGACCCCAAGTGAAGTGAATTTCTTGAATTCGAAAGC 1026
 QY 1021 TTGTTGGGCGGCGAGAAAGAGAGCTGAAGTTGAAGTCTTGGCGCATCCCTTCTTC 1080

CURRENT APPLICATION NUMBER: US/09/916,204
CURRENT FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1133
TYPE: DNA
ORGANISM: Human
US-09-916-204-1

Query Match 12.3%; Score 756.4; DB 4; Length 1133;
Best Local Similarity 99.9%; Pred. No. 6.3e-188;
Matches 757; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGCTGTAACCAATT 60
DB 54 ATGTGAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGCTGTAACCAATT 113
QY 61 GCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAACACCCCTTATGACTCAA 120
DB 114 GCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAACACCCCTTATGACTCAA 173
QY 121 CACAGATGTCCTCTCTTCCGAGAGGATATTAATGATCCCTCTTGTCTTTGAA 180
DB 174 CACAGATGTCCTCTCTTCCGAGAGGATATTAATGATCCCTCTTGTCTTTGAA 233
QY 181 GAATGAGTACGCTGCTGTAAGATTAAGACCTGAGCACTTTGTCCGAAGTAT 240
DB 234 GAATGAGTACGCTGCTGTAAGATTAAGACCTGAGCACTTTGTCCGAAGTAT 293
QY 241 TCCGACCACTAGCTGATGATGAGAGCTCCAGCTCCGCAAGAGCTCGAAGTCAGA 300
DB 294 TCCGACCACTAGCTGATGATGAGAGCTCCAGCTCCGCAAGAGCTCGAAGTCAGA 353
QY 301 AGTCTTGAGTTGTGCTCACTTTGCTGAAGTCAAGTGTGTAAGAGAGCAACCGGG 360
DB 354 AGTCTTGAGTTGTGCTCACTTTGCTGAAGTCAAGTGTGTAAGAGAGCAACCGGG 413
QY 361 GACATCTATGCTATGAAAGTGAAGAGAGAGCTTTATTTGGCCCAAGAGAGCTTTCA 420
DB 414 GACATCTATGCTATGAAAGTGAAGAGAGAGCTTTATTTGGCCCAAGAGAGCTTTCA 473
QY 421 TTTTGGAG 480
DB 474 TTTTGGAG 533
QY 481 CAGTATGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 534 CAGTATGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 593
QY 541 GACTTGTCTGCTCACTTTTGAATGATATGAGAGCAAGTATGATGATGATGATGAT 600
DB 594 GACTTGTCTGCTCACTTTTGAATGATATGAGAGCAAGTATGATGATGATGATGAT 653
QY 601 TACCTAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 654 TACCTAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713
QY 661 GACATCAAGCTGAG 720
DB 714 GACATCAAGCTGAG 773
QY 721 GGATCTGCCGCGAGAAATGAATTCAAACAGATGTGAA 758
DB 774 GGATCTGCCGCGAGAAATGAATTCAAACAGATGTGAA 811

RESULT 7
US-10-282-048-1
Sequence 1, Application US/10282048
Patent No. 6692948
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
THEREOF
FILE REFERENCE: CL001164CIP-DIV
CURRENT APPLICATION NUMBER: US/10/282,048
CURRENT FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1133
TYPE: DNA
ORGANISM: Human
US-10-282-048-1

Query Match 12.3%; Score 756.4; DB 4; Length 1133;
Best Local Similarity 99.9%; Pred. No. 6.3e-188;
Matches 757; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGTGAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGCTGTAACCAATT 60
DB 54 ATGTGAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGCTGTAACCAATT 113
QY 61 GCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAACACCCCTTATGACTCAA 120
DB 114 GCCAGCGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAACACCCCTTATGACTCAA 173
QY 121 CACAGATGTCCTCTCTTCCGAGAGGATATTAATGATCCCTCTTGTCTTTGAA 180
DB 174 CACAGATGTCCTCTCTTCCGAGAGGATATTAATGATCCCTCTTGTCTTTGAA 233
QY 181 GAATGAGTACGCTGCTGTAAGATTAAGACCTGAGCACTTTGTCCGAAGTAT 240
DB 234 GAATGAGTACGCTGCTGTAAGATTAAGACCTGAGCACTTTGTCCGAAGTAT 293
QY 241 TCCGACCACTAGCTGATGATGAGAGCTCCAGCTCCGCAAGAGCTCGAAGTCAGA 300
DB 294 TCCGACCACTAGCTGATGATGAGAGCTCCAGCTCCGCAAGAGCTCGAAGTCAGA 353
QY 301 AGTCTTGAGTTGTGCTCACTTTGCTGAAGTCAAGTGTGTAAGAGAGCAACCGGG 360
DB 354 AGTCTTGAGTTGTGCTCACTTTGCTGAAGTCAAGTGTGTAAGAGAGCAACCGGG 413
QY 361 GACATCTATGCTATGAAAGTGAAGAGAGAGAGCTTTATTTGGCCCAAGAGAGCTTTCA 420
DB 414 GACATCTATGCTATGAAAGTGAAGAGAGAGAGCTTTATTTGGCCCAAGAGAGCTTTCA 473
QY 421 TTTTGGAG 480
DB 474 TTTTGGAG 533
QY 481 CAGTATGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 534 CAGTATGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 593
QY 541 GACTTGTCTGCTCACTTTTGAATGATATGAGAGCAAGTATGATGATGATGATGAT 600
DB 594 GACTTGTCTGCTCACTTTTGAATGATATGAGAGCAAGTATGATGATGATGATGAT 653
QY 601 TACCTAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 654 TACCTAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713
QY 661 GACATCAAGCTGAG 720
DB 714 GACATCAAGCTGAG 773
QY 721 GGATCTGCCGCGAGAAATGAATTCAAACAGATGTGAA 758
DB 774 GGATCTGCCGCGAGAAATGAATTCAAACAGATGTGAA 811

RESULT 8
US-09-016-434-513

Sequence 513, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 513:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAINON01
CLONE: 2290031
US-09-016-434-513

Query Match 4.2%; Score 258; DB 4; Length 258;

Best Local Similarity 100.0%; Pred. No. 1.8e-57;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5204 GCAAGTCGTCATTCCTCGCTACACGAAACCTCAGCAATATGCTCGGAAAGGA 5263
DB 1 GCAAGTCGTCATTCCTCGCTACACGAAACCTCAGCAATATGCTCGGAAAGGA 60
QY 5264 TAGAGACTCAGAGCCCTGAGCTGATCCACTTCACCAATTAAGTATCTCATTTGGA 5323
DB 61 TAGAGACTCAGAGCCCTGAGCTGATCCACTTCACCAATTAAGTATCTCATTTGGA 120
QY 5324 CCAATTAATTTCTAGCAATGACATGAAGCAGTACAGCTCGAGGAATTTCTGTGATAGA 5383
DB 121 CCAATTAATTTCTAGCAATGACATGAAGCAGTACAGCTCGAGGAATTTCTGTGATAGA 180
QY 5384 ATGACCTTCTTGAGCAGCTGCTGTGTTGGCGCTCTTCAAGAGCTTCCCTGCTCAA 5443
DB 181 ATGACCTTCTTGAGCAGCTGCTGTGTTGGCGCTCTTCAAGAGCTTCCCTGCTCAA 240
QY 5444 TCGTGAGGTGACAGCG 5461
DB 241 TCGTGAGGTGACAGCG 258

RESULT 9
US-09-949-016-2640

Sequence 2640, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2640
LENGTH: 2423
TYPE: DNA
ORGANISM: Human
US-09-949-016-2640

Query Match 3.8%; Score 233; DB 4; Length 2423;
Best Local Similarity 52.4%; Pred. No. 2.6e-50;
Matches 590; Conservative 0; Mismatches 520; Indels 15; Gaps 3;

QY 152 TATTAGATGCCCTTTGTTCTCTTTGAGATGACAGTCCGCTGTGATGAAGATTA 211
DB 1021 TACTGATATATCTATCTGCTTTATATGATGAATCAATATTTCTCATTTGAAAGAGAGA 1080
QY 212 AGCAGTGAGCAACTTTGTCGGAAGTATTCGACACCATAGTGAATGACAGAGCTCC 271
DB 1081 AGAATCTTCGATATCTGATGAATGGCTAAACCATTTACTTTAAAGTGAACAAATGC 1140
QY 272 AGCTTGCGAAGAGACTTGAAGTCAAGCTTGAAGTTGTTGTCATCTTCTGTAAG 331
DB 1141 GATTACATAGAGAGACTTGAATATTAAGTGAATGTCGAGAGCTTTGGGGAGG 1200
QY 332 TGCAGTGTGTAAGAGAAAGCAACGGGGCATCTAGTATGAATGATGAAGAGA 391
DB 1201 TTGCTGTAGTAATCACTAAATGACATTAAGTGTGTCATTAATATTAATTAAT 1260
QY 392 AGCTTTATTTGGCCAGAGAGCTTTCAATTTTGTGAGAGAGCGGAACATTAATCTC 451
DB 1261 GGGAAATGCTGAAGAGCTGAGACAGCATGTTTTGTAAGAGAGATGATTAAGTA 1320
QY 452 GAAGCAGAGCCCTGATCCCAATTAAGTATGCTTTGAGACAAATCACTTT 511
DB 1321 ATGAGACAATTAATGATTAACAACCTTGACATGCTTTCCAGAGATGACAAATTAAT 1380
QY 512 ATCTGTATGATATATACAGCTGAGAGGAGCTTGCTGCTCTTTGAATGATATAGG 571
DB 1381 ACCGTGTATGATATATATGTTGAGAGATTTGCTTACTCTACGCAAAATTTGAAG 1440
QY 572 ACCAGTATGAGAAACCTGATACAGTTTACTAGCTGAGCTGATTTTGCTGTTACA 631
DB 1441 ATGATTTGCTGAGAGATATGCTGATTTTACTTGCTGAGATGATATGACATTAAGT 1500
QY 632 GCGTTATCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
DB 1501 CAGTTATCAGCTACATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
QY 692 GCAAGAGACATCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 751
DB 1561 TGAATGACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
QY 752 TGTGATGACCAATCTCCGATTTGGAGCCCAAGATTAAGTCTGTAAGTGTGATG 811
DB 1621 CGGTTACGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 812 TGATGAACGGGAGTGAAGAAAGCACTTACGGCTGAGCTGATGATGATGATGATGATG 871

Db 1681 CCATGGAAG---ATGGAAGAGAGATATGACCTGATATGATGCTGTGCTTTGGGG 1737
Qy 872 TGATTCCTTATGATGATTTATGAGAGATCCCTTCGACAGAGAACTTCGACGAA 931
Db 1738 TCTGTATGATGAATGCTTTTACGAGAAACCACTTTTATGAGAAATGCTGGTGAGA 1797
Qy 932 CCTTCATTAACATTAATGAAATTTCCAGGCGTTTGAATTTCCAG---ATGACCCCAAG 988
Db 1798 CATACGAAATATCATGAAACCAAGAGAGTTTCAGTTTCCAGCCCAAGTGAAGTGTG 1857
Qy 989 TGACAGTGAAGTCTTTCATGATTCATGAACTTGTGTGCGCAGAAAGAGAGACT-- 1046
Db 1858 TGTGTGAAATGCTAAGAGATCTTATGGAAGCTCATTTGTAGAGAGAAATGAGACTTG 1917
Qy 1047 -----GAAGTTGAAGGTTTGTGCTCCCATCTTCTTCTTCTTAAATGATGGAACA 1099
Db 1918 GTCAAAATGAAATGAAGACTTTTAAAGAACCCCATTTTTCAGTGAATGATGGGATA 1977
Qy 1100 ACATTGTAACCTCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC 1159
Db 1978 ATATTGGAAGTGTGAAGACCTTATATTCAGAAAGTTAGAGCCCAAGATGACATGA 2037
Qy 1160 ATTGTTGAACCAAGAGAAATTCGTGGGTTTCATCTCTCCGTCAGCTGAGCCCT 1219
Db 2038 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2097
Qy 1220 CAGGCTCTCGGCTGAAGAACTCCGCTTTGTGGGCTTTGTGATCA 1264
Db 2098 CTGCAATTTCTGGCCACATCTGCAATTTGTGTTTACATATA 2142

RESULT 10
US-08-422-699A-12
Sequence 12, Application US/08422699A
Patent No. 5955265
GENERAL INFORMATION:
APPLICANT: Brook, J. David
APPLICANT: Housman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Hartley, Helen G.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
City: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/422,699A
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2726 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-422-699A-12

Query Match 3.7%; Score 227.2; DB 2; Length 2726;
Best Local Similarity 54.1%; Pred. No. 9.3e-49;
Matches 535; Conservative 0; Mismatches 438; Indels 15; Gaps 3;

Qy 194 CTGCTGATGAAGATTAGACAGTGAACATTTGTCCGAAATTCGACACATAG 253
Db 243 CCGAAGCTGGCCCGAGCAAGTACGTGGCGGACCTTTCAGTGGGCGAGCCATCGTGG 302
Qy 254 CTGAGTTTACAGAGCTCCAGCCCTTCGCAAGAGCTTCGAAGTCAGAGCTTGTAGTT 313
Db 303 TGAAGCTTAAAGAGGTCCTGACCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 362
Qy 314 GTGCTCATTTGCTGAAGTGCAGGTGTAAAGAGAAAGCAACCGGAGCATCTATGCTA 373
Db 363 GCGGGCGGTTACAGCGAGTACAGCGTGTAGTGAATGAAGAGAGAGAGAGAGAGAGAG 422
Qy 374 TGAAGTGAAGAAAGAGGCTTTATTTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 433
Db 423 TGAAGTCAATGAACAGTGGACATGCTGAAGAGGCGGAGGTGTGCTCCGTGAGG 482
Qy 434 AGCGAACAATATATTCGAAGCAAGCCCGTGTATCCCAATTAAGTATGCTTTC 493
Db 483 AGAGGACGTGTGTGAATGGGACCGGCGGTGATACGACGTGCACTTCGCTTCC 542
Qy 494 AGGCAAAATATCACTTTATCTGTATGATGAATATCAGCCTGAGGAGAGAGAGAGAGAG 553
Db 543 AGATAGAGAACTACCTGTACCTGTATGATGAATATCAGCCTGAGGAGAGAGAGAGAG 602
Qy 554 TTTTGAATGATATGAGACCAAGTATGATGAAGAAACCTGATTAACATTAAGTATGAG 613
Db 603 TGCTGAGCAAGTTTGGGAGCGGATTCGCGCGAGATGCGGCTTCTACCTGGCGAGA 662
Qy 614 TGATTTTGGCTGTTCACACGCTTCATCTGATGAGATGAGATGAGATGAGATGAGATGAG 673
Db 663 TTGTATGCTCATTAAGCTGTGACCGGCTTGTGCTACGTGCAAGAGAGATTAACCCG 722
Qy 674 AGAACAATTCCTGTGACCGCAGAGACATCAAGCTGTGATTTTGTGATCTGCGCGA 733
Db 723 ACAACATCTGCTGAGCGGCTGTGCGGCTGTGCGACATCGGCTGCGACATTCGCTTCA 782
Qy 734 AATGATTTCAACAAAGATGATGATGCAAACTCCCATTTGGAGCCCAAGTATACATG 793
Db 783 AGCTGCGGCGAGATGAGACGCTGCGGTGTGCTGTGCTGTGCGCACCCAGACTACTGT 842
Qy 794 CTCCTGAAGTGTGA---CTGTGATGAAGCGGGAGATGAAAGACCTTACGCTGAGCT 850
Db 843 CCCCCGAGATCTGAGAGCTGTGCGGCTGTGCGGCTGTGCGGAGCAAGCTACCGGAGT 902
Qy 851 GTGACTGTGTGCTAGTGGCGGTGATTTGCTATGAGATGATTTATGAGAGATCCCTTGG 910
Db 903 GTGATCTGTGTGGCGGCTGTGCTGTATGATGATGATTTCTATGAGAGAGAGAGAGAG 962
Qy 911 CAGAGGAACTCTGCGCAAGACTTCAATTAACATTATGATTTCCAGCGGTTTGAAT 970

Qy 1079 TCTTAAATGACGTGAGACAACTGTAATCTCTCCCTGCTTCCACCTCA 1138
Db 1143 TCTTTGGCTGACCTGGATGCTCTCCGGACAGCGTCCCCCTTACACCGGATTTGG 1202
Qy 1139 AGTCTGACGATGACACCTCCAAATTTTGA 1166
Db 1203 AAGGTGCCACCGACATGCAACTTTCGA 1230

RESULT 12

US-08-422-699A-8
Sequence 8, Application US/08422699A
Patent No. 5955265
GENERAL INFORMATION:
APPLICANT: Brook, J. David
APPLICANT: Houseman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Harley, Helen G.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,699A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/422,706
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1746

US-08-422-699A-8

Query Match 3.6%; Score 220.4; DB 2; Length 2511;
Best Local Similarity 54.6%; Pred. No. 5,4e-47;
Matches 512; Conservative 0; Mismatches 411; Indels 15; Gaps 3;

Qy 244 GACACCTAGCTGATGATGACGAGCTTCAGCCTTCGGCAAGGACTTCGAAGTCAAGT 303
Db 43 GCCATCGTGTGAGGCTTAAAGAGTCCGACTGACGAGGAGCAGCTTCGAGATTCGAA 102
Qy 304 CTGTGATGTTGTGTGCTCTTTGCTGAAGTCCAGGCTGTGTAAGAGAAAGCAACCGGGGAC 363
Db 103 GTGATCGACGCGGGGCTTACAGGAGTACCGGTAGTGAAGTGAAGACAGACGAGCAG 162
Qy 364 ATCTATGCTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCAGAGAGAGTTCATTT 423
Db 163 GTGATGCTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCAGAGAGAGTTCATTT 222
Qy 424 TTTGAGGAGAGCGGAAATATTTATCTGAAAGCAAGCCGCTGATCCCAATTAAG 483
Db 223 TTCCGTGAGGAGAGGACGCTGTGTAATGGGACCGGCGTGTGATCAGCAGCTGCAC 282
Qy 484 TATGCTTTGAGGACAAATTCACCTTTATCTGTGATGAAATATACGCTGAGAGGAG 543
Db 283 TTGCTTCCAGGATGAACTATCTGTGATGATGATGATGATGATGATGATGATGATG 342
Qy 544 TTGCTGCTCATTTTGAATGATGATGAGACCAATGATGATGATGATGATGATGATGAT 603
Db 343 CTGCTGACACTGTGATGAGCAAGTTTGGGAGCGGATTCGCGGCAAGATGAGCGCTTCT 402
Qy 604 CTAGCTGAGCTGATTTTGGCTGTTCACAGCTTCATCTGATGATGATGATGATGATG 663
Db 403 CTGCGGAGATGCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 462
Qy 664 ATCAAGCTGAGAACTTCTGTTGACCCGACAGACATCAAGCTGTGTGATTTTGA 723
Db 463 ATCAAGCTGAGAACTTCTGTTGACCCGACAGACATCAAGCTGTGTGATTTTGA 522
Qy 724 TCTGCGGCAAAATGATTTCAAAAGATGATGATGATGATGATGATGATGATGATGAT 783
Db 523 TCTTGGCTCAGCTGCGGCAAGTGAAGCGTGTGATGATGATGATGATGATGATGATG 582
Qy 784 GATTAATGAGCTCTGTA--AGTCTGATGATGATGATGATGATGATGATGATGATG 840
Db 583 GATTAATGAGCTCTGTA--AGTCTGATGATGATGATGATGATGATGATGATGATG 642
Qy 841 GAGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 643 GAGCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 702
Qy 901 TCCCTCTTGCAGAGGAACTCTGCGAGAACTTCAATTAATTAATTAATTAATTAAT 960
Db 703 AGCCCTTCTAGCGGATTTCCACGCGGAGACTTATGGAATGCTCACTCAAGAGAG 762
Qy 961 TTTTGAATTTCCAGATGACCCCAAGTGAAGT--GACTTCTTGTATGATGATTA 1017
Db 763 CACTCTCTCTGCGCTGTGTGAGCAAGGGGTCTGAGAGAGGCTGAGACTTCAATTG 822
Qy 1018 AACTTGTGTGCGGCAAGAAAGAGACTGAAAGTGTGAAGTCTTGTCTGCTC----- 1068
Db 823 CGGTGTGTGTGCTTCCCGGAGACAGCGCTGGGCGGGGTGAGAGCGCACTTCCGAG 882
Qy 1069 CATCTCTTCTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1128
Db 883 CATCTCTTCTTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 942
Qy 1129 CCGACCTTCAAGTGTGAGGATGACCTTCAATTTTGA 1166
Db 943 CCGATTTTCAAGTGTGAGGATGACCTTCAATTTTGA 980

RESULT 13
US-08-422-706B-8

Sequence 8, Application US/08422706B
Patent No. 597733
GENERAL INFORMATION:
APPLICANT: Brook, J. David
APPLICANT: Houman, David E.
APPLICANT: Shaw, Duncan J.
APPLICANT: Hatley, Helen G.
APPLICANT: Johnson, Keith J.
TITLE OF INVENTION: DNA SEQUENCE ENCODING THE MYOTONIC
TITLE OF INVENTION: DYSTROPHY GENE AND USES THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: US
ZIP: 02713
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,706B
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,543
FILING DATE: 08-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/023,612
FILING DATE: 26-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/839,255
FILING DATE: 20-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01545
FILING DATE: 19-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00253
FILING DATE: 05-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB9202485.0
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-5830A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1746
US-08-422-706B-8

Query Match 3.6%; Score 220.4; DB 2; Length 2511;
Best Local Similarity 54.6%; Pred. No. 5.4e-47;
Matches 512; Conservative 0; Mismatches 411; Indels 15; Gaps 3;

244 GACACATAGCTGAGTTACAGAGCTCAGGCTTCGGCAAGCACTTCGAGTCAAGT 303
43 GCCATCTGTGTGAGGCTTAAGAGAGTCCGACTGCAGAGGAGCGACTTCGATTTCTGAG 102
304 CTTGTAGTTGTGTCACTTTGTCTGAAGTGCAGGTGTGTAAAGAGAAAGCAACCGGGGAC 363

103 GTGATCGAAGCGGGGGCTTCAGGAGTACGGCTAATGAAGATGAAGACAGCGGGCAG 162
364 ATCTATGCTATGAAGATGAAGAGAGAGCTTTATTTGGCCAGAGCAAGTTCAATT 423
163 GTGATGCCATGAAGATCAAGACATGAGGACATGCTGAAGAGGGGCGAGTCTCGC 222
424 TTGAGAGAGCGGAACATATTATCTCGAAGACAGAACCCGTGATCCCAATTACG 483
223 TTCCGTGAGAGAGGAGCGTGTGTGTAATGGGGACCGGGCGTGTGATACCGACCTGCAC 282
484 TATGCCCTTTGAGAGCAAAATACCTTATCTGTGATGAAATATACGCTGAGGGGAC 543
283 TTGGCTTTGAGAGTGAACCTACTGTACTGTGTCAATGATATACGTGGGCGGGAC 342
544 TTGCTGTCACTTTGAATATGATATGAGACCAAGTTAATGAAAACCTGATACAGTTTAC 603
343 CTGCTGACATCTGCTGACACAGTTTGGGGAGCGGATTCGGCCGAGATGGCGGCTTCTAC 402
604 CTAGCTGAGCTGATTTTGGCTGTTACAGCGGTTCACTGATGAGATACGTGATCAGAC 663
403 CTGGCGGAGATTGTCATGCGCATATGACTCGGTGACCGGCTTGCTACGTGACAGAGGAC 462
664 ATCAAGCTGAGAACTTCTGCTGTGACCGCAGAGACATCAAGCTGTGAGATTTTGA 723
463 ATCAAGCGGACCAATCTGCTGTGACCGGCTGTGACCAATCCGCTGGCCGACTTGGC 522
724 TCTGCGCGGAAATGAATTCMAACAGATGATGATCCAAATCCGATTTGGAGCCCA 783
523 TCTTGCTCAAGCTGCGGGGAGATGAGACGGTGGGCTGCTGTGCTGTGGGACACCCCA 582
784 GATTACATGAGCTCTCTGA--AGTGTGACTGTGTATGAGACGGGAGTGAAGAGGACCTTAC 840
583 GACTACCTGTCCCGGAGATCTGTGACAGGCTGTGGCGGTGGGCTTGGGACAGGACTAC 642
841 GGCTGAGCTGTACTGTGTGTGATGAGTGGGCTGATTTGCTATGAGATTTATGGAGA 900
643 GGGGCCAGGTGTGCTGTGGGCGCTGTGTGTATTCCTATGAAATGTTCTATGGGCGAG 702
901 TCCGCTTGGCAGAGGAGCACTGTGCGAGAACCTTCAATATGATTAATTTTCACGCG 960
703 AGGCTTCTTACGCGGATTCACGCGGAGACCTATGAGCAAGATCTGCTACATCAAGAG 762
961 TTTTGAATTTCCAGATGACCCCAAGTGAAGT--GACTTCTTGATCTGATTCAA 1017
763 CACCTCTCTGCGCGTGTGAGACGAGGGGTCCCTGAGAGGCTCGAGACTTATTCAG 822
1018 AGCTTGTGTGCGGCGCAAGAGAGACTGAATTGAAGTCTTTGCTG----- 1068
823 CGGTGTGTGTCTCCCGGAGACACGGCTGTGGCCGGGTGAGAGCGGCACTTCGAGACA 882
1069 CATCCTTCTTCTTAATTAATGACTGGAACAATGTAATCTCTCCCTCCCTGCTT 1128
883 CATCCTTCTTCTTGTGCTGACTGAGATGTCTCCGGGACAGCGTGGCCCCCTTAC 942
1129 CCCACCTCAAGTCTGAGATGACACCTCCCAATTTGA 1166
943 CCGGATTTGAGAGTGCACCGACATGCACTTGA 980

RESULT 14
US-08-484-044-11
Sequence 11, Application US/08484044
Patent No. 5552282
GENERAL INFORMATION:
APPLICANT: Caskey, C. T.
APPLICANT: Fu, Ying-Hui
APPLICANT: Friedman, David L.
APPLICANT: Pizutti, Antonio
APPLICANT: Fenwick, Raymond G.
TITLE OF INVENTION: Diagnosis of Myotonic Muscular Dystrophy
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: U.S.A.
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,044
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/019,940
FILING DATE: 19-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5443
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5325
TELEFAX: 713/651-5246
TELEX: 762829
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-044-11

Query Match 3.6%; Score 220; DB 1; Length 3182;
Best Local Similarity 54.6%; Pred. No. 7.9e-47;

Matches 511; Conservative 0; Mismatches 410; Indels 15; Gaps 3;

QY 246 CACCATAGCTGAGTTACAGAGCTCCAGCTTCGGCAAGAACTTCAGATCAGAACTCT 305
DB 743 CATCGTGTAGAGCTTAAGAGGTCGACCTGCAGAGAGGAGCACTTCAGATTCTGAAGT 802
QY 306 TGTAGTTGTGTCATCTTCTGTAAGTGCAGGTGTGAAGAGAAACCAACCGGGGACAT 365
DB 803 GATCGGACGGGGCGCTTCAGCCAGGTAGCGGTAGTGAATGAAGACGAGCGGCGACGT 862
QY 366 CTATGCTATGAAGTGTGAAGAAAGGCTTATTGGCCAGAGAGAGTTTCATTTT 425
DB 863 GTATGCTATGAATCATGTGAACAAGTGGACATGCTGAAGAGGCGGAGGTGTCTGCTT 922
QY 426 TGAGGAAGACGGGAACATATTATCTCGAAGCACAAAGCCCTGTGATCCCAATTAACGTA 485
DB 923 CCGTGAAGAGGAGCGTGTGTGTAATGGGACCGGCGGTGATACAGAGCTGCATT 982
QY 486 TGGCTTTGAGCAAAATATCACTTTATCTGTCATGTAATATCACTGAGAGGACCTT 545
DB 983 CGCTTCAGAGAGAACTTACCTGTACCTGTGTCATGTAGTATTACGTGGCGGGACCT 1042
QY 546 GCTGTCACTTTGAATVAGATATGAGACCAAGTATGAAAACTGATACGTTTAACT 605
DB 1043 GCTGACACTGTGAGCAAGTTTGGGAGCGGATTCGGGCGGAATGACGGCTTCTAAGT 1102
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DB 1103 GGGGAGGATTTGTCATGTGCAATAGACTCGGTGACCGGCTTGGTTAGCTGACAGGAGCAT 1162
QY 666 CAAGCTGAGAACTTCTGTTGACCGCAAGAGACATCAAGCTGTGATTTTGATC 725
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DB 1643 GAATTCGAAGTGTGCCACGACACATGCAACTTGA 1678

RESULT 15
US-09-804-471A-3
; Sequence 3, Application US/09804471A
; Patent No. 6479269

; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 174493
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(174493)
; OTHER INFORMATION: n = A, T, C or G
US-09-804-471A-3

Query Match 3.3%; Score 205; DB 4; Length 174493;
Best Local Similarity 100.0%; Pred. No. 7.6e-42;

Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Wed May 18 09:47:51 2005

us-10-791-666-1.rn1

Page 17

Db 130469 CTTCAATPACATTATGAAATTTCCAG 130493

Search completed: May 16, 2005, 18:37:09
Job time : 660 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2005, 15:06:39 / Search time 2152 Seconds
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Perfect score: 6165
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Scoring table: IDENTITY NUC
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Searched: 5662332 seqs, 3060109652 residues 11324664
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Post-processing: Minimum Match 0%
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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	6161.8	99.9	6298 17 US-10-415-011-43	Sequence 43, Appl1
4	6144	99.7	8656 18 US-10-618-941-1	Sequence 1, Appl1
5	6121.8	99.3	6189 11 US-09-964-956-10	Sequence 10, Appl1
6	6121.8	99.3	6189 17 US-10-262-511-1	Sequence 1, Appl1
7	6105.4	99.0	6201 11 US-09-964-956-8	Sequence 8, Appl1
8	6105.4	99.0	6201 17 US-10-262-511-13	Sequence 13, Appl1
9	5837	94.7	5877 13 US-10-028-946-3	Sequence 3, Appl1
10	5837	94.7	5877 18 US-10-791-666-3	Sequence 3, Appl1
11	5661.4	91.8	6159 13 US-10-017-216-3	Sequence 3, Appl1

12	5661.4	91.8	6162 16 US-10-325-430-11	Sequence 11, Appl1
13	5661.4	91.8	6574 16 US-10-017-216-1	Sequence 1, Appl1
14	5661.4	91.8	6574 16 US-10-325-430-10	Sequence 10, Appl1
15	5661.4	91.8	6574 18 US-10-757-262-51	Sequence 51, Appl1
16	2928.2	47.5	3131 17 US-10-276-774-137	Sequence 137, Appl1
17	2682.8	43.5	2896 18 US-10-357-930-30150	Sequence 30150, A
18	2476.6	40.2	2497 17 US-10-262-511-5	Sequence 5, Appl1
19	2476.6	39.3	2542 17 US-10-262-511-7	Sequence 7, Appl1
20	1847.8	30.0	1870 17 US-10-262-511-9	Sequence 9, Appl1
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23	1398.8	22.7	2066 17 US-10-311-034-33	Sequence 33, Appl1
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25	1398.2	22.7	1515 14 US-10-238-709-1	Sequence 1, Appl1
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38	246.8	4.0	5372 17 US-10-333-314-40	Sequence 40, Appl1
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42	241.6	3.9	6335 17 US-10-388-934-85	Sequence 85, Appl1
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ALIGNMENTS

RESULT 1
US-10-028-946-1
Sequence 1, Application US/10028946
Publication No. US20020123622A1
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
FILE REFERENCE: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
CURRENT FILING DATE: 2001-12-20
PRIORITY APPLICATION NUMBER: US 60/256,335
PRIORITY FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6165
TYPE: DNA
ORGANISM: homo sapiens
US-10-028-946-1
Query Match 100.0%; Score 6165; DB 13; Length 6165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 GCCAGCGGGGCTCCAGGCTGAATCTTCTTCAGGGGAACACCTTATGACTCAA 120

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DB 121 CAGAGATGTCCTCTTCCCGAAGGATATTAGATGCCCTCTTGTCTCTTTGAA 180
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Db 3421 GAGATTTCCGCTCTGACAGGCTCTCAAAAGAGCAAGTGAAGGCCGAGAGCTCTCT 3480
Qy 3481 GACAGCTCAATGACCTGAGAGAGCAATGCTATGCTGTAATGAATGAGCCGAGATTA 3540
Db 3481 GACAGCTCAATGACCTGAGAGAGCAATGCTATGCTGTAATGAATGAGCCGAGATTA 3540
Qy 3541 CAGCAGAGCTGAGACTGAAAGAGAGCTCAACAGAGGCTTCTGAAAGAGCAAGCCAA 3600
Db 3541 CAGCAGAGCTGAGACTGAAAGAGAGCTCAACAGAGGCTTCTGAAAGAGCAAGCCAA 3600
Qy 3601 TTACAGAGAGATGAGCTGAGAGAAATATCAATTTCCGCTGATCAAGAGCTGCA 3660
Db 3601 TTACAGAGAGATGAGCTGAGAGAAATATCAATTTCCGCTGATCAAGAGCTGCA 3660
Qy 3661 GAAGCTTGAATGGGCTGATCTATCTGAAGCAAGAAAGTGAAGCTTGAAGTATCAGCTG 3720
Db 3661 GAAGCTTGAATGGGCTGATCTATCTGAAGCAAGAAAGTGAAGCTTGAAGTATCAGCTG 3720
Qy 3721 GAAGAATTGAGTTCTCTATTTCTCATGAAAGGTGAAGATGAAGGCACTATTTCTCA 3780
Db 3721 GAAGAATTGAGTTCTCTATTTCTCATGAAAGGTGAAGATGAAGGCACTATTTCTCA 3780
Qy 3781 CAACCAAACTCATGATTTTCTGCAAGCCAAATGACCAACTGCTTAAAGAAAG 3840
Db 3781 CAACCAAACTCATGATTTTCTGCAAGCCAAATGACCAACTGCTTAAAGAAAG 3840
Qy 3841 GTTCTCTGCAAGTCAATGAGCTGAAGTGGCCCTGAGAGAGAGAAAGCTGCTGCA 3900
Db 3841 GTTCTCTGCAAGTCAATGAGCTGAAGTGGCCCTGAGAGAGAGAAAGCTGCTGCA 3900
Qy 3901 GAGCTAGAGAGAGCCCTTCAAGAAAGCCGACATCGAGCTCGGCTCGCCGGAGAGAGCT 3960
Db 3901 GAGCTAGAGAGAGCCCTTCAAGAAAGCCGACATCGAGCTCGGCTCGCCGGAGAGAGCT 3960
Qy 3961 GAGCTAGAGAGAGCCCTTCAAGAAAGCCGACATCGAGCTCGGCTCGCCGGAGAGAGCT 3960
Db 3961 GAGCTAGAGAGAGCCCTTCAAGAAAGCCGACATCGAGCTCGGCTCGCCGGAGAGAGCT 3960
Qy 4021 ATGCGCATGCTGCGCATCTGAGAGTGGGCTGCGCAAGACCAAGCCATGCAATGCTGCTG 4080
Db 4021 ATGCGCATGCTGCGCATCTGAGAGTGGGCTGCGCAAGACCAAGCCATGCAATGCTGCTG 4080
Qy 4081 GCGCGGCAATCAGCGGAGAGAGATCTTCAACTCAGAGAGATTTAGTCCGCGCTT 4140
Db 4081 GCGCGGCAATCAGCGGAGAGAGATCTTCAACTCAGAGAGATTTAGTCCGCGCTT 4140
Qy 4141 AAGGAGCAGTGCACCAATATTTCTCAACGATTCACAGTGAAGCTGAACATGAGAGCC 4200
Db 4141 AAGGAGCAGTGCACCAATATTTCTCAACGATTCACAGTGAAGCTGAACATGAGAGCC 4200
Qy 4201 ACAAGTGTGCTGTGTGTCTGAGATACGCTGCACTTTGAGAGCCAGGCAATGTCTC 4260
Db 4201 ACAAGTGTGCTGTGTGTCTGAGATACGCTGCACTTTGAGAGCCAGGCAATGTCTC 4260
Qy 4261 GAATGTCAGAGTGTGTGACCCCAAGTGTGCAAGTGTGCTGAGAGCCAGCTGCGGCTTG 4320
Db 4261 GAATGTCAGAGTGTGTGACCCCAAGTGTGCAAGTGTGCTGAGAGCCAGCTGCGGCTTG 4320
Qy 4321 CTTGCTGAATATGCAACACTTCAACGAGGCTTCTGCGCTGCAAAATGAATGCCCA 4380
Db 4321 CTTGCTGAATATGCAACACTTCAACGAGGCTTCTGCGCTGCAAAATGAATGCCCA 4380
Qy 4381 GGTCTCAGAGCAAGAGCCGAGAGAGCTTGAACCTGGAAGAGGTGATGAAGTGTGCC 4440
Db 4381 GGTCTCAGAGCAAGAGCCGAGAGAGCTTGAACCTGGAAGAGGTGATGAAGTGTGCC 4440
Qy 4441 AGGAATTAACAAAGAGCAGCAAGGCTGGAGCAGAAATGATCATTTGCTGAGAGGATCA 4500
Db 4441 AGGAATTAACAAAGAGCAGCAAGGCTGGAGCAGAAATGATCATTTGCTGAGAGGATCA 4500

QY 4501 AAAGTCCTATTATGACATGAAAGCCAGAGAGCTGAGACAGAGCCCGGTGAAAGATT 4560
 DB 4501 AAAATCTCTATTATGACATGAAAGCCAGAGAGCTGAGACAGAGCCCGGTGAAAGATT 4560
 QY 4561 GAGCTGTGCTTCCGAGCGGGGATGTATCTATCATGAGTGCCTGTGCTTCCGAACTC 4620
 DB 4561 GAGCTGTGCTTCCGAGCGGGGATGTATCTATCATGAGTGCCTGTGCTTCCGAACTC 4620
 QY 4621 GCAAAATCAGCCAAAGCAGATGTCCCATCATCTGAAAGATGAAATCTCAACCCGACAC 4680
 DB 4621 GCAAAATCAGCCAAAGCAGATGTCCCATCATCTGAAAGATGAAATCTCAACCCGACAC 4680
 QY 4681 ACCTGTGCCCCGGGAGAACCTCTACTGTAGCTCCAGCTTCCCGCAAAACAGGCG 4740
 DB 4681 ACCTGTGCCCCGGGAGAACCTCTACTGTAGCTCCAGCTTCCCGCAAAACAGGCG 4740
 QY 4741 TGGGTCAACCGCTTAGATGATGATGTGTGCGAGGTGGAGAGTTTCTAGGGAAAAAGCAGAA 4800
 DB 4741 TGGGTCAACCGCTTAGATGATGATGTGTGCGAGGTGGAGAGTTTCTAGGGAAAAAGCAGAA 4800
 QY 4801 GCTGATGCTAACTGTGCTTGGAAATCTCCCTGCTGAACTGGAAAGGTATGACCTGTAGAC 4860
 DB 4801 GCTGATGCTAACTGTGCTTGGAAATCTCCCTGCTGAACTGGAAAGGTATGACCTGTAGAC 4860
 QY 4861 ATGAACTGCAAGCTGACCTTCAAGTACAGAGTGGTGTGGGAGCAACGAGGAGGCTC 4920
 DB 4861 ATGAACTGCAAGCTGACCTTCAAGTACAGAGTGGTGTGGGAGCAACGAGGAGGCTC 4920
 QY 4921 TACGCCCTGAATGTCTTGAAGAACTCCCTTAACCCATGTCCAGAGATTTGAGAGCTTTC 4980
 DB 4921 TACGCCCTGAATGTCTTGAAGAACTCCCTTAACCCATGTCCAGAGATTTGAGAGCTTTC 4980
 QY 4981 CAAATTTATTTATCAAGAGCTTGGAGAGAGTACTCATGATAGAGAGAAAGCGGGCA 5040
 DB 4981 CAAATTTATTTATCAAGAGAGCTTGGAGAGAGTACTCATGATAGAGAGAAAGCGGGCA 5040
 QY 5041 CTGTGCTTGTGAGCGTGAAGAAAGTGAACAGTCCCTGAGCCAGTCCCACTGCTGCGC 5100
 DB 5041 CTGTGCTTGTGAGCGTGAAGAAAGTGAACAGTCCCTGAGCCAGTCCCACTGCTGCGC 5100
 QY 5101 CAGCCCGACATCTCACCCCAATTTTGAAGCTGTCAAGGGCTGCCACTGTTTGGGGCA 5160
 DB 5101 CAGCCCGACATCTCACCCCAATTTTGAAGCTGTCAAGGGCTGCCACTGTTTGGGGCA 5160
 QY 5161 GCGAAATTTGAGAACGGGCTTGCATCTGTGACGCCATGCCAGCAAAAGTGTCTATCTC 5220
 DB 5161 GCGAAATTTGAGAACGGGCTTGCATCTGTGACGCCATGCCAGCAAAAGTGTCTATCTC 5220
 QY 5221 CGCTACAGGAAACCTCAGCAAACTCTGATCCGAGAAAGATAGAGACTTCAAGGCC 5280
 DB 5221 CGCTACAGGAAACCTCAGCAAACTCTGATCCGAGAAAGATAGAGACTTCAAGGCC 5280
 QY 5281 TGCAGCTGTATCCACTTCAACCAATTCAGATCTCTGATTTGGAACCAATTAATCTAGAA 5340
 DB 5281 TGCAGCTGTATCCACTTCAACCAATTCAGATCTCTGATTTGGAACCAATTAATCTAGAA 5340
 QY 5341 ATCGACATGAGAGTACAGCTCGAGGAATTCCTGATTAAGATGACCAATTCCTTGGCA 5400
 DB 5341 ATCGACATGAGAGTACAGCTCGAGGAATTCCTGATTAAGATGACCAATTCCTTGGCA 5400
 QY 5401 CCGTGTGTGTTGGCGGCTTCCCAACAGCTTCCCTGTCTCAATCTGTGACAGGTGAACAGC 5460
 DB 5401 CCGTGTGTGTTGGCGGCTTCCCAACAGCTTCCCTGTCTCAATCTGTGACAGGTGAACAGC 5460
 QY 5461 GCGAGGCGAGAGAGAGTACTGTGTGTTTCCAGAAATTTGAGAGTGTTCGAGATTC 5520
 DB 5461 GCGAGGCGAGAGAGAGTACTGTGTGTTTCCAGAAATTTGAGAGTGTTCGAGATTC 5520
 QY 5521 TACGGAAGAGTACCGCGACAGACGATCTCAAGTGAAGTGTGCTTACCTTTGGCCTTTGCC 5580
 DB 5521 TACGGAAGAGTACCGCGACAGACGATCTCAAGTGAAGTGTGCTTACCTTTGGCCTTTGCC 5580
 QY 5581 TACAGAGAACCTATCTGTTTGTGACCCCACTTCACTCACTGGAAGTAAATGAGATCCAG 5640

DB 5581 TACAGAGAACCTATCTGTTTGTGACCACTTCACTCACTGGAATTAATGAGATCCAG 5640
 QY 5641 GCACGCTCTCAGCAGGAGACCCCTGCCCCAGCGTACCTGAGCATCCGAAACCCGCTAC 5700
 DB 5641 GCACGCTCTCAGCAGGAGACCCCTGCCCCAGCGTACCTGAGCATCCGAAACCCGCTAC 5700
 QY 5701 CTGGGCTTGCATTTCTTCTCAGAGCATTTACTTGGCGTCTCTATACCAAGATTAATTA 5760
 DB 5701 CTGGGCTTGCATTTCTTCTCAGAGCATTTACTTGGCGTCTCTATACCAAGATTAATTA 5760
 QY 5761 AGGTGATTTGTGCAAGGGAACCTGTGAAGAGTCCGCAATTAACCAACAGCGGGC 5820
 DB 5761 AGGTGATTTGTGCAAGGGAACCTGTGAAGAGTCCGCAATTAACCAACAGCGGGC 5820
 QY 5821 CCGTCACTCTCCGACAGCAGCCCAACAGCAGGAGCCCAACCACTGTAACAGACATC 5880
 DB 5821 CCGTCACTCTCCGACAGCAGCCCAACAGCAGGAGCCCAACCACTGTAACAGACATC 5880
 QY 5881 ACCAAGCGGTGCTTCAGCCCAAGCGCGCCGGAAGGCCCAAGCCACCCGAGAGCCA 5940
 DB 5881 ACCAAGCGGTGCTTCAGCCCAAGCGCGCCGGAAGGCCCAAGCCACCCGAGAGCCA 5940
 QY 5941 AGCAGACCCCAACCGCTAACCGCGAGGGGCGGACCGAGCTGGCGAGGACAAAGTCTCTGCG 6000
 DB 5941 AGCAGACCCCAACCGCTAACCGCGAGGGGCGGACCGAGCTGGCGAGGACAAAGTCTCTGCG 6000
 QY 6001 CGCCCCCTGAGGAGGAGAAAGTCCCGCGCGGATCTACAGCAGCGGAGAGAGCGGTCC 6060
 DB 6001 CGCCCCCTGAGGAGGAGAAAGTCCCGCGCGGATCTACAGCAGCGGAGAGAGCGGTCC 6060
 QY 6061 CCGCGAGGCTGTTTGAAGACAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6120
 DB 6061 CCGCGAGGCTGTTTGAAGACAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6120
 QY 6121 CCGCTGTCCAGGTGAACAAAGTCTGAGACCACTTCACTTAATA 6165
 DB 6121 CCGCTGTCCAGGTGAACAAAGTCTGAGACCACTTCACTTAATA 6165

RESULT 2
 US-10-791-666-1
 ; Sequence 1, Application US/10791666
 ; Publication No. US20040209297A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu, Xuanchuan
 ; APPLICANT: Miranda, Maricar
 ; APPLICANT: Fiedler, Carl Johan
 ; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0289-USA
 ; CURRENT APPLICATION NUMBER: US/10/791,666
 ; PRIOR FILING DATE: 2004-03-02
 ; PRIOR APPLICATION NUMBER: US/10/028,946
 ; PRIOR FILING DATE: 2001-12-20
 ; PRIOR APPLICATION NUMBER: US 60/258,335
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 6165
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-791-666-1

Query Match 100.0%; Score 6165; DB 18; Length 6165;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGAAGTTCAATATGAGCGCGGAATCTTTGATGCTGTGCTGAACCATTT 60
 DB 1 ATGTTGAAGTTCAATATGAGCGCGGAATCTTTGATGCTGTGCTGAACCATTT 60
 QY 61 GCGAGCCGGGCTCCAGGCTGAATCTGTTTTCAGAGGAGAAACACCTTTATGACTCAA 120


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QY 2281 CAGCACTATGAGAAAGATTAAAGTTGTCATATCATTAAGAAAGACCTGGCTGAC 2340
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Db 2281 CAGCACTATGAGAAAGATTAAAGTTGTCATATCATTAAGAAAGACCTGGCTGAC 2340
QY 2341 AAGGAGACACTGAGAAACATGATCAGAGACACGAGAGAGAGGCCCATGAGAGGGGCAA 2400
|||
Db 2341 AAGGAGACACTGAGAAACATGATCAGAGACACGAGAGAGAGGCCCATGAGAGGGGCAA 2400
QY 2401 ATTCTCAGCGAACAAGAGCGATGATCAATGCTATGATTCAGAGATCAGATCCCTGAA 2460
|||
Db 2401 ATTCTCAGCGAACAAGAGCGATGATCAATGCTATGATTCAGAGATCAGATCCCTGAA 2460
QY 2461 CAGGAGATTGTCGACTCTGTCGAGCCAAATTAACCTTGACGAATAGCAGCTTTTAAAC 2520
|||
Db 2461 CAGGAGATTGTCGACTCTGTCGAGCCAAATTAACCTTGACGAATAGCAGCTTTTAAAC 2520
QY 2521 CAAAGGAACATGAAAGGCCCAAGAGATGATTTCTGAACTCAGAGCAACAGAAATTTTAC 2580
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Db 2521 CAAAGGAACATGAAAGGCCCAAGAGATGATTTCTGAACTCAGAGCAACAGAAATTTTAC 2580
QY 2581 CTGGAGACACAGGCTGGAGAGTTGAGAGCCCAAGAACGAAACTGAGAGCAGCTGGAG 2640
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Db 2581 CTGGAGACACAGGCTGGAGAGTTGAGAGCCCAAGAACGAAACTGAGAGCAGCTGGAG 2640
QY 2641 AAGATCGCCACCAAGACCAAGTGAACAAGATTCGGCTGTCGAACTGAGAGCAAGATTG 2700
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Db 2641 AAGATCGCCACCAAGACCAAGTGAACAAGATTCGGCTGTCGAACTGAGAGCAAGATTG 2700
QY 2701 CGGAGAGCTCAGTCTAGAGCAAGAGAGCAAGAACTGAGAGCTCAAGGCCAGCTCAGAG 2760
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Db 2701 CGGAGAGCTCAGTCTAGAGCAAGAGAGCAAGAACTGAGAGCTCAAGGCCAGCTCAGAG 2760
QY 2761 CTACAGCTCTCCCTGAGAGCGCGAGTCAAGTTGAACGCCCTGACAGCTGCAACGGCG 2820
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Db 2761 CTACAGCTCTCCCTGAGAGCGCGAGTCAAGTTGAACGCCCTGACAGCTGCAACGGCG 2820
QY 2821 GCCCTGAGAGCCAGACTTCCGCGAGCAAGAGCAAGAGCTGAGAGACCAAGAAAGCT 2880
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Db 2821 GCCCTGAGAGCCAGACTTCCGCGAGCAAGAGCAAGAGCTGAGAGACCAAGAAAGCT 2880
QY 2881 GAAGAGAGATCCAGGCACTCAGGCGCATAGAGATGAATCCAGGCGCAATTTGATGCT 2940
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Db 2881 GAAGAGAGATCCAGGCACTCAGGCGCATAGAGATGAATCCAGGCGCAATTTGATGCT 2940
QY 2941 CTTCTGTAACAGCTGTACTGTAAATCAAGACTGAGAGAGCAAGCTTAACAGCTGACCGAG 3000
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Db 2941 CTTCTGTAACAGCTGTACTGTAAATCAAGACTGAGAGAGCAAGCTTAACAGCTGACCGAG 3000
QY 3001 GACACGCTGAATCTCAACCAACCAAACTTTACTTGTCCAAACAATCTCGATGAGGCTTCT 3060
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Db 3001 GACACGCTGAATCTCAACCAACCAAACTTTACTTGTCCAAACAATCTCGATGAGGCTTCT 3060
QY 3061 GGGCGCAACGACGAGATTGTAACTGCGAAGTGAAGTGGACCATCTCGCGCGGGAGATC 3120
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Db 3061 GGGCGCAACGACGAGATTGTAACTGCGAAGTGAAGTGGACCATCTCGCGCGGGAGATC 3120
QY 3121 ACGGAAACGAGAGTGCAGCTTACCAAGCAAGAACCAAGATGAGGCTTGAAGACCAAG 3180
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QY 3181 TGCACCATCTGAGAGAAACAGGTCATGATTTGGAAGGCCCTTAAACGATGAGCTGTAGAA 3240
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Db 3181 TGCACCATCTGAGAGAAACAGGTCATGATTTGGAAGGCCCTTAAACGATGAGCTGTAGAA 3240
QY 3241 AAAAGACGCGAGTGGAGGCTTGGAGAGAGTCTGGGTGATGAGAAATCCCAAGTTTGAAG 3300
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QY 3301 TGTGGGTTTCAGAGCTGCAAGATGCTGCAACCGAGAAACAGAGCAGGGGAGAGGCC 3360
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Db 3301 TGTGGGTTTCAGAGCTGCAAGATGCTGCAACCGAGAAACAGAGCAGGGGAGAGGCC 3360
QY 3361 GATCAGCGGATCACCGAGTCTCCGACAGGTGTGAGCTGGCATGAAAGAGCAACAGGCT 3420
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Db 3361 GATCAGCGGATCACCGAGTCTCCGACAGGTGTGAGCTGGCATGAAAGAGCAACAGGCT 3420
QY 3421 GAGATTCCTGCTGACGACAGGCTCTCAAGAGAGCAAGAGCTGAGAGGCTGAGGCTCTCT 3480
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Db 3421 GAGATTCCTGCTGACGACAGGCTCTCAAGAGAGCAAGAGCTGAGAGGCTGAGGCTCTCT 3480
QY 3481 GACAAAGCTCAATGACTGAGAGAGAACATGCTATGCTTGAATATGAAATGCCCCGAAGCTTA 3540
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Db 3481 GACAAAGCTCAATGACTGAGAGAGAACATGCTATGCTTGAATATGAAATGCCCCGAAGCTTA 3540
QY 3541 CAGCAGAAAGCTGAGAGATGAAACGAGAGCTCAACAGAGGCTTCTGAAAGACCAAGCAA 3600
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Db 3541 CAGCAGAAAGCTGAGAGATGAAACGAGAGCTCAACAGAGGCTTCTGAAAGACCAAGCAA 3600
QY 3601 TTACAGCAGAGATGAGCTCGCAAGAAATCAACTTTCCGTGACTCAAGGACTGCAAA 3660
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Db 3601 TTACAGCAGAGATGAGCTCGCAAGAAATCAACTTTCCGTGACTCAAGGACTGCAAA 3660
QY 3661 GAAGCTCTAGATCGGCTGATCTTACTGAAAGACAGAAAGAAAGTGAAGTGAAGTCAAGCTG 3720
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Db 3661 GAAGCTCTAGATCGGCTGATCTTACTGAAAGACAGAAAGAAAGTGAAGTGAAGTCAAGCTG 3720
QY 3721 GAAAACTTCAAGTTCTTATTTCTCATGAAAGGTGAAATGGAAGGCACTATTTCTCAA 3780
|||
Db 3721 GAAAACTTCAAGTTCTTATTTCTCATGAAAGGTGAAATGGAAGGCACTATTTCTCAA 3780
QY 3781 CAAACCAAACTCATGATTTTCTGCAAGGCCAAATGGAACCACTGCTAAAGAAAGAAAG 3840
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Db 3781 CAAACCAAACTCATGATTTTCTGCAAGGCCAAATGGAACCACTGCTAAAGAAAGAAAG 3840
QY 3841 GTTCTCTGAGTACATGAGTGAAGCTGAGCTGAGCCCTGAGAGAGAGAAAGCTCGCTGCA 3900
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Db 3841 GTTCTCTGAGTACATGAGTGAAGCTGAGCTGAGCCCTGAGAGAGAGAAAGCTCGCTGCA 3900
QY 3901 GAGCTGAGAGAGCCCTTGAAGAAAGCCGATGAGCTCGGCTCGCGCGGAGAAAGCT 3960
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Db 3901 GAGCTGAGAGAGCCCTTGAAGAAAGCCGATGAGCTCGGCTCGCGCGGAGAAAGCT 3960
QY 3961 GCCCAGCGAAGCAACGAGCAACCCATCCATCCAGCCAGCCACCGGAGAGGACAGAG 4020
|||
Db 3961 GCCCAGCGAAGCAACGAGCAACCCATCCATCCAGCCAGCCACCGGAGAGGACAGAG 4020
QY 4021 ATGCCATGTCGCGCATCTGTCGAGTGCAGAGACCAAGCCAGTGCATGAGCTGCTG 4080
|||
Db 4021 ATGCCATGTCGCGCATCTGTCGAGTGCAGAGACCAAGCCAGTGCATGAGCTGCTG 4080
QY 4081 GCCCGGCATCCAGCCGCAAGAAAGAGTCTTCAACTCCAGAGAAATTTAGTGGCGTCTT 4140
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Db 4081 GCCCGGCATCCAGCCGCAAGAAAGAGTCTTCAACTCCAGAGAAATTTAGTGGCGTCTT 4140
QY 4141 AAGGAACGATGACCAACCAATTTCTCAACGATTCAGAGTGAAGTGAACATGCGAGGC 4200
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Db 4141 AAGGAACGATGACCAACCAATTTCTCAACGATTCAGAGTGAAGTGAACATGCGAGGC 4200
QY 4201 ACAAAGTGTGCTGTGTGTGATACCGTGCATTGTGACAGCCAGGATCCAAATGTCTC 4260
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Db 4201 ACAAAGTGTGCTGTGTGTGATACCGTGCATTGTGACAGCCAGGATCCAAATGTCTC 4260
QY 4261 GAATGTCAAGTATGTATGATCAACCCCAAGTGTCTCAAGTGTCTCCAGCCACCTGGCTTG 4320
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Db 4321 CCTGCTGAATATGCCACCACTTCAACGAGGCTTCTGCGGTGACAAATGAATCTCCCA 4380
QY 4381 GGTCTCCAGACCAAGAGCCCGACAGCAGCTTGCACCTGGAAGGTTGATGAAGGAGGCC 4440
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Db 4381 GGTCTCCAGACCAAGAGCCCGACAGCAGCTTGCACCTGGAAGGTTGATGAAGGAGGCC 4440
QY 4441 AGGAATTAACAAACGAGGACAGCAAGGCTGGGACAGAGAAATCAATTGTCTGTGAGGAGATCA 4500
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4441 AGGAATTAACAAACGAGACAGCAGGCTGGAGAGAAATCATTTGCTGGAGAGATCA 4500
4501 AAAGTCTCATTTATATGACATTAAGCAGAGAGAGAGAGAGAGAGAGAGAGATTT 4560
4501 AAAGTCTCATTTATATGACATTAAGCAGAGAGAGAGAGAGAGAGAGAGAGATTT 4560
4561 GAGGTGCTTCCGAGCGGGAGATGATCTATTGATGATGATGATGATGATGATGATG 4620
4561 GAGGTGCTTCCGAGCGGGAGATGATCTATTGATGATGATGATGATGATGATGATG 4620
4621 GCAAAATACAGCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 4680
4621 GCAAAATACAGCAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 4680
4681 ACCGTGCTGAGCGGGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 4740
4681 ACCGTGCTGAGCGGGAGAGAGAGATGATGATGATGATGATGATGATGATGATGATG 4740
4741 TGGGTCAACGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4800
4741 TGGGTCAACGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4800
4801 GCTGATCTAACTGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4860
4801 GCTGATCTAACTGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4860
4861 ATGAACTGACGCGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4920
4861 ATGAACTGACGCGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATG 4920
4921 TACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4980
4921 TACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4980
4981 CAAATTTATATTAATCAAG 5040
4981 CAAATTTATATTAATCAAG 5040
5041 CTGCTGCTTGAAG 5100
5041 CTGCTGCTTGAAG 5100
5101 CAGCCGACATCTCAACCAATTTTGAAGCTGTCAAGAGAGAGAGAGAGAGAGAGAGAG 5160
5101 CAGCCGACATCTCAACCAATTTTGAAGCTGTCAAGAGAGAGAGAGAGAGAGAGAGAG 5160
5161 GCGAAGATTGAG 5220
5161 GCGAAGATTGAG 5220
5221 GCGTACACGAG 5280
5221 GCGTACACGAG 5280
5281 TGCAGCTGATCTCACTTCAACCAATTTTGAAGCTGTCAAGAGAGAGAGAGAGAGAGAG 5340
5281 TGCAGCTGATCTCACTTCAACCAATTTTGAAGCTGTCAAGAGAGAGAGAGAGAGAGAG 5340
5341 ATGCAATGAG 5400
5341 ATGCAATGAG 5400
5401 CTGCTGCTTGAAG 5460
5401 CTGCTGCTTGAAG 5460
5461 GCAGGAG 5520
5461 GCAGGAG 5520
5521 TACGGAAG 5580
5521 TACGGAAG 5580

5521 TACGGAAG 5580
5581 TACGGAAG 5640
5581 TACGGAAG 5640
5641 GCAGGAG 5700
5641 GCAGGAG 5700
5701 CTGCTGCTTGAAG 5760
5701 CTGCTGCTTGAAG 5760
5761 AGGATCATTTGCTGAG 5820
5761 AGGATCATTTGCTGAG 5820
5821 CCGTCACTTCCGAG 5880
5821 CCGTCACTTCCGAG 5880
5881 ACAG 5940
5881 ACAG 5940
5941 AGCAG 6000
5941 AGCAG 6000
6001 CCGCTGCTTGAAG 6060
6001 CCGCTGCTTGAAG 6060
6061 CCGGAG 6120
6061 CCGGAG 6120
6121 CCGCTGCTTGAAG 6180
6121 CCGCTGCTTGAAG 6180

RESULT 3
US-10-415-011-43
Sequence 43, Application US/10415011
Publication No. US20040035394A1
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION
APPLICANT: GURURAJAN, Rajagopal
APPLICANT: BAUGHN, Mariah R.
APPLICANT: CHAWLA, Narinder K.
APPLICANT: ELLIOTT, Vicki S.
APPLICANT: XU, Yuming
APPLICANT: ARVIZU, Chandra S.
APPLICANT: YAO, Monique G.
APPLICANT: RAMKUMAR, Jayalaxmi
APPLICANT: DING, Li
APPLICANT: TANG, Y. Tom
APPLICANT: HAFALIA, April J.A.
APPLICANT: NGUYEN, Daniel B.
APPLICANT: GANDHI, Ameena R.
APPLICANT: LU, Van
APPLICANT: YUE, Henry
APPLICANT: BURFORD, Neil
APPLICANT: BANDMAN, Olga
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: LAL, Preeti G.
APPLICANT: RECIPION, Shirley A.
APPLICANT: LU, Dying Aina M.
APPLICANT: BOROMSKY, Mark L.
APPLICANT: THORNTON, Michael B.
APPLICANT: SWARNAKER Anita

APPLICANT: THANGAVELU, Kavitha
APPLICANT: KHAN, Farrah A.
APPLICANT: ISON, Craig H.
TITLE OR INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0262 USN
CURRENT APPLICATION NUMBER: US/10/415, 011
CURRENT FILING DATE: 2003-04-18
PRIORITY APPLICATION NUMBER: PCT/US01/47728
PRIORITY FILING DATE: 2001-10-20
PRIORITY APPLICATION NUMBER: US 60/242,410
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: US 60/244,068
PRIORITY FILING DATE: 2000-10-27
PRIORITY APPLICATION NUMBER: US 60/245,708
PRIORITY FILING DATE: 2000-11-03
PRIORITY APPLICATION NUMBER: US 60/247,672
PRIORITY FILING DATE: 2000-11-09
PRIORITY APPLICATION NUMBER: US 60/249,565
PRIORITY FILING DATE: 2000-11-16
PRIORITY APPLICATION NUMBER: US 60/252,730
PRIORITY FILING DATE: 2000-11-22
PRIORITY APPLICATION NUMBER: US 60/250,807
PRIORITY FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL Program
SEQ ID NO 43
LENGTH: 6298
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US2004005394A1 7484498CBI
US-10-415-011-43

Query Match 99.9%; Score 6161.8; DB 17; Length 6298;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGGAAGTTCAATATGAGCGCGGAATCTTTGATGCTGCTGTAACCCATT 60
DB 55 ATGTGGAAGTTCAATATGAGCGCGGAATCTTTGATGCTGCTGTAACCCATT 114
QY 61 GCCAGCGGCGCTCCAGCTGTAATCTGTCTCCAGGGAACACCCCTTATGACCTCA 120
DB 115 GCCAGCGGCGCTCCAGCTGTAATCTGTCTCCAGGGAACACCCCTTATGACCTCA 174
QY 121 CAGCAGATGTCCTCTTTCCGAGAGGATATTAGATCCCTCTTTGTTCTTTGAA 180
DB 175 CAGCAGATGTCCTCTTTCCGAGAGGATATTAGATCCCTCTTTGTTCTTTGAA 234
QY 181 GAATGCAGTAGCCTGCTGTGATGAAGATTAAAGCAGTGAACCTTTGTCCGAAATAT 240
DB 235 GAATGCAGTAGCCTGCTGTGATGAAGATTAAAGCAGTGAACCTTTGTCCGAAATAT 294
QY 241 TCCGACACCATAGCTAGTGAAGAGAGCTCCAGCTCCGCAAGAGACTTCCGAAGTCA 300
DB 295 TCCGACACCATAGCTAGTGAAGAGAGCTCCAGCTCCGCAAGAGACTTCCGAAGTCA 354
QY 301 AGTCTTGAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTTAAGAGAAAGCAACCGG 360
DB 355 AGTCTTGAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTTAAGAGAAAGCAACCGG 414
QY 361 GACATTAATGCTATGAAGATGAAGAAAGGCTTTTATTTGGCCAGAGGAGGTTTCA 420
DB 415 GACATTAATGCTATGAAGATGAAGAAAGGCTTTTATTTGGCCAGAGGAGGTTTCA 474
QY 421 TTTTGTGAGAGAGGAGGAACATATATCTCCGAAGACACCCCTGGATCCCCCAATTA 480
DB 475 TTTTGTGAGAGAGGAGGAACATATATCTCCGAAGACACCCCTGGATCCCCCAATTA 534
QY 481 CAGTATGCTTTTCAGAGCAAAATACCTTTATCTGTCATGGAATATAGCTGGAGGG 540
DB 535 CAGTATGCTTTTCAGAGCAAAATACCTTTATCTGTCATGGAATATAGCTGGAGGG 594

QY 541 GACTTGCTGTCACTTTGAATAGATATAGAGCAAGTTAGTGAACCTGTATACAGTTT 600
DB 595 GACTTGCTGTCACTTTGAATAGATATAGAGCAAGTTAGTGAACCTGTATACAGTTT 654
QY 601 TACCTAGCTGAGCTGATTTTGGCTGTCAAGAGCTTATCTGAAGGATACGTCAATGCA 660
DB 655 TACCTAGCTGAGCTGATTTTGGCTGTCAAGAGCTTATCTGAAGGATACGTCAATGCA 714
QY 661 GACATCAAGCTGAGAACATTTCTGTGACCGACAGACATCAAGCTGTGGATTTT 720
DB 715 GACATCAAGCTGAGAACATTTCTGTGACCGACAGACATCAAGCTGTGGATTTT 774
QY 721 GGAATCTCCCGAAATGAAATTCAAACAAGATGTGAATGCCAACTCCGATTTGGAGC 780
DB 775 GGAATCTCCCGAAATGAAATTCAAACAAGATGTGAATGCCAACTCCGATTTGGAGC 834
QY 781 CCGATTAACATAGCTCTGTGAAGTGTGACCTGTATGAACGGGATGGAACCAAGCTTAC 840
DB 835 CCGATTAACATAGCTCTGTGAAGTGTGACCTGTATGAACGGGATGGAACCAAGCTTAC 894
QY 841 GGCTGGAATGTAAGTGTGATGAGTGGGAGTATGCTATGATGATTTATGGAGA 900
DB 895 GGCTGGAATGTAAGTGTGATGAGTGGGAGTATGCTATGATGATTTATGGAGA 954
QY 901 TCCCTCTTGCAGAGGGAACCTTGCAGAACCTTCAATTAATTAATGAATTTCCAGCG 960
DB 955 TCCCTCTTGCAGAGGGAACCTTGCAGAACCTTCAATTAATTAATGAATTTCCAGCG 1014
QY 961 TTTTGAATTTTCCAAATGACCCCAAGAGAGAGATCTTTGTGATCTGATTTCAAGC 1020
DB 1015 TTTTGAATTTTCCAAATGACCCCAAGAGAGAGATCTTTGTGATCTGATTTCAAGC 1074
QY 1021 TTGTTGCGCGGCAGAAAGAGAGATGAAGTTGAAGTCTTTGCTGCCATCTTCTTC 1080
DB 1075 TTGTTGCGCGGCAGAAAGAGAGATGAAGTTGAAGTCTTTGCTGCCATCTTCTTC 1134
QY 1081 TCTAAATTTGACTGGAACCAATTCGTAACTCTTCCCTTCTGCTCCACCTTCAAG 1140
DB 1135 TCTAAATTTGACTGGAACCAATTCGTAACTCTTCCCTTCTGCTCCACCTTCAAG 1194
QY 1141 TCTGAGATGACACCTTCCAAATTTTGAATGAACCAAGAAATTCGTGGTTTATCTCT 1200
DB 1195 TCTGAGATGACACCTTCCAAATTTTGAATGAACCAAGAAATTCGTGGTTTATCTCT 1254
QY 1201 CCGTGCACGTGACCCCTCAAGCTTCTCGGGTGAAGAACTGCGTTTGAGGGGTTTTCG 1260
DB 1255 CCGTGCACGTGACCCCTCAAGCTTCTCGGGTGAAGAACTGCGTTTGAGGGGTTTTCG 1314
QY 1261 TACAGCAAGGCACTGGGAAATCTTGGTAGATCTGATCTGTGTGTGCGGGTCTGACTCC 1320
DB 1315 TACAGCAAGGCACTGGGAAATCTTGGTAGATCTGATCTGTGTGTGCGGGTCTGACTCC 1374
QY 1321 CCTGCCAAGACTAGCTTCCATGGAAGAAATCTTCTATCAAAAGCAAAAGCTTACAGAC 1380
DB 1375 CCTGCCAAGACTAGCTTCCATGGAAGAAATCTTCTATCAAAAGCAAAAGCTTACAGAC 1434
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DB 1435 TCTCAGAGCAAGTGTCACAAGATGAGCAGAGAAATGACCCGGTTACATGAGAGTGTCA 1494
QY 1441 GAGGTGAGGCTGTGCTTAGTACAGAAAGATGAGCTGAAAGCTTCTGAGACTCAGAGA 1500
DB 1495 GAGGTGAGGCTGTGCTTAGTACAGAAAGATGAGCTGAAAGCTTCTGAGACTCAGAGA 1554
QY 1501 TCCCTTCTGAGACAGAGCTTCTCTACCTACATCAAGATGCAATGACTTTAAAGGAAGT 1560
DB 1555 TCCCTTCTGAGACAGAGCTTCTCTACCTACATCAAGATGCAATGACTTTAAAGGAAGT 1614
QY 1561 TTGAGAGCAAGCAGATGAGAGGTGCCAGAGGATGCAAAAGCACTGAGCTTCTCCAT 1620
DB 1615 TTGAGAGCAAGCAGATGAGAGGTGCCAGAGGATGCAAAAGCACTGAGCTTCTCCAT 1674

QY 1621 GATATCAGAGCAGAGCCGGAAGCTCCAGAAATCAAGAGCAGAGCTACAGGCTCAA 1680
Db 1675 GATATCAGAGCAGAGCCGGAAGCTCCAGAAATCAAGAGCAGAGCTACAGGCTCAA 1734
QY 1681 GTGGAAGAAATGAGGTGATGATGATCAATGATGGAAGAGATCTTGTCTCAGCAAGAA 1740
Db 1735 GTGGAAGAAATGAGGTGATGATGATCAATGATGGAAGAGATCTTGTCTCAGCAAGAA 1794
QY 1741 CGAGGTGATCTCTACGAATCTGAGCTGAGAGAGTCTCGGCTTGTCTGAAAGAAATTCAG 1800
Db 1795 CGAGGTGATCTCTACGAATCTGAGCTGAGAGAGTCTCGGCTTGTCTGAAAGAAATTCAG 1854
QY 1801 CGGAAGCAGACAGAAATGTCAGCATTAATCTTTGAAGCTTAAGATCAAGGAGACCTGAA 1860
Db 1855 CGGAAGCAGACAGAAATGTCAGCATTAATCTTTGAAGCTTAAGATCAAGGAGACCTGAA 1914
QY 1861 GTGGAGAAATATGGGAACTGGAGAAAGATCAATGCTGAGCAGAGCTCAAAATTCAGAG 1920
Db 1915 GTGGAGAAATATGGGAACTGGAGAAAGATCAATGCTGAGCAGAGCTCAAAATTCAGAG 1974
QY 1921 CTCGAAGGAAATCTGAGAAAGCTGTAAAGCCAGCAACGAGGCCACCGAGCTGTCAG 1980
Db 1975 CTCGAAGGAAATCTGAGAAAGCTGTAAAGCCAGCAACGAGGCCACCGAGCTGTCAG 2034
QY 1981 AATATCCGCCAGGCAAGAGAGCCGAGCGAGGGAGCTGGAAGAGCTGCAAGACCGAGAG 2040
Db 2035 AATATCCGCCAGGCAAGAGAGCCGAGCGAGGGAGCTGGAAGAGCTGCAAGACCGAGAG 2094
QY 2041 GATCTTCTGAAGGATTCAGAAAGAGCTGGTGAAGGTGAGAAACGCGCATTTCTCTG 2100
Db 2095 GATCTTCTGAAGGATTCAGAAAGAGCTGGTGAAGGTGAGAAACGCGCATTTCTCTG 2154
QY 2101 GAGAAACAAGATTAAGAGACTAGAGACCATGAGCGTGAAGAGAAACAGACTGAAGATGAC 2160
Db 2155 GAGAAACAAGATTAAGAGACTAGAGACCATGAGCGTGAAGAGAAACAGACTGAAGATGAC 2214
QY 2161 ATTCAGACAAAATCCCAACAGATCCAGCATGAGTGAATTAATTTCTGAGCTGGAAGAG 2220
Db 2215 ATTCAGACAAAATCCCAACAGATCCAGCATGAGTGAATTAATTTCTGAGCTGGAAGAG 2274
QY 2221 AAAATGCGGAGGCGCAAGTCTCAGCCGAGCACTGAGAGTGCACCTGAAACAGAAAGAG 2280
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QY 2281 CAGCACTATGAGGAAAGATTAAGTGTGGAACAATCAGATTAAGAAAGACCTGAGCTGAC 2340
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QY 2341 AAGGAGACACTGAGAAACATGATGCAAGACACGAGAGAGGCCCATGAGAGGGCATA 2400
Db 2395 AAGGAGACACTGAGAAACATGATGCAAGACACGAGAGAGAGGCCCATGAGAGGGCATA 2454
QY 2401 ATTTCTCAGCGAAACGAAGGCCATGATCAATGCTATGATTTCCAGATTAAGATTCCTTGGAA 2460
Db 2455 ATTTCTCAGCGAAACGAAGGCCATGATCAATGCTATGATTTCCAGATTAAGATTCCTTGGAA 2514
QY 2461 CAGAGATTGTGGAATGTCTGAAGCCAAATAACTCTGACGAAATAGCAGCTTTTAAAC 2520
Db 2515 CAGAGATTGTGGAATGTCTGAAGCCAAATAACTCTGACGAAATAGCAGCTTTTAAAC 2574
QY 2521 CAAAGGAACATGAAGGCCCAAGAAAGATGATTTCTGAATCTCAGGCAACAGAAATTTTAC 2580
Db 2575 CAAAGGAACATGAAGGCCCAAGAAAGATGATTTCTGAATCTCAGGCAACAGAAATTTTAC 2634
QY 2581 CTGAGAGACAGGGCTGGGAATTTGGAGGCCCAAGAACGAAACTGGAGAGACAGCTGGAG 2640
Db 2635 CTGAGAGACAGGGCTGGGAATTTGGAGGCCCAAGAACGAAACTGGAGAGACAGCTGGAG 2694
QY 2641 AAGATTCAGCCACCAAGACACACAGTGAACAAGATCGGCTGTGAACCTGAGACAAGATTG 2700
Db 2695 AAGATTCAGCCACCAAGACACACAGTGAACAAGATCGGCTGTGAACCTGAGACAAGATTG 2754
QY 2701 CGGAGGTCAGTCTTAGACACGAGAGGAGAACTGAGACTCAAGCGCCAGCTCACAAGAG 2760

Db 2755 CGGAGGTCAGTCTTAGACACGAGAGGAGAGAACTGAGAGCTCAAGCCGCAAGCTCACAAG 2814
QY 2761 CTAAGCTCTTCCCTGCAAGAGCCGGAATCAAGTTGAACAGCCCTGCAAGCTGCAACGGCG 2820
Db 2815 CTAAGCTCTTCCCTGCAAGAGCCGGAATCAAGTTGAACAGCCCTGCAAGCTGCAACGGCG 2874
QY 2821 GCCCTGAGAGCCAGCTTCCGCAAGGCCAAGACAGAGCTGGAAGAGACCAACGAGAGCT 2880
Db 2875 GCCCTGAGAGCCAGCTTCCGCAAGGCCAAGACAGAGCTGGAAGAGACCAACGAGAGCT 2934
QY 2881 GAAGAGAGATCCAGGCACTCAAGGCAATAGAGATGAATCCAGCGCAATTTGATGCT 2940
Db 2935 GAAGAGAGATCCAGGCACTCAAGGCAATAGAGATGAATCCAGCGCAATTTGATGCT 2994
QY 2941 CTTGCTAAACAGCTGTACTGTATATCAGACACTGAGAGGACGATTAACAGCTGACCGAG 3000
Db 2995 CTTGCTAAACAGCTGTACTGTATATCAGACACTGAGAGGACGATTAACAGCTGACCGAG 3054
QY 3001 GACAAAGCTGAATCTCAACCAACCAAACTTCTTATGTCGCAACCACTGATGAGGCTTCT 3060
Db 3055 GACAAAGCTGAATCTCAACCAACCAAACTTCTTATGTCGCAACCACTGATGAGGCTTCT 3114
QY 3061 GCGCGCAACGACGAGATTGTATCAACCTGCAAGTGAAGTGAACATCTCCGCGGAGATC 3120
Db 3115 GCGCGCAACGACGAGATTGTATCAACCTGCAAGTGAAGTGAACATCTCCGCGGAGATC 3174
QY 3121 ACGGAACGAGAGATGCAAGCTTACCAAGCAGAAAGCAACGATGAGGCTTGAACACAG 3180
Db 3175 ACGGAACGAGAGATGCAAGCTTACCAAGCAGAAAGCAACGATGAGGCTTGAACACAG 3234
QY 3181 TGCACATGCTGAGGAAACAGGTCATGATTTGGAGGCCCTTAAACGATGAGCTCTAGAA 3240
Db 3235 TGCACATGCTGAGGAAACAGGTCATGATTTGGAGGCCCTTAAACGATGAGCTCTAGAA 3294
QY 3241 AAAAGGGGCAATGGAGAGGCTTGAAGAGGCTCCTGGGTATGAGAAATCCCAATTTGAG 3300
Db 3295 AAAAGGGGCAATGGAGAGGCTTGAAGAGGCTCCTGGGTATGAGAAATCCCAATTTGAG 3354
QY 3301 TGTGCGGTTGAGAGGCTGCAAGAGATCTGGAACCAAGAAACAGAGCAGGCGAGAGCC 3360
Db 3355 TGTGCGGTTGAGAGGCTGCAAGAGATCTGGAACCAAGAAACAGAGCAGGCGAGAGCC 3414
QY 3361 GATCAGCGGATCACCGAGTCTCGCAGGTGCTGAGGCTGAGGATGAAGAGCACAGGCT 3420
Db 3415 GATCAGCGGATCACCGAGTCTCGCAGGTGCTGAGGCTGAGGATGAAGAGCACAGGCT 3474
QY 3421 GAGATTTCTCGCTTGCAGCAGGCTCTCAAGAGACGAAGGCTGAAGGCCGAGAGCTCTCT 3480
Db 3475 GAGATTTCTCGCTTGCAGCAGGCTCTCAAGAGACGAAGGCTGAAGGCCGAGAGCTCTCT 3534
QY 3481 GACAAAGCTCAATGACCTGGAAGAACATGCTATGCTTGAATGAATGCCGGAAGCTTA 3540
Db 3535 GACAAAGCTCAATGACCTGGAAGAACATGCTATGCTTGAATGAATGCCGGAAGCTTA 3594
QY 3541 CAGCAAGAGCTGAGACTGGAACGAGACTCAACAGAGGCTTCTGGAAGAGCAAGCCAA 3600
Db 3595 CAGCAAGAGCTGAGACTGGAACGAGACTCAACAGAGGCTTCTGGAAGAGCAAGCCAA 3654
QY 3601 TTACAGACAGATGACCTGCAAGAAATCAATTTCCGCTGACTCAAGGACTGCAA 3660
Db 3655 TTACAGACAGATGACCTGCAAGAAATCAATTTCCGCTGACTCAAGGACTGCAA 3714
QY 3661 GAAGCTCTAAGTGGGGCTGATCTATCTGAAGACAAAGAGTGAAGCTTGGAGTATCAGCTG 3720
Db 3715 GAAGCTCTAAGTGGGGCTGATCTATCTGAAGACAAAGAGTGAAGCTTGGAGTATCAGCTG 3774
QY 3721 GAAGATTCAGGTTCTCTATTTCTCATGAAGAGGTGAAGTGAAGGACATATTTCTCAA 3780
Db 3775 GAAGATTCAGGTTCTCTATTTCTCATGAAGAGGTGAAGTGAAGGACATATTTCTCAA 3834
QY 3781 CAAACCAACTCATTTATTTTCTGCAAGCCAAATGCAACCACTGCTAAAAAGAAAAAG 3840

Db 3835 CAACCAAACTCATTTATTTCTGCAAGCCAAATGACCAAACTGCTMAAAGAAAAAG 3894
Qy 3841 GTTCTCTGCGATCAATAGACTGAAGTGGCCCTGAGAAAGAGAAAGTCCGTGTGCA 3900
Db 3895 GTTCTCTGCGATCAATAGACTGAAGTGGCCCTGAGAAAGAGAAAGTCCGTGTGCA 3954
Qy 3901 GAGCTAGAGAAAGCCCTTCAGAAAGCCCGCATTCAGAGTCCGGTCCCGCCGGAGAAAGCT 3960
Db 3955 GAGCTAGAGAAAGCCCTTCAGAAAGCCCGCATTCAGAGTCCGGTCCCGCCGGAGAAAGCT 4014
Qy 3961 GCCCACCAGAAAGCAAGGACCAACCAACCATTCAGAGGACCAAGGACGAGAGAG 4020
Db 4015 GCCCACCAGAAAGCAAGGACCAACCAACCATTCAGAGGACCAAGGACGAGAGAG 4074
Qy 4021 ATGCCCATGTCCTGCGATGTCGGTCCGACAGAGCAAGCCAGTCCCATGAGCTGTG 4080
Db 4075 ATGCCCATGTCCTGCGATGTCGGTCCGACAGAGCAAGCCAGTCCCATGAGCTGTG 4134
Qy 4081 GCCCCGCGCATCAGCCGAGAAAGAGTCTCACTCAGAGAAATTTAGTGGCGCTT 4140
Db 4135 GCCCCGCGCATCAGCCGAGAAAGAGTCTCACTCAGAGAAATTTAGTGGCGCTT 4194
Qy 4141 AAGGAACGATGCAACCAATATTCTCAGCGATTCAACGTAGAGACTGAACATGCGAGCC 4200
Db 4195 AAGGAACGATGCAACCAATATTCTCAGCGATTCAACGTAGAGACTGAACATGCGAGCC 4254
Qy 4201 ACAAAGTGTGTGTGTCTGAGATCCGTGCACTTTGAGCGCAGGATCCAAATGTCTC 4260
Db 4255 ACAAAGTGTGTGTGTCTGAGATCCGTGCACTTTGAGCGCAGGATCCAAATGTCTC 4314
Qy 4261 GAATGTAGAGTATGTGTACCCCAAGTGTCCAGCGCTTGGCCAGGCACTGTGGGCTTG 4320
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Db 4375 CTTGCTGAATATGCAACACTTCAACGAGGCTTCTGCGGTGCAAAATGAACTCCCA 4434
Qy 4381 GGTCTCCAGACCAAGAGCCCAAGAGAGCTTGTGCACTTGGAGGGTGAATGAAGTGGCC 4440
Db 4435 GGTCTCCAGACCAAGAGAGCCCAAGAGAGCTTGTGCACTTGGAGGGTGAATGAAGTGGCC 4494
Qy 4441 AGGAATPACAAAGAGAGCAAGAGGTGGAGACAGAAAGTACATTTGCTCTGGAGGATCA 4500
Db 4495 AGGAATPACAAAGAGAGCAAGAGGTGGAGACAGAAAGTACATTTGCTCTGGAGGATCA 4554
Qy 4501 AAAGTCTCATTTATGCAATGAAGCAGAGAGCTGAGACAGAGGCGGTGAGAAATTT 4560
Db 4555 AAAGTCTCATTTATGCAATGAAGCAGAGAGCTGAGACAGAGGCGGTGAGAAATTT 4614
Qy 4561 GAGCTGTGCTTCCGACGAGGAGTGTATCTATTCAATGTGCGTGTGGTCTTCCGAATC 4620
Db 4615 GAGCTGTGCTTCCGACGAGGAGTGTATCTATTCAATGTGCGTGTGGTCTTCCGAATC 4674
Qy 4621 GCAATATACGCCCAAGACAGATGTCATATCATATCTGAAGTGAATCTCACCCGACAC 4680
Db 4675 GCAATATACGCCCAAGACAGATGTCATATCATATCTGAAGTGAATCTCACCCGACAC 4734
Qy 4681 ACCTGTGCGCCCGGAGAAAGCCCTCTACTTGTAGCTCCGAGCTTCCCTGCAAAAGCGG 4740
Db 4735 ACCTGTGCGCCCGGAGAAAGCCCTCTACTTGTAGCTCCGAGCTTCCCTGCAAAAGCGG 4794
Qy 4741 TGGGTACCGCTTAAATCAATGTTGTGCGAGGTGGAGAGTTTCTAGGAGAAAGACAGAA 4800
Db 4795 TGGGTACCGCTTAAATCAATGTTGTGCGAGGTGGAGAGTTTCTAGGAGAAAGACAGAA 4854
Qy 4801 GCTGAATGCTAACTGTTTGGAAATCTCCCTGTCTAAATCTGGAAGTATGACCTTACAG 4860
Db 4855 GCTGAATGCTAACTGTTTGGAAATCTCCCTGTCTAAATCTGGAAGTATGACCTTACAG 4914
Qy 4861 ATGAATGACGCTGCTTCAAGTACCAAGTGTGTTGGTGGGCAACGAGAGAGGGCTC 4920
Db 4915 ATGAATGACGCTGCTTCAAGTACCAAGTGTGTTGGTGGGCAACGAGAGAGGGCTC 4974

Qy 4921 TACGCTGAAATGTCTTGAAGAAATCTCCCTAACCCATGTCCGAGAAATTGAGAGTCTTC 4980
Db 4975 TACGCTGAAATGTCTTGAAGAAATCTCCCTAACCCATGTCCGAGAAATTGAGAGTCTTC 5034
Qy 4981 CAATTTATTTATCAAGAGACTTGGAGAACTACTCATGATAGAGAGAGAGCGGCA 5040
Db 5035 CAATTTATTTATCAAGAGACTTGGAGAACTACTCATGATAGAGAGAGAGCGGCA 5094
Qy 5041 CTGTGTCTTGTGACGTGAAGAAAGTGAACAGTCCCTGGCCAGTCCCACTGTGCGC 5100
Db 5095 CTGTGTCTTGTGACGTGAAGAAAGTGAACAGTCCCTGGCCAGTCCCACTGTGCGC 5154
Qy 5101 CAGCCGACATCTCACCCCAATTTTGAAGCTGTCAAGGGCTGCGCACTGTGTGGGCA 5160
Db 5155 CAGCCGACATCTCACCCCAATTTTGAAGCTGTCAAGGGCTGCGCACTGTGTGGGCA 5214
Qy 5161 GCGAAGATTGAGAAAGCGGCTCTGATCTGTGACAGCCATGCCCAAGAAAGTGTATCTC 5220
Db 5215 GCGAAGATTGAGAAAGCGGCTCTGATCTGTGACAGCCATGCCCAAGAAAGTGTATCTC 5274
Qy 5221 CGCTAACAGAAACCTCAGCAATATCTGATCCGAGAAAGATAGAGACTCAGAGCC 5280
Db 5275 CGCTAACAGAAACCTCAGCAATATCTGATCCGAGAAAGATAGAGACTCAGAGCC 5334
Qy 5281 TGAAGCTGATTCACATTTACCAATTAAGTATCTCATTTGAAACCAATAAATCTACGAA 5340
Db 5335 TGAAGCTGATTCACATTTACCAATTAAGTATCTCATTTGAAACCAATAAATCTACGAA 5394
Qy 5341 ATGACATGAGAGAGATACAGCTCGAGAAATTCCTGATAGAAATGACCTTCTTGCA 5400
Db 5395 ATGACATGAGAGAGATACAGCTCGAGAAATTCCTGATAGAAATGACCTTCTTGCA 5454
Qy 5401 CTTGCTGTGTTTCCGCTCTTCCAAAGCTTCCCTGTCTCAATTCGAGAGTGAACAG 5460
Db 5455 CTTGCTGTGTTTCCGCTCTTCCAAAGCTTCCCTGTCTCAATTCGAGAGTGAACAG 5514
Qy 5461 GCAGGCGAGGAGAGAGTACTTGTGTGTTTCAAGAAATTTGAGTGTCTGTGATTC 5520
Db 5515 GCAGGCGAGGAGAGAGTACTTGTGTGTTTCAAGAAATTTGAGTGTCTGTGATTC 5574
Qy 5521 TACGAAAGATGATGCGGACACAGCATCTCAAGTGAATGCTTACTTGTGCTTGGC 5580
Db 5575 TACGAAAGATGATGCGGACACAGCATCTCAAGTGAATGCTTACTTGTGCTTGGC 5634
Qy 5581 TACAGAAACCCATCTGTTTGTGACCACTTCAACTCTCGAAGTAAATTGATCCAG 5640
Db 5635 TACAGAAACCCATCTGTTTGTGACCACTTCAACTCTCGAAGTAAATTGATCCAG 5694
Qy 5641 GCAAGCTCTCAGCAGAGGACCCCTGCGAGGATCTTGAACATCCCGAACCCGCGCTAC 5700
Db 5695 GCAAGCTCTCAGCAGAGGACCCCTGCGAGGATCTTGAACATCCCGAACCCGCGCTAC 5754
Qy 5701 CTGGGCTCTGCAATTTCTCAGAGAGGATTTACTTGGCTCTCATACAGATTAATTA 5760
Db 5755 CTGGGCTCTGCAATTTCTCAGAGAGGATTTACTTGGCTCTCATACAGATTAATTA 5814
Qy 5761 AGGGTCAATTTGCTGCAAGGAAACCTCGTGAAGAGTCCGAGCATGGAACCAACCGGGG 5820
Db 5815 AGGGTCAATTTGCTGCAAGGAAACCTCGTGAAGAGTCCGAGCATGGAACCAACCGGGG 5874
Qy 5821 CCGTCAACTCCGAGACAGCCCAACAGCAGGACCAACCAAGTACAAACAGACATC 5880
Db 5875 CCGTCAACTCCGAGACAGCCCAACAGCAGGACCAACCAAGTACAAACAGACATC 5934
Qy 5881 ACCAAGCGGTGGCTTCCAGCCAGCGCGCCGAAAGGCCAGCCACCCGAGAGCCA 5940
Db 5935 ACCAAGCGGTGGCTTCCAGCCAGCGCGCCGAAAGGCCAGCCACCCGAGAGCCA 5994
Qy 5941 AGCACACCCACCGCTACCGAGGAGGAGGAGCCAGAGTGGCGAGGAGCAAGTCTCTGGC 6000
Db 5995 AGCACACCCACCGCTACCGAGGAGGAGGAGCCAGAGTGGCGAGGAGCAAGTCTCTGGC 6054

Qy 6001 CGCCCCCTGAGACGAGAAAGTCCCGGCGGATCTACAGACGCGGAGAGAGCGGTCC 6060
Db 6055 CGCCCCCTGAGACGAGAAAGTCCCGGCGGATCTACAGACGCGGAGAGAGCGGTCC 6114
Qy 6061 CCGCGAGGCTGTTGAAGACAGACGAGGCGGCGCTGCGGAGCGCTGAGGACC 6120
Db 6115 CCGCGAGGCTGTTGAAGACAGACGAGGCGGCGCTGCGGAGCGCTGAGGACC 6174
Qy 6121 CCGCTGCTCCAGGTGAACAAGGTCTGGAGACCACTTCAGATATA 6165
Db 6175 CCGCTGCTCCAGGTGAACAAGGTCTGGAGACCACTTCAGATATA 6219

RESULT 4

US-10-618-941-1
; Sequence 1, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CANEBEDEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618, 941
; CURRENT FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395, 632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 8656
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-618-941-1

Query Match 99.7%; Score 6144; DB 18; Length 8656;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6160; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

Qy 1 ATGTTGAAGTTCAAAATATGAGGCGGAAATCCTTGATGCTGGTGTGATGAACCAT 60
Db 51 ATGTTGAAGTTCAAAATATGAGGCGGAAATCCTTGATGCTGGTGTGATGAACCAT 110
Qy 61 GCCAGCGGCGCTCCAGGCTGAATCTGTCTTCCAGGAGAAACCACTTATGACTCAA 120
Db 111 GCCAGCGGCGCTCCAGGCTGAATCTGTCTTCCAGGAGAAACCACTTATGACTCAA 170
Qy 121 CAGCAGATGCTCTCTCTTCCGAGAAAGGATATTAAGTCCCTTTGTTCTTTGAA 180
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Qy 298 AGAAGCTTGTAGGTGTGCTCACTTGTGTAAGTGAAGTGTGAAGAGAAAGCAAC 357
Db 351 AGAAGCTTGTAGGTGTGCTCACTTGTGTAAGTGAAGTGTGAAGAGAAAGCAAC 410
Qy 358 GGGGACATCTATGCTATGAAGATGAAGAAAGGCTTATTTAGGCCGAGAGCAAGT 417
Db 411 GGGGACATCTATGCTATGAAGATGAAGAAAGGCTTATTTAGGCCGAGAGCAAGT 470
Qy 418 TCAATTTTGAAGAGAGCGAACAATATCTGAGACCAAGCCGCTGATCCGCCAA 477
Db 471 TCAATTTTGAAGAGAGCGAACAATATCTGAGACCAAGCCGCTGATCCGCCAA 530
Qy 478 TTACAGTATGCTTTCAAGACCAAAATCACTTTATCTGATCAATATCAAGCTTGA 537
Db 537 TTACAGTATGCTTTCAAGACCAAAATCACTTTATCTGATCAATATCAAGCTTGA 590

Db 531 TTACAGTATGCTTTCAAGACCAAAATCACTTTATCTGATCAATATCAAGCTTGA 590
Qy 538 GGGGACATCTGCTCACTTTGAATAGATAGAGACCAAGTTAGTGAACCTGATACAG 597
Db 591 GGGGACATCTGCTCACTTTGAATAGATAGAGACCAAGTTAGTGAACCTGATACAG 650
Qy 598 TTTTACTAGCTGAGCTGATTTTGGCTTTCAAGAGCTTCACTGATGGGATAGTGCAT 657
Db 651 TTTTACTAGCTGAGCTGATTTTGGCTTTCAAGAGCTTCACTGATGGGATAGTGCAT 710
Qy 658 CGAGACATCAAGCCTGAGAACATTTCTGTTGACCGACAGACACATCAAGCTGTGGAT 717
Db 711 CGAGACATCAAGCCTGAGAACATTTCTGTTGACCGACAGACACATCAAGCTGTGGAT 770
Qy 718 TTTGATCTGCGCGAAATGAATTCACACAGATGATGCAATCCGATTTGG 777
Db 771 TTTGATCTGCGCGAAATGAATTCACACAGATGATGCAATCCGATTTGG 830
Qy 778 ACCCGAGTTACATGCTCTGAAAGTCTGATGTAAGACGGGATGGAAGAGCAC 837
Db 831 ACCCGAGTTACATGCTCTGAAAGTCTGATGTAAGACGGGATGGAAGAGCAC 890
Qy 838 TACGGCCTGAGCTGATGCTGTGCTGATGAGTGGGCTGATGATGATGATTTATGG 897
Db 891 TACGGCCTGAGCTGATGCTGTGCTGATGAGTGGGCTGATGATGATGATTTATGG 950
Qy 898 AGATCCCTCTGAGAGAGGACCTTGCAGAACCTTCAATACATTAATGAATTTTCAG 957
Db 951 AGATCCCTCTGAGAGAGGACCTTGCAGAACCTTCAATACATTAATGAATTTTCAG 1010
Qy 958 CGGTTTGAATTTCCAGATGACCCCAAGATGAGAGTGAATTTCTTATCTGATTTCA 1017
Db 1011 CGGTTTGAATTTCCAGATGACCCCAAGATGAGAGTGAATTTCTTATCTGATTTCA 1070
Qy 1018 AGCTGTGTGCGGCGCAAGAGAGACCTGAAGTTGAAGTCTTCTGCAATCTTTC 1077
Db 1071 AGCTGTGTGCGGCGCAAGAGAGACCTGAAGTTGAAGTCTTCTGCAATCTTTC 1130
Qy 1078 TTTCTTAAATTTGATGGAACCAATTCGTACTCTCTCCCTTCTGTTCCACCTTC 1137
Db 1131 TTTCTTAAATTTGATGGAACCAATTCGTACTCTCTCCCTTCTGTTCCACCTTC 1190
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Qy 1258 TCGTACAGCAAGGACCTGGGAAATTCGTGATGATCTGATCTGTGTTGTCGGGCTGAG 1317
Db 1311 TCGTACAGCAAGGACCTGGGAAATTCGTGATGATCTGATCTGTGTTGTCGGGCTGAG 1370
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Db 1371 TCCCTGCAAGACTAGCTCATGGAAGAAATTCATCAAAAGCAAAAGACTTCAAA 1430
Qy 1378 GACTCTAGAGCAAGTGTCAAGATGAGACAGAAATGACCCGGTTCAATCCGAGAGTG 1437
Db 1431 GACTCTAGAGCAAGTGTCAAGATGAGACAGAAATGACCCGGTTCAATCCGAGAGTG 1490
Qy 1438 TCAAGGTGAGAGGCTGTGTTAGTCAAGAGAGGTGAGCTGAAGGCTCTGAGACTCAG 1497
Db 1491 TCAAGGTGAGAGGCTGTGTTAGTCAAGAGAGGTGAGCTGAAGGCTCTGAGACTCAG 1550
Qy 1498 AGATCCCTCTGAGAGAGACTTGTCTACTACATCAAGATGCAAGTCAATTAACGA 1557
Db 1551 AGATCCCTCTGAGAGAGACTTGTCTACTACATCAAGATGCAAGTCAATTAACGA 1610
Qy 1558 AGTTGAGAGAGAGAGAGAGTGTCCAGAGAGATGACCAAGCACTGCACTTCTC 1617
Db 1611 AGTTGAGAGAGAGAGAGAGTGTCCAGAGAGATGACCAAGCACTGCACTTCTC 1670

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Db	1671	CATGATATCAAGAGACAAGCCCGAAGCTTCAAGAAATCAAGAGACGAGTACCAAGCT	1730
Qy	1678	CAGTGGAAAGAAATGAGCTTGATGATGAAATCACTTGGAAAGAGATCTTGTCTACAGAGA	1737
Db	1731	CAAGTGAAGAAATGAGCTTGATGATGAAATCACTTGGAAAGAGATCTTGTCTACAGAGA	1790
Qy	1738	AGACGAGTATCTTACGAATCTGAGCTGAGAGAGTCTCGGCTTGTCTGCTCAAGATTC	1797
Db	1791	AGACGAGTATCTTACGAATCTGAGCTGAGAGAGTCTCGGCTTGTCTGCTCAAGATTC	1850
Qy	1798	AAGCGGAAACCGACAGATGTGCATTAACCTGTTGAAGGCTTAAGATCAAGGAAAGCT	1857
Db	1851	AAGCGGAAACCGACAGATGTGCATTAACCTGTTGAAGGCTTAAGATCAAGGAAAGCT	1910
Qy	1858	GAAGTGGGGAATATTCGGAACCTGGAGAGATCAATTCGTGAGACACACTCAAAATTGAG	1917
Db	1911	GAAGTGGGGAATATTCGGAACCTGGAGAGATCAATTCGTGAGACACACTCAAAATTGAG	1970
Qy	1918	GAAGCTCAAGAGAACTGAGAGAGGCTGTAAAGCCAGACACGAGGCCACGAGCTGCTG	1977
Db	1971	GAAGCTCAAGAGAACTGAGAGAGGCTGTAAAGCCAGACACGAGGCCACGAGCTGCTG	2030
Qy	1978	CAGATATTCCTCCGACGAAAGAGCGGACCTGAGAGGAGCTGAGAGACCTGCAGAACCGA	2037
Db	2031	CAGAAATATCCGACGAGCAAGAGGAGCGGACCTGAGAGACCTGCAGAACCGA	2090
Qy	2038	GAGGATTTCTTGAAGGCAATCGAAGAAAGCTGGTGGAAAGCTGAGGAACGCGGCAATTC	2097
Db	2091	GAGGATTTCTTGAAGGCAATCGAAGAAAGCTGGTGGAAAGCTGAGGAACGCGGCAATTC	2150
Qy	2098	CTGGAGAACCAAGGTAAAGAGCTAGAGACCAATGAGCGGTAGAGAAACAGACTGAAGAT	2157
Db	2151	CTGGAGAACCAAGGTAAAGAGCTAGAGACCAATGAGCGGTAGAGAAACAGACTGAAGAT	2210
Qy	2158	GACATCCGACAAATATCCCAACAGATCCAGACAGATGCTGTAAATTTCTGAGCTGGAA	2217
Db	2211	GACATCCGACAAATATCCCAACAGATCCAGACAGATGCTGTGTAAATTTCTGAGCTGGAA	2270
Qy	2218	GAGAAACATCGGAGAGGCCCAAGTCTCAGCCCGACCTAGAGAGTGCACCTGAACAGAAA	2277
Db	2271	GAGAAACATCGGAGAGGCCCAAGTCTCAGCCCGACCTAGAGAGTGCACCTGAACAGAAA	2330
Qy	2278	GAGCAGCACTATGAGAGAAAGATTAAAGTGTGGCAATCAATGATTAAGAAAGACTGCGCT	2337
Db	2331	GAGCAGCACTATGAGAGAAAGATTAAAGTGTGGCAATCAATGATTAAGAAAGACTGCGCT	2390
Qy	2338	GACAAGAGAGACACTGAGAGACATGATGAGAGACACGAGGAGGAGGCCAATGAGAGGCG	2397
Db	2391	GACAAGAGAGACACTGAGAGACATGATGAGAGACACGAGGAGGAGGCCAATGAGAGGCG	2450
Qy	2398	AAAAATTCCTCAGCGAACAGAGGCGCATGATCAATGCTATGATATTCGAATCAGATCCCTG	2457
Db	2451	AAAAATTCCTCAGCGAACAGAGGCGCATGATCAATGCTATGATATTCGAATCAGATCCCTG	2510
Qy	2458	GAAAGAGAGATTGTGGAACTGTGTGAAGCCCAATAACTTGGACGAATATGACGCTTTTT	2517
Db	2511	GAAAGAGAGATTGTGGAACTGTGTGAAGCCCAATAACTTGGACGAATATGACGCTTTTT	2570
Qy	2518	AACCCAAAGAACATGAGAGGCCCAAGAGAGATGATTTCTGAACCTCAGGCAACAGAAATTT	2577
Db	2571	AACCCAAAGAACATGAGAGGCCCAAGAGAGATGATTTCTGAACCTCAGGCAACAGAAATTT	2630
Qy	2578	TACCTTGAGACACAGGCTGGAGAGTTGGAGGCCAGAACCGAAAACTGAGAGACAGCTG	2637
Db	2631	TACCTTGAGACACAGGCTGGAGAGTTGGAGGCCAGAACCGAAAACTGAGAGACAGCTG	2690
Qy	2638	GAGAAAGATCAAGCCCAAGACCAAGTGAAGAGATGGGCTGCTGGAACTTGGAGACAAAG	2697
Db	2691	GAGAAAGATCAAGCCCAAGACCAAGTGAAGAGATGGGCTGCTGGAACTTGGAGACAAAG	2750

QY	2698	TTGCGGAGGATCAGTCTVAGAGCAGAGAGCAGAAACTGGAGCTCAAGCCGCACTCA	2757
Db	2751	TTGCGGAGGATCAGTCTAGAGCAGAGAGCAGAAACTGGAGCTCAAGCCGCACTCA	2810
QY	2758	GAGCTACAGCTCTCCCTCGAGGAGGCGAGTCAAGTTGACAGCCCTGCAAGCTGCACGG	2817
Db	2811	GAGCTACAGCTCTCCCTCGAGGAGGCGAGTCAAGTTGACAGCCCTGCAAGCTGCACGG	2870
QY	2818	GGGGCCCTGAGAGCCAGCTTGCGCAGGCGGAAGACAGAGCTGGAAAGAGACCAAGAGAA	2877
Db	2871	GGGGCCCTGAGAGGCAAGCTTGCGCAGGCGGAAGACAGAGCTGGAAAGAGACCAAGAGAA	2930
QY	2878	GCTTGAAGAGAGATTCAGGCACTCAGCGCACATAGAGATGAATTCAGCGCAAAATTTGAT	2937
Db	2931	GCTTGAAGAGAGATTCAGGCACTCAGCGCACATAGAGATGAATTCAGCGCAAAATTTGAT	2990
QY	2938	GCTCTTGGTAAAGGCTGTACTGTATTCACACCTGGAGGAGCAGCTTAAACCACTGACC	2997
Db	2991	GCTCTTGGTAAAGGCTGTACTGTATTCACACCTGGAGGAGCAGCTTAAACCACTGACC	3050
QY	2998	GAGGACAAAGCTGAATCAACAAACCAAACTTCTACTGTTGCATAACCACTGCATGAGAGCT	3057
Db	3051	GAGGACAAAGCTGAATCAACAAACCAAACTTCTACTGTTGCATAACCACTGCATGAGAGCT	3110
QY	3058	TCTGGCGCCAAAGCAGAGATTGTACAACTCGGAAGTGAATGAGCACTCTCCGCGGAG	3117
Db	3111	TCTGGCGCCAAAGCAGAGATTGTACAACTCGGAAGTGAATGAGCACTCTCCGCGGAG	3170
QY	3118	ATCAGGGAACGAGAGATGACAGCTTACCAGCCAGAACCAACGATGAGGCTCTGAGAAC	3177
Db	3171	ATCAGGGAACGAGAGATGACAGCTTACCAGCCAGAACCAACGATGAGGCTCTGAGAAC	3230
QY	3178	ACGTGCACCATGTCTGGAGAGAACAGATCATGATTGGAGGCCCTTAAACGATGAGCTCTA	3237
Db	3231	ACGTGCACCATGTCTGGAGAGAACAGATCATGATTGGAGGCCCTTAAACGATGAGCTCTA	3290
QY	3238	GAATAAAGCGGCAAGTGGAGGAGCCTGAGAGAGCGTCTCGGATGATGAGAAATCCAGTTT	3297
Db	3291	GAATAAAGCGGCAAGTGGAGGAGCCTGAGAGAGCGTCTCGGATGATGAGAAATCCAGTTT	3350
QY	3298	GAGGTCCGGGTTTCAGAGCTGCAAGGATGTGTGACACCGAAGAACAGACGAGGCGAGA	3357
Db	3351	GAGGTCCGGGTTTCAGAGCTGCAAGGATGTGTGACACCGAAGAACAGACGAGGCGAGA	3410
QY	3358	GCCGATCAGCGGATTCACCGAGTCTCGCAGGCTGTGAGGCTGCGAGTGAAGAGACCAAG	3417
Db	3411	GCCGATCAGCGGATTCACCGAGTCTCGCAGGCTGTGAGGCTGCGAGTGAAGAGACCAAG	3470
QY	3418	GCTGAGATTTCGCTCTGCAGCAGGCTCTAAAGAGCAGAAAGCTGAAGGCCGAGAGCTTC	3477
Db	3471	GCTGAGATTTCGCTCTGCAGCAGGCTCTAAAGAGCAGAAAGCTGAAGGCCGAGAGCTTC	3530
QY	3478	TCTGACAAAGCTCAATGACCTGGAGAGAGACATGCTATGCTTGAATGAATGCCCGAAGC	3537
Db	3531	TCTGACAAAGCTCAATGACCTGGAGAGAGACATGCTATGCTTGAATGAATGCCCGAAGC	3590
QY	3538	TTACAGAGAAAGCTGAGAGCTGAAACGAGACTCAACAGAGGCTTTCGAAAGGCAAGCC	3597
Db	3591	TTACAGAGAAAGCTGAGAGCTGAAACGAGACTCAACAGAGGCTTTCGAAAGGCAAGCC	3650
QY	3598	AAATTACAGAGCAGATGAGACTTGCAGAAAAATCACTTTCCGTCTGACTCAAGACTG	3657
Db	3651	AAATTACAGAGCAGATGAGACTTGCAGAAAAATCACTTTCCGTCTGACTCAAGACTG	3710
QY	3658	CAAGAGCTTAGATCGGCTGATCTATCTGAGAGCAGAAAGAGTGACTTGGAGTACAG	3717
Db	3711	CAAGAGCTTAGATCGGCTGATCTATCTGAGAGCAGAAAGAGTGACTTGGAGTACAG	3770
QY	3718	CTGGAAGAAACATCAAGGTTCTCTATTTCTCATGAAAGAGTGAATGGAAGCACTAATTTCT	3777
Db	3771	CTGGAAGAAACATCAAGGTTCTCTATTTCTCATGAAAGAGTGAATGGAAGCACTAATTTCT	3830
QY	3778	CAACCAAAACCAACTCATTTGATTTTCTGCAAGCCAAATAGGACCAACCTGCTAATAAAAGAA	3837

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Qy 3838 AAGGTCCTCTGAGTACAAATGAGCTGAAGCTGGCCCTGAGAGAGAAAGCTCGCTGT 3897
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Qy 3898 GCAGAGCTAAGAGAGAGCCCTTCAGAGAGACCCGATCGAGCTCCGGTCCCGCGGAGAA 3957
Db 3951 GCAGAGCTAAGAGAGAGCCCTTCAGAGAGACCCGATCGAGCTCCGGTCCCGCGGAGAA 4010
Qy 3958 GCGGCCCAACCGCAAGAGAGAGAGCAACCCATCCAGCCAGGCAACCGGAGGAG 4017
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Db 5031 TTCCAAATTTATTTATTCAG 5090
Qy 5038 GCACTGTGCTTGTGAG 5097
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Db 5631 GCTTACAG 5690
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RESULT 5
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GENERAL INFORMATION:
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APPLICANT: Stone, David
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APPLICANT: Ellerman, Karen
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APPLICANT: Shimkets, Richard A.
TITLE OF INVENTION: No. US20040043926A1 Proteins and Nucleic Acids Encoding Same
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NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 6189
TYPE: DNA
ORGANISM: Homo sapiens

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Query Match 99.3%; Score 6121.8; DB 11; Length 6189;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 6145; Conservative 0; Mismatches 17; Indels 3; Gaps 1;
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Db 301 AGTCTGTAGTGTGCTGCTCACTTGTGTAAGTGAAGTGAAGAGAAAGCAACCGG 360
QY 361 GACATCTATGCTATGAAGATGAAGAAAGGCTTTATTTGGCCAGAGAGAGTTTCA 420
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RESULT 6
US-10-262-511-1
Sequence 1, Application US/10262511
Publication No. US20040038223A1

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APPLICANT: Miller, Isabelle
APPLICANT: Peyman, John A.
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APPLICANT: Yu, Jinfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Saeha)
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APPLICANT: Spytek, Kimberly A.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda

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APPLICANT: Caterton, Elina
APPLICANT: Ji, Weizhen
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APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
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APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
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LENGTH: 6189
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(6159)
US-10-262-511-1

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Query Match 99.3%; Score 6121.8; DB 17; Length 6189;
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RESULT 7
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; GENERAL INFORMATION:
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; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
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NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 6201
TYPE: DNA
ORGANISM: Homo sapiens
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Query Match 99.0%; Score 6105.4; DB 11; Length 6201;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 6131; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

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QY 4021 ATGCGCATGTCGCGCATGTGTGCGGTGCGCAAGAGCCAGCCCATGAGAGCTGCTG 4080
| | | | |

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GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Miller, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
APPLICANT: Guo, Xiaojia (Sasha)
APPLICANT: Paturajan, Meera
APPLICANT: Spytek, Kimberly R.
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M.
APPLICANT: Ort, Tatiana
APPLICANT: Gorman, Linda
APPLICANT: Zernhusen, Bryan D.
APPLICANT: Anderson, David W.
APPLICANT: Zhong, Mei
APPLICANT: Catterton, Elina
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Pena, Carol E. A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OR INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuroSeqIst version 0.1
SEQ ID NO 13
LENGTH: 6201
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(6198)
US-10-262-511-13

Query Match 99.0%; Score 6105.4; DB 17; Length 6201;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 6131; Conservative 0; Mismatches 21; Indels 3; Gaps 1;
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|||||

Db 1 ATGTTGAAGTTCAATAATATGAGCGCGGAATCCTTTGATGCTGCTGCTGAACCAATT 60
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Qy 781 CCAGATTTACATGCTCCGTAAGTCTGATGATGATGATGATGATGATGATGATGATGAT 840
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QY 5641 GCAAGCTCTCAGACAGAGACCCCTGCGCAGCTACCTGAGCATCCCGAACCCGCTAC 5700
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QY 5701 CTGGGCTCTGCAAGAGGAACTCTGTAAGAGAGTCCGGCATCTGAACCAACCGGGGC 5760
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QY 5761 AGGATATTTGCTGCAAGAGGAACTCTGTAAGAGAGTCCGGCATCTGAACCAACCGGGGC 5820
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QY 5821 CCGTCCACCTCCCGCAGACGACCCCAACAGAGGACCCCACTGTAACAGAGCATC 5880
DB 5818 CCGTCCACCTCCCGCAGACGACCCCAACAGAGGACCCCACTGTAACAGAGCATC 5877
QY 5881 ACCAAGCGCGTGGCTCTCAGACGACCCGCGCCGAAAGGCCCAACCGGAGAGCCA 5940
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QY 5941 AGACACACCCCAACCGCTACCGCGAGAGGAGGAGCCGAGTGGCGAGGAGCAAGTCTCTGGC 6000
DB 5938 AGACACACCCCAACCGCTACCGCGAGAGGAGGAGCCGAGTGGCGAGGAGCAAGTCTCTGGC 5997
QY 6001 CGCCCTCTGAGAGAGAGAGATCCCGCGCGAGTACTAGCAAGAGAGAGAGCGGTCC 6060
DB 5998 CGCCCTCTGAGAGAGAGAGATCCCGCGCGAGTACTAGCAAGAGAGAGAGCGGTCC 6057
QY 6061 CCGCAGAGGCTGTTGAGAGACAGACAGAGAGGAGCGGTGCTGCGGAGCGCTGAGAGACC 6120
DB 6058 CCGCAGAGGCTGTTGAGAGACAGACAGAGAGGAGCGGTGCTGCGGAGCGCTGAGAGACC 6117
QY 6121 CCGCTGTCCAGGTAACAGAGTCTGGAGCAAGTC 6155
DB 6118 CCGCTGTCCAGGTAACAGAGTCTGGAGCAAGTC 6152

RESULT 9
US-10-028-946-3
Sequence 3, Application US/10028946
Publication No. US20020123622A1
GENERAL INFORMATION:

APPLICANT: Yu, Xuanhuan
APPLICANT: Miranda, Maricar
APPLICANT: Fridlie, Carl Johan
TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
FILE REFERENCES: LEX-0289-USA
CURRENT APPLICATION NUMBER: US/10/028,946
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: US 60/258,335
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5877
TYPE: DNA
ORGANISM: homo sapiens
US-10-028-946-3

Query Match 94.7%; Score 5837; DB 13; Length 5877;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGAAGTTCAAAATATGAGCGCGAATCTTTGATGCTGTGCTGTAACCATTT 60

DB 1 ATGTTGAAGTTCAAAATATGAGCGCGAATCTTTGATGCTGTGCTGTAACCATTT 60
QY 61 GCCAGCGGGGCTCCAGAGTGAATCTTTTCCAGAGGAGAAACACCTTTATGACTCAA 120
DB 61 GCCAGCGGGGCTCCAGAGTGAATCTTTTCCAGAGGAGAAACACCTTTATGACTCAA 120
QY 121 CAGCAGATGCTCTCTTTCCCGAAGAGGAGATTAAGATGCTCTTTGTTCTTTGAA 180
DB 121 CAGCAGATGCTCTCTTTCCCGAAGAGGAGATTAAGATGCTCTTTGTTCTTTGAA 180
QY 181 GAATGAGTACGCTGCTCTGATGAAGATTAAGCAAGTGAACAATTTGTCGGGAATAT 240
DB 181 GAATGAGTACGCTGCTCTGATGAAGATTAAGCAAGTGAACAATTTGTCGGGAATAT 240
QY 241 TCCGACACCAATAGCTAGTTACAGAGCTCCAGCTTCCGCAAGAGACTTCGAAGTCAGA 300
DB 241 TCCGACACCAATAGCTAGTTACAGAGCTCCAGCTTCCGCAAGAGACTTCGAAGTCAGA 300
QY 301 AGTCTTGAAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTGAAGAGAAAGCAACCGG 360
DB 301 AGTCTTGAAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTGAAGAGAAAGCAACCGG 360
QY 361 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTTGGCCAGAGAGAGTTTCA 420
DB 361 GACATCTATGCTATGAAGTGAAGAGAGAGGCTTTATTTGGCCAGAGAGAGTTTCA 420
QY 421 TTTTGAAGAGAGGAGCAATATATCTGAGAGCAAGCCGCTGATCCCGCAATTA 480
DB 421 TTTTGAAGAGAGGAGCAATATATCTGAGAGCAAGCCGCTGATCCCGCAATTA 480
QY 481 CAGTATGCTTTTCAAGACAAATATCACTTTATCTGATGATGATATACGCTGAGAGG 540
DB 481 CAGTATGCTTTTCAAGACAAATATCACTTTATCTGATGATGATATACGCTGAGAGG 540
QY 541 GACTTCTGCTCACTTTTGAATGATATGAGAGCACTTATGATTAATTAACCTGATACGTTT 600
DB 541 GACTTCTGCTCACTTTTGAATGATATGAGAGCACTTATGATTAATTAACCTGATACGTTT 600
QY 601 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGCTTCACTGATGATGATGATGATGATGAT 660
DB 601 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGCTTCACTGATGATGATGATGATGATGAT 660
QY 661 GACATCAAGCTGAGAAATCTCTGTTGACCGCAGACACATCAAGCTGATGATTTT 720
DB 661 GACATCAAGCTGAGAAATCTCTGTTGACCGCAGACACATCAAGCTGATGATTTT 720
QY 721 GATCTGCGCGAAATGAAATTCAAACAGATGATGATGATGATGATGATGATGATGATGAT 780
DB 721 GATCTGCGCGCGAAATGAAATTCAAACAGATGATGATGATGATGATGATGATGATGATGAT 780
QY 781 CCAATTAATGATGCTCTGTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 840
DB 781 CCAATTAATGATGCTCTGTAAGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 841 GGCCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 GGCCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 TCCCTCTGAGAGAGGAACTCTGCGAAGCTTCAATTAATTAATTAATTAATTAATTAATTAAT 960
DB 901 TCCCTCTGAGAGAGGAACTCTGCGAAGCTTCAATTAATTAATTAATTAATTAATTAATTAAT 960
QY 961 TTTTGAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 961 TTTTGAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
QY 1021 TTTTGAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080
DB 1021 TTTTGAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080
QY 1081 TTTTGAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1140

Db 1081 TCTAAATGTGACGGAACAACATTGCTAATCTCTCCCTCCCTGTTCCACCCCTCAAG 1140
Qy 1141 TCTGACATGACATCTCCCAATTTTGTATGAACGAGAAAGATTGCGGTTTCATCCCTCT 1200
Db 1141 TCTGACATGACATCTCCCAATTTTGTATGAACAAGAAAGATTGCGGTTTCATCTCTCT 1200
Qy 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAACAACCTCCGTTTGTGGGGTTTTCG 1260
Db 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTCGGGTGAACAACCTCCGTTTGTGGGGTTTTCG 1260
Qy 1261 TACAGCAGGCACTGCGGATTTCTTTGTAGATCTGAGTCTGTGTGTGCGGCTTGAATCC 1320
Db 1261 TACAGCAGGCACTGCGGATTTCTTTGTAGATCTGAGTCTGTGTGTGCGGCTTGAATCC 1320
Qy 1321 CTTGCCAAGCTTACTGCTCATGAGAAAGAACTTCTCATCAAAAGCAAGACTTACAGAC 1380
Db 1321 CTTGCCAAGCTTACTGCTCATGAGAAAGAACTTCTCATCAAAAGCAAGACTTACAGAC 1380
Qy 1381 TCTCAGGACAAGTGTCACAAGATGAGCAGGAAATGACCCGGTTACATTCGGAAGTGTCA 1440
Db 1381 TCTCAGGACAAGTGTCACAAGATGAGCAGGAAATGACCCGGTTACATTCGGAAGTGTCA 1440
Qy 1441 GAGGTGAGGCTGTGCTTAAGTCAAGAGAGGTGAGGCTTGAAGGCTTGAAGTCAAGAGA 1500
Db 1441 GAGGTGAGGCTGTGCTTAAGTCAAGAGAGGTGAGGCTTGAAGGCTTGAAGTCAAGAGA 1500
Qy 1501 TCCCTCTCTGAGCAGACCTTGTCTACCTACATCAAGATGACAGTACTTAAAGCGAAGT 1560
Db 1501 TCCCTCTCTGAGCAGACCTTGTCTACCTACATCAAGATGACAGTACTTAAAGCGAAGT 1560
Qy 1561 TTGGAGCAAGCAGGATGAGGTGTCCAGAGAGATGACAAGCACTGACGCTTTCAT 1620
Db 1561 TTGGAGCAAGCAGGATGAGGTGTCCAGAGAGATGACAAGCACTGACGCTTTCAT 1620
Qy 1621 GATATCAGAGCAGAGCCCGAAGCTTCAAGAAATCAAAAGCAGAGTACAGGCTCAA 1680
Db 1621 GATATCAGAGCAGAGCCCGAAGCTTCAAGAAATCAAAAGCAGAGTACAGGCTCAA 1680
Qy 1681 GTGGAGAAATGAGTTGATGATGAATCAAGTTGAAAGAGATCTTGTCTCAGCAAGAGA 1740
Db 1681 GTGGAGAAATGAGTTGATGATGAATCAAGTTGAAAGAGATCTTGTCTCAGCAAGAGA 1740
Qy 1741 CGGAGTATCTTACGAATCTGAGCTGAGAGAGTCTCGGTTGCTCTGAAGAAATTCAG 1800
Db 1741 CGGAGTATCTTACGAATCTGAGCTGAGAGAGTCTCGGTTGCTCTGAAGAAATTCAG 1800
Qy 1801 CGGAAAGCAGAGATGTGAGCATTAACCTGTTGAAGGCTTAAGGCTAAGGGAAGCTTGA 1860
Db 1801 CGGAAAGCAGAGATGTGAGCATTAACCTGTTGAAGGCTTAAGGCTAAGGGAAGCTTGA 1860
Qy 1861 GTGGAGAAATGAGTGAATCTGAGAAATGATGCTGAGCAGAGCTCAAAATTCAGAG 1920
Db 1861 GTGGAGAAATGAGTGAATCTGAGAAATGATGCTGAGCAGAGCTCAAAATTCAGAG 1920
Qy 1921 GTCCAAAGAAATCTGAGAAAGGCTGTTAAAGCCAGACCGAGGCTCAGAGCTTGCAG 1980
Db 1921 GTCCAAAGAAATCTGAGAAAGGCTGTTAAAGCCAGACCGAGGCTCAGAGCTTGCAG 1980
Qy 1981 AATATCCGCAAGCAGAGCAGCCGAGAGGAGCTGAGAAAGCTGAGAAACCGAGAG 2040
Db 1981 AATATCCGCAAGCAGAGCAGCCGAGAGGAGCTGAGAAAGCTGAGAAACCGAGAG 2040
Qy 2041 GATTCTTCTGAGGATCAAGAAAGAAAGCTGTGAGAGCTGAGAGAGCCGCCATTTCTCG 2100
Db 2041 GATTCTTCTGAGGATCAAGAAAGAAAGCTGTGAGAGCTGAGAGAGCCGCCATTTCTCG 2100
Qy 2101 GAGAACAAAGTAAAGAGACTAGAGACATGAGAGCTGAGAGAAACAGACTGAAGGTGAC 2160
Db 2101 GAGAACAAAGTAAAGAGACTAGAGACATGAGAGCTGAGAGAAACAGACTGAAGGTGAC 2160
Qy 2161 ATCCAGACAAATCCCAACAGATCCAGAGAGTGGCTGATTAATTCGAGGCTCGAAGAG 2220
Db 2161 ATCCAGACAAATCCCAACAGATCCAGAGAGTGGCTGATTAATTCGAGGCTCGAAGAG 2220

Qy 2221 AAAATCGGAGGCCCAAGTCTCAGCCAGCACCTAGAAAGTGAACCTGAAGCAGAAAGAG 2280
Db 2221 AAAATCGGAGGCCCAAGTCTCAGCCAGCACCTAGAAAGTGAACCTGAAGCAGAAAGAG 2280
Qy 2281 CAGCATTATGAGAAATTAAGTTAAGTTGAGCAATCAGTAAAGAAAGCTGGCTGAC 2340
Db 2281 CAGCATTATGAGAAATTAAGTTAAGTTGAGCAATCAGTAAAGAAAGCTGGCTGAC 2340
Qy 2341 AAGAGACATCTGAGAAACATGATCAGAGACACAGAGAGAGGCCCATGAGAGGCGAAA 2400
Db 2341 AAGAGACATCTGAGAAACATGATCAGAGACACAGAGAGAGGCCCATGAGAGGCGAAA 2400
Qy 2401 ATTCTAGCGAACAAGAGCGATGATCATGATGATGATGATGATGATGATGATGATGATG 2460
Db 2401 ATTCTAGCGAACAAGAGCGATGATCATGATGATGATGATGATGATGATGATGATGATG 2460
Qy 2461 CAGAGATTTGTGAACCTGTCTGAAGCCAAATTAACCTTGACCAATATGCAATCTTTTACC 2520
Db 2461 CAGAGATTTGTGAACCTGTCTGAAGCCAAATTAACCTTGACCAATATGCAATCTTTTACC 2520
Qy 2521 CAAAGGAACATGAAGGCCCAAGAGATGATTTCTGAACCTCAGGCAACAGAAATTTTAC 2580
Db 2521 CAAAGGAACATGAAGGCCCAAGAGATGATTTCTGAACCTCAGGCAACAGAAATTTTAC 2580
Qy 2581 CTGGAGACACAGGCTGGAAAGTTGAGGCTCAGAACCGAAAATGAGAGAGCAGCTGAG 2640
Db 2581 CTGGAGACACAGGCTGGAAAGTTGAGGCTCAGAACCGAAAATGAGAGAGCAGCTGAG 2640
Qy 2641 AAGATGAGCACAACACACACAGTGAACAAGATTCGGCTCTGGAATCTGAGACCAATTTG 2700
Db 2641 AAGATGAGCACAACACACACAGTGAACAAGATTCGGCTCTGGAATCTGAGACCAATTTG 2700
Qy 2701 CCGGAGGTGATCTAGAGACAGAGCAGAGAACTGAACTCAAGGCCAGCTCAGAGAG 2760
Db 2701 CCGGAGGTGATCTAGAGACAGAGCAGAGAACTGAACTCAAGGCCAGCTCAGAGAG 2760
Qy 2761 CTACAGCTCTCCCTGAGAGGCGCGAGTCAAGTTGACAGCCCTGACGAGCTGACCGGCG 2820
Db 2761 CTACAGCTCTCCCTGAGAGGCGCGAGTCAAGTTGACAGCCCTGACGAGCTGACCGGCG 2820
Qy 2821 GCCCTGAGAGGCAAGCTTGGCAGAGGAGACAGAGCTGGAAGAGCCACAGAGAGCT 2880
Db 2821 GCCCTGAGAGGCAAGCTTGGCAGAGGAGACAGAGCTGGAAGAGCCACAGAGAGCT 2880
Qy 2881 GAAAGAGATCAGGCACTCAGGCACTAGAGATGAAGTCAAGGCAAAATTTGATGCT 2940
Db 2881 GAAAGAGATCAGGCACTCAGGCACTAGAGATGAAGTCAAGGCAAAATTTGATGCT 2940
Qy 2941 GTTCTGAACGCTGTATCTGTATCAACAGCTGAGAGAGCAGCTAAACAGCTGACCGAG 3000
Db 2941 GTTCTGAACGCTGTATCTGTATCAACAGCTGAGAGAGCAGCTAAACAGCTGACCGAG 3000
Qy 3001 GACAAAGCTGAACCTCAACCAAACTTCTTCTGAACTGATGAGGCTTCT 3060
Db 3001 GACAAAGCTGAACCTCAACCAAACTTCTTCTGAACTGATGAGGCTTCT 3060
Qy 3061 GCGGCAACGAGAGATTTGAACAATGAGAGTGAAGTGAACATCTCGGCGGAGATC 3120
Db 3061 GCGGCAACGAGAGATTTGAACAATGAGAGTGAAGTGAACATCTCGGCGGAGATC 3120
Qy 3121 ACGGAACGAGAGATCAGCTTACAGCCAGCAAGCAAAAGATGAGGCTTGAAGACAG 3180
Db 3121 ACGGAACGAGAGATCAGCTTACAGCCAGCAAGCAAAAGATGAGGCTTGAAGACAG 3180
Qy 3181 TGCAACATGCTGAGAGAAACAGGTCAATGATTTGAGGCTTGAAGAGTCTGAGAA 3240
Db 3181 TGCAACATGCTGAGAGAAACAGGTCAATGATTTGAGGCTTGAAGAGTCTGAGAA 3240
Qy 3241 AAAAGCGGAGTGGAGGCTCGAGAGGCGCTGAGGATGAGAAATCCAGTTTGAAG 3300
Db 3241 AAAAGCGGAGTGGAGGCTCGAGAGGCGCTGAGGATGAGAAATCCAGTTTGAAG 3300

QY 3301 TGTGGGTTGAGAGCTGCAGAGATGCTGGAACCCGAGAAACAGAGACAGGCGAGAGCC 3360
DB 3301 TGTGGGTTGAGAGCTGCAGAGATGCTGGAACCCGAGAAACAGAGACAGGCGAGAGCC 3360
QY 3361 GATCAGCGAGTCAACGAGTCTCCGACAGTGTGAGAGCTGGCAGTGAAGAGACAAAGCT 3420
DB 3361 GATCAGCGAGTCAACGAGTCTCCGACAGTGTGAGAGCTGGCAGTGAAGAGACAAAGCT 3420
QY 3421 GAGATTCTGCTCTGCAGACAGGCTCTCAAGAGACAGAAAGCTGAGAGGCTCTCT 3480
DB 3421 GAGATTCTGCTCTGCAGACAGGCTCTCAAGAGACAGAAAGCTGAGAGGCTCTCT 3480
QY 3481 GACAACTCAATGACTCTGAGAGAGAGAGATGCTATGCTTGAATGAATGCCAAAGCTTA 3540
DB 3481 GACAACTCAATGACTCTGAGAGAGAGAGATGCTATGCTTGAATGAATGCCAAAGCTTA 3540
QY 3541 CAGAGAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGGCTTCTGAGAGAGCAAGCCAA 3600
DB 3541 CAGAGAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGGCTTCTGAGAGAGCAAGCCAA 3600
QY 3601 TTACAGCAGAGATGAGACTGTCAGAGAAATCAATTTCCGCTGACTCAAGAGACTGCA 3660
DB 3601 TTACAGCAGAGATGAGACTGTCAGAGAAATCAATTTCCGCTGACTCAAGAGACTGCA 3660
QY 3661 GAAGCTCTAAGTCCGGCTGATCTACTGAGAGACAGAAAGAAAGTGAAGTATCAAGCTG 3720
DB 3661 GAAGCTCTAAGTCCGGCTGATCTACTGAGAGACAGAAAGAAAGTGAAGTATCAAGCTG 3720
QY 3721 GAAAACTTCAAGTCTCTATTTCTCATGAAAAAGGTGAAAAATGAGAGCACTATTTCTCA 3780
DB 3721 GAAAACTTCAAGTCTCTATTTCTCATGAAAAAGGTGAAAAATGAGAGCACTATTTCTCA 3780
QY 3781 CAAACCAACTGATTTGATTTTCTGCAAGCCAAATGAGACCACTGCTAAAAAGAAAAAG 3840
DB 3781 CAAACCAACTGATTTGATTTTCTGCAAGCCAAATGAGACCACTGCTAAAAAGAAAAAG 3840
QY 3841 GTTCTCTGAGATCAATGAGCTGAGCTGGCTTGAGAAAGAAAGTCTGCTGTGCA 3900
DB 3841 GTTCTCTGAGATCAATGAGCTGAGCTGGCTTGAGAAAGAAAGTCTGCTGTGCA 3900
QY 3901 GAGCTAAGAGAGCCCTTCAAGAAACCCGATTCGAGCTCCGCTCCGCGAGAGAGAGCT 3960
DB 3901 GAGCTAAGAGAGCCCTTCAAGAAACCCGATTCGAGCTCCGCTCCGCGAGAGAGAGCT 3960
QY 3961 GCCACCGCAAAAGCAGACCAACCCATCCAGCCAGGCAACGCGAGGCAAG 4020
DB 3961 GCCACCGCAAAAGCAGACCAACCCATCCAGCCAGGCAACGCGAGGCAAG 4020
QY 4021 ATGCGCATGTCGCGCATCTGTCGAGTCCGAGAGCAGAGCCAGTGCATGAGCTGCTG 4080
DB 4021 ATGCGCATGTCGCGCATCTGTCGAGTCCGAGAGCAGAGCCAGTGCATGAGCTGCTG 4080
QY 4081 GCCCGGCAATCCAGCCGAGAAAGAGTCTTCACTCAAGAGAAATTAATGTCGCGCTT 4140
DB 4081 GCCCGGCAATCCAGCCGAGAAAGAGTCTTCACTCAAGAGAAATTAATGTCGCGCTT 4140
QY 4141 AAGGAGAGCAGTGCACCAATATTCCTCAACGATTCGAAAGAGAGCTGGAACATGCGAGC 4200
DB 4141 AAGGAGAGCAGTGCACCAATATTCCTCAACGATTCGAAAGAGAGCTGGAACATGCGAGC 4200
QY 4201 ACAAGT 4260
DB 4201 ACAAGT 4260
QY 4261 GAATGTCAAGT 4320
DB 4261 GAATGTCAAGT 4320
QY 4321 CTGT 4380
DB 4321 CTGT 4380
QY 4381 GGTCTCCAGACCAAGAGCCAGAGAGCTTGTGCACTGTGAAGGAGTGAAGGTGCTC 4440

DB 4381 GGTCTCCAGACCAAGAGCCAGAGAGCTTGTGCACTGTGAAGGAGTGAAGGTGCTC 4440
QY 4441 AGGAATTAACAAACGAGAGCAGCAAGCTGAGAGAGAGATGATTTGCTTGAAGGATCA 4500
DB 4441 AGGAATTAACAAACGAGAGCAGCAAGCTGAGAGAGAGATGATTTGCTTGAAGGATCA 4500
QY 4501 AAAGTCTCAATTTATGACAAATGAAGCAGAGAAAGCTGACAGAGCCGCTGGAAGATTT 4560
DB 4501 AAAGTCTCAATTTATGACAAATGAAGCAGAGAAAGCTGACAGAGCCGCTGGAAGATTT 4560
QY 4561 GAGCTGTGCTTCCGAGCGGAGATGATCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTG 4620
DB 4561 GAGCTGTGCTTCCGAGCGGAGATGATCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTG 4620
QY 4621 GCAAAATACAGCCAAAGCAGATGTCCTCATATCTGAAGATGAGATCTCAACCCGACACC 4680
DB 4621 GCAAAATACAGCCAAAGCAGATGTCCTCATATCTGAAGATGAGATCTCAACCCGACACC 4680
QY 4681 ACCGTGAGCCGAGAGAACCTCTACTGCTGAGCTCCAGCTTCCCTGACAAACAGCGC 4740
DB 4681 ACCGTGAGCCGAGAGAACCTCTACTGCTGAGCTCCAGCTTCCCTGACAAACAGCGC 4740
QY 4741 TGGGTACCGGCTTGAATGATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4800
DB 4741 TGGGTACCGGCTTGAATGATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4800
QY 4801 GCTGATGCTAACTGCTGTGAAACTCCCTGCTGAACTGGAAGGTGATGACCTGAGAC 4860
DB 4801 GCTGATGCTAACTGCTGTGAAACTCCCTGCTGAACTGGAAGGTGATGACCTGAGAC 4860
QY 4861 ATGAACTGACGCTGCTTCACTGAGCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920
DB 4861 ATGAACTGACGCTGCTTCACTGAGCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920
QY 4921 TAGGCTTGAATGCTTGAAGAACTCCCTTAACCAATGCTCCAGGAATTTGAGAGCTTTC 4980
DB 4921 TAGGCTTGAATGCTTGAAGAACTCCCTTAACCAATGCTCCAGGAATTTGAGAGCTTTC 4980
QY 4981 CAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5040
DB 4981 CAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5040
QY 5041 CTGTGTCTGT 5100
DB 5041 CTGTGTCTGT 5100
QY 5101 CAGCCGCAATCTCAACCAATTTTGAAGCTGTCAAGGCTGCACTGTGTGTGTGTGTGTGT 5160
DB 5101 CAGCCGCAATCTCAACCAATTTTGAAGCTGTCAAGGCTGCACTGTGTGTGTGTGTGTGT 5160
QY 5161 GGCAGATGAGAACGGGCTCTGATCTGTGACGCAATGCGCAGCAAGTGTGATTTCTC 5220
DB 5161 GGCAGATGAGAACGGGCTCTGATCTGTGACGCAATGCGCAGCAAGTGTGATTTCTC 5220
QY 5221 CGCTACAAGAAACCTCAGCAAAATATCTGATCCGAAAGAGATAGAGACTCAGAGCC 5280
DB 5221 CGCTACAAGAAACCTCAGCAAAATATCTGATCCGAAAGAGATAGAGACTCAGAGCC 5280
QY 5281 TGCACTGTATTCATCTTCACTTACAGTATCTCATTTGGAACCAATTAATTTTACGAA 5340
DB 5281 TGCACTGTATTCATCTTCACTTACAGTATCTCATTTGGAACCAATTAATTTTACGAA 5340
QY 5341 ATGCACTGAAGAGATGACAGCTGAGAGATTCCTGATTAAGATGACATTTCTTGGCA 5400
DB 5341 ATGCACTGAAGAGATGACAGCTGAGAGATTCCTGATTAAGATGACATTTCTTGGCA 5400
QY 5401 CTGT 5460
DB 5401 CTGT 5460
QY 5461 GCAAGGAGAGAGAGATCTGT 5520

Db 5461 GCAGGCGAGGAGAGTACTGTGCTGCTTCCACGAATTGGAGTGTGTGATTTCT 5520
Qy 5521 TACGGAAGAGCTAGCCGACAGAGATCTCAAGTGAAGTGGCTTACTTTGGCTTGGCC 5580
Db 5521 TACGGAAGAGCTAGCCGACAGAGATCTCAAGTGAAGTGGCTTACTTTGGCTTGGCC 5580
Qy 5581 TACGGAAGAGCTAGCTTGTGTGTGACCACTTCAACTCACTGAGTAATTGAATCCAG 5640
Db 5581 TACGGAAGAGCTTACTTGTGTGTGACCACTTCAACTCACTGAGTAATTGAATCCAG 5640
Qy 5641 GCAGCTCTCAGAGGAGGAGCCCTGCGGAGCGTACCTGACATCCGGAACCCGCGTAC 5700
Db 5641 GCAGCTCTCAGAGGAGGAGCCCTGCGGAGCGTACCTGACATCCGGAACCCGCGTAC 5700
Qy 5701 CTGGGCGCTGCTGCTTCTCTCAGAGCGATTTACTTGGCTGCTCATACAGATAAATTA 5760
Db 5701 CTGGGCGCTGCTGCTTCTCTCAGAGCGATTTACTTGGCTGCTCATACAGATAAATTA 5760
Qy 5761 AGGGTCATTTGCTGCTGAGGAGAACTGTGAAGAGTCCGCACTGAAACCCGAGGCG 5820
Db 5761 AGGGTCATTTGCTGCTGAGGAGAACTGTGAAGAGTCCGCACTGAAACCCGAGGCG 5820
Qy 5821 CCGTCCACCTCCGCGAG 5837
Db 5821 CCGTCCACCTCCGCGAG 5837

RESULT 10
US-10-791-666-3
; Sequence 3, Application US/10791666
; Publication No. US20040209297A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanhuan
; APPLICANT: Miranda, Maricar
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/791,666
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5877
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-791-666-3

Query Match 94.7%; Score 5837; DB 18; Length 5877;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTTAAAGTTCAAATATGAGGCGGAAATCTTTGATGCTGTGCTGTAACCCATT 60
Db 1 ATGTTAAAGTTCAAATATGAGGCGGAAATCTTTGATGCTGTGCTGTAACCCATT 60
Qy 61 GCCAGCGCGGAGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCTTTATGACTCA 120
Db 61 GCCAGCGCGGAGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCTTTATGACTCA 120
Qy 121 CAGCAGATGTCTCTCTTCCGAGAAAGGATATTAGATGCTCTTTGTTCTCTTTGAA 180
Db 121 CAGCAGATGTCTCTCTTCCGAGAAAGGATATTAGATGCTCTCTTTGTTCTCTTTGAA 180
Qy 181 GAATGAGTCAAGCTGCTCTGATGAAGATTAAAGCACTGAGCAACTTTGTCCGGAAGTAT 240
Db 181 GAATGAGTCAAGCTGCTCTGATGAAGATTAAAGCACTGAGCAACTTTGTCCGGAAGTAT 240
Qy 241 TCCGACACATGATGATTTAGAGAGCTCCAGCTTCGCAAGAGACTTCCAGAGTCA 300
Db 241 TCCGACACATGATGATTTAGAGAGCTCCAGCTTCGCAAGAGACTTCCAGAGTCA 300

Db 241 TCCGACACATGATGATTTAGAGAGCTCCAGCTTCGCAAGAGACTTCCAGAGTCA 300
Qy 301 AGCTTTAGATTTGTGTGCTCACTTTGCTGAAGTGCAGGTGTGAAGAGAAAGCAACCGGG 360
Db 301 AGCTTTAGATTTGTGTGCTCACTTTGCTGAAGTGCAGGTGTGAAGAGAAAGCAACCGGG 360
Qy 361 GACATCTATGTATGAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 GACATCTATGTATGAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 TTTTGTGAG 480
Db 421 TTTTGTGAG 480
Qy 481 CAGTATGCTTTTCAAGCAAAATCACTTTATCTGTGCTCAAGTAATACAGCTTGAGGG 540
Db 481 CAGTATGCTTTTCAAGCAAAATCACTTTATCTGTGCTCAAGTAATACAGCTTGAGGG 540
Qy 541 GACTTGCTGCTCACTTTTGAATGATATGAGAGACAGTTAGATGAAAACCTGATACATTT 600
Db 541 GACTTGCTGCTCACTTTTGAATGATATGAGAGACAGTTAGATGAAAACCTGATACATTT 600
Qy 601 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGCTTCATGATGAGGATACGTGACATGA 660
Db 601 TACCTAGCTGAGCTGATTTTGGCTGTTCAAGGCTTCATGATGAGGATACGTGACATGA 660
Qy 661 GACATCAAGCTGAGAAATCTCTGTTGACCGACAGACACATCAAGCTGTGTGATTTT 720
Db 661 GACATCAAGCTGAGAAATCTCTGTTGACCGACAGACACATCAAGCTGTGTGATTTT 720
Qy 721 GATCTGCGCGGAAATGAATTTAAACAGATGTGTGAATGCCAACTCCGATTTGGAGCC 780
Db 721 GATCTGCGCGGAAATGAATTTAAACAGATGTGTGAATGCCAACTCCGATTTGGAGCC 780
Qy 781 CCAGATTACATGCTCTGTAAGTGTGACGTGATGAAAGGGAGTGAAGAAAGCACCTAC 840
Db 781 CCAGATTACATGCTCTGTAAGTGTGACGTGATGAAAGGGAGTGAAGAAAGCACCTAC 840
Qy 841 GGCCTGAGCTGTGACTGTGTGTGCTGAGTGGGCGTGAATGCTATGAGATGATTTATGGGAGA 900
Db 841 GGCCTGAGCTGTGACTGTGTGTGCTGAGTGGGCGTGAATGCTATGAGATGATTTATGGGAGA 900
Qy 901 TCCCTCTTGGCAGAGGAACTCTGCGCAACCTTAAATACATTAATGAATTTCCAGCGG 960
Db 901 TCCCTCTTGGCAGAGGAACTCTGCGCAACCTTAAATACATTAATGAATTTCCAGCGG 960
Qy 961 TTTTGAATTTCCAGATGACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 TTTTGAATTTCCAGATGACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 TTGTTGTGCGGCGCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1021 TTGTTGTGCGGCGCAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy 1081 TCTAAATTTGACTGGAACAACATTTGTAACTCTCTCCCTTGTGTTCCACCTTCAAG 1140
Db 1081 TCTAAATTTGACTGGAACAACATTTGTAACTCTCTCCCTTGTGTTCCACCTTCAAG 1140
Qy 1141 TCTGAGATGACACCTCCCAATTTTGAATGAACAAGAGAAATTCGAGGTTTCACTCT 1200
Db 1141 TCTGAGATGACACCTCCCAATTTTGAATGAACAAGAGAAATTCGAGGTTTCACTCT 1200
Qy 1201 CCGTGCAGCTGAGCCCTCAAGCTTCTGAGGTGAAGAACTCCGTTGTGTGGGTTTTCG 1260
Db 1201 CCGTGCAGCTGAGCCCTCAAGCTTCTGAGGTGAAGAACTCCGTTGTGTGGGTTTTCG 1260
Qy 1261 TACAGCAAGCACTGAGGATTTCTGTGTGATCTGATCTGTGTGTGTGTGTGTGTGTGT 1320
Db 1261 TACAGCAAGCACTGAGGATTTCTGTGTGATCTGATCTGTGTGTGTGTGTGTGTGTGT 1320
Qy 1321 CCTGCAAGACTGATCTCAATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTTACAGAGC 1380
Db 1321 CCTGCAAGACTGATCTCAATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTTACAGAGC 1380

D	b	3541	CAGCAGAGCTGGAGACTGAAACGAGACTAAACAGAGGCTTTCTGGAAAGCAAGCCAAA	3600
Q	y	3601	TTACAGCAGCAGATGGAACCTTGCAAGAAAATCATTTCCTGCTGACTCAAGGACTGCAA	3660
D	b	3601	TTACAGCAGCAGATGGAACCTTGCAAGAAAATCATTTCCTGCTGACTCAAGGACTGCAA	3660
Q	y	3661	GAAGCTTTAATGAGGGCTGATCTAATGAGACAGAAAGAAAGTAGACTTGGATATCAGCTG	3720
D	b	3661	GAAGCTTTAATGAGGGCTGATCTAATGAGACAGAAAGAAAGTAGACTTGGATATCAGCTG	3720
Q	y	3721	GAAGCTTTAATGAGGGCTGATCTAATGAGAAAGTGAAGTGAAGGCACTATTTCTCAA	3780
D	b	3721	GAAGCTTTAATGAGGGCTGATCTAATGAGAAAGTGAAGTGAAGGCACTATTTCTCAA	3780
Q	y	3781	CAAAACCAATCTATTGATTTTCTGCAAGCCAAATGSAACCACTGCTAAAAAGAAAAG	3840
D	b	3781	CAAAACCAATCTATTGATTTTCTGCAAGCCAAATGSAACCACTGCTAAAAAGAAAAG	3840
Q	y	3841	GTTCTCTGCAATGATGAGCTGAAGCTGGCCCTGGAAGAGAGAAAGCTCGCTGTGCA	3900
D	b	3841	GTTCTCTGCAATGATGAGCTGAAGCTGGCCCTGGAAGAGAGAAAGCTCGCTGTGCA	3900
Q	y	3901	GAGCTAGAGAGACCCCTTGAGAAACCCGCAATGAGACTCCGGTCCGGCCGGAGAGAGCT	3960
D	b	3901	GAGCTAGAGAGACCCCTTGAGAAACCCGCAATGAGACTCCGGTCCGGCCGGAGAGAGCT	3960
Q	y	3961	GCCCAACGGAAGCAACGACCAACCCATCCAGCCGCAACCCGCAAGGAGAGAGAG	4020
D	b	3961	GCCCAACGGAAGCAACGACCAACCCATCCAGCCGCAACCCGCAAGGAGAGAGAG	4020
Q	y	4021	ATGCGCATGTCGGCCATCGTGCGGTGCGAAGACACAGCCCAAGTGCATGAGAGCTGTG	4080
D	b	4021	ATGCGCATGTCGGCCATCGTGCGGTGCGAAGACACAGCCCAAGTGCATGAGAGCTGTG	4080
Q	y	4081	GCCCGCCCATCCAGCCGGAAGAGAGTCTTCACTCCAGAGAAATTTAGTGGGCTCTT	4140
D	b	4081	GCCCGCCCATCCAGCCGGAAGAGAGTCTTCACTCCAGAGAAATTTAGTGGGCTCTT	4140
Q	y	4141	AAGGAACGCAATGATATTCCTCAACCGATTCAAGTAGAGCTGAACATGCGAGCC	4200
D	b	4141	AAGGAACGCAATGATATTCCTCAACCGATTCAAGTAGAGCTGAACATGCGAGCC	4200
Q	y	4201	ACAAAGTGTCTGTGTCTGAGTACCGTGCACTTTGGAACGCGCAGAGCATCCAAATGTCTC	4260
D	b	4201	ACAAAGTGTGTGTGTCTGAGTACCGTGCACTTTGGAACGCGCAGAGCATCCAAATGTCTC	4260
Q	y	4261	GAATGTCAAGTATGTGTCAACCCAAAGTGTCAAGTGTCTGCGCAGCCACTGCGGCTTG	4320
D	b	4261	GAATGTCAAGTATGTGTCAACCCAAAGTGTCAAGTGTCTGCGCAGCCACTGCGGCTTG	4320
Q	y	4321	CCTGCTGAATATGCAACACTTCAACGAGGCTTCTGCGCGTGAACAAATGAACTCCCCA	4380
D	b	4321	CCTGCTGAATATGCAACACTTCAACGAGGCTTCTGCGCGTGAACAAATGAACTCCCCA	4380
Q	y	4381	GCTTCCAGACCAAGAGCCCAAGAGACTTGCACCTGGAAGGTGATGAAGGTGCC	4440
D	b	4381	GCTTCCAGACCAAGAGCCCAAGAGACTTGCACCTGGAAGGTGATGAAGGTGCC	4440
Q	y	4441	AGGAATTAACAAACGAGACAGCAAGGCTGGGACAGAAAGTACATTGTCTGGAAGGATCA	4500
D	b	4441	AGGAATTAACAAACGAGACAGCAAGGCTGGGACAGAAAGTACATTGTCTGGAAGGATCA	4500
Q	y	4501	AAAGCTCATTTATGACATGAAAGCCAGAGAGCTGACAGAGCCGGTGGAAAGATTT	4560
D	b	4501	AAAGCTCATTTATGACATGAAAGCCAGAGAGCTGACAGAGCCGGTGGAAAGATTT	4560
Q	y	4561	GAGCTGTGCTTCCGACGGGAGTGTATCTATTATGATGTGCTTGGTGTCTTCCGAATC	4620
D	b	4561	GAGCTGTGCTTCCGACGGGAGTGTATCTATTATGATGTGCTTGGTGTCTTCCGAATC	4620
Q	y	4621	GCAATATACGCCAAAGCAGATGTCCATATCTGAAGATGAAATTCACCGGCACACC	4680
D	b	4621	GCAATATACGCCAAAGCAGATGTCCATATCTGAAGATGAAATTCACCGGCACACC	4680
D	b	4681	GCAATATACGCCAAAGCAGATGTCCATATCTGAAGATGAAATTCACCGGCACACC	4680
Q	y	4681	ACCTGTGAGCCCGGAGAGAACCTCTACTGTGTACTGCCACCTTCCCTGACAAACAGGCG	4740
D	b	4681	ACCTGTGAGCCCGGAGAGAACCTCTACTGTGTACTGCCACCTTCCCTGACAAACAGGCG	4740
Q	y	4741	TGGGTACCGGCTTAAAGATCAAGTGTGCAAGGTGGAGAGTGTCTGAGGAAAAGCAGAA	4800
D	b	4741	TGGGTACCGGCTTAAAGATCAAGTGTGCAAGGTGGAGAGTGTCTGAGGAAAAGCAGAA	4800
Q	y	4801	GCTATGTAAATCTGCTTGGAAATCTCCCTGCTGAAACTGGAAGGTGATGACCGTCTAGAC	4860
D	b	4801	GCTATGTAAATCTGCTTGGAAATCTCCCTGCTGAAACTGGAAGGTGATGACCGTCTAGAC	4860
Q	y	4861	ATGAATGCAACGCTGACGCTTCAAGGACCAAGGTGTGTGGTGGGCAACCGAGAGAGCTC	4920
D	b	4861	ATGAATGCAACGCTGACGCTTCAAGGACCAAGGTGTGTGGTGGGCAACCGAGAGAGCTC	4920
Q	y	4921	TAGCCCTGAAATGTCTTGAAGAACTCCCTAACCATTGCTCCAGAGAAATGAGAGCTTC	4980
D	b	4921	TAGCCCTGAAATGTCTTGAAGAACTCCCTAACCATTGCTCCAGAGAAATGAGAGCTTC	4980
Q	y	4981	CAAAATTTATTTATTCAGAGACCTGAGAGAGCTATCATATGACAGAGAAAGCGGCA	5040
D	b	4981	CAAAATTTATTTATTCAGAGACCTGAGAGAGCTATCATATGACAGAGAAAGCGGCA	5040
Q	y	5041	CTGTGTCTGTGACGATGGAAGAAAGTGAACAGTCCCTGGCCAGTCCCACTGCGCTGCC	5100
D	b	5041	CTGTGTCTGTGACGATGGAAGAAAGTGAACAGTCCCTGGCCAGTCCCACTGCGCTGCC	5100
Q	y	5101	CAGCCGCAATCTTCAACCAACATTTTGAAGCTGTCAAGGGCTGCACATTGTTGGGGCA	5160
D	b	5101	CAGCCGCAATCTTCAACCAACATTTTGAAGCTGTCAAGGGCTGCACATTGTTGGGGCA	5160
Q	y	5161	GGCAAGTTGAAGACGGGCTCTGATCTGTGCAAGCAGATGCCAGAAAGTGTCTATCTTC	5220
D	b	5161	GGCAAGTTGAAGACGGGCTCTGATCTGTGCAAGCAGATGCCAGAAAGTGTCTATCTTC	5220
Q	y	5221	CGCTACAGAGAAACCTCAGCAATATCTGATCCGGAAGAGATGAGACCTGAGAGCC	5280
D	b	5221	CGCTACAGAGAAACCTCAGCAATATCTGATCCGGAAGAGATGAGACCTGAGAGCC	5280
Q	y	5281	TGCACTGTATCCACTTCAACCAATTAACGATTCCTGATGGAACCAATAATTTCTAGAA	5340
D	b	5281	TGCACTGTATCCACTTCAACCAATTAACGATTCCTGATGGAACCAATAATTTCTAGAA	5340
Q	y	5341	ATGCAATGAAGAGTACACGCTGCGAGAAATTCCTGATPAGATGATCAATTCCTTGGCA	5400
D	b	5341	ATGCAATGAAGAGTACACGCTGCGAGAAATTCCTGATPAGATGATCAATTCCTTGGCA	5400
Q	y	5401	CCTGCTGTGTTTGGCGCTTTCCAACAGTTCCTCCGTCTCAATGCTGAGAGTGAACAC	5460
D	b	5401	CCTGCTGTGTTTGGCGCTTTCCAACAGTTCCTCCGTCTCAATGCTGAGAGTGAACAC	5460
Q	y	5461	GCAAGGACGAGAGAGAGTACTGTGTGTTTCAAGAAATTTGAGATGCTGAGATTC	5520
D	b	5461	GCAAGGACGAGAGAGAGAGTACTGTGTGTTTCAAGAAATTTGAGATGCTGAGATTC	5520
Q	y	5521	TACGGAAGAGTACCGGCAACAGCATCTCAAGTGAAGTCCGCTTACCTTGGCCTTTGCC	5580
D	b	5521	TACGGAAGAGTACCGGCAACAGCATCTCAAGTGAAGTCCGCTTACCTTGGCCTTTGCC	5580
Q	y	5581	TACAGGAACCTTATCTGTTTGTGACCCCACTTCACTCACTGGAAGTAAATGAGATCCAG	5640
D	b	5581	TACAGGAACCTTATCTGTTTGTGACCCCACTTCACTCACTGGAAGTAAATGAGATCCAG	5640
Q	y	5641	GCAAGCTCTCAGAGAGAGACCCCTGCGAGAGGTACTGACATCCCGAGCCGCTTAC	5700
D	b	5641	GCAAGCTCTCAGAGAGAGACCCCTGCGAGAGGTACTGACATCCCGAGCCGCTTAC	5700
Q	y	5701	CTGGGCTTGCACATTTCTCAGAGAGATTTATCTTGCGCTCTCATACAGAGTAAATTA	5760
D	b	5701	CTGGGCTTGCACATTTCTCAGAGAGATTTATCTTGCGCTCTCATACAGAGTAAATTA	5760
D	b	5701	CTGGGCTTGCACATTTCTCAGAGAGATTTATCTTGCGCTCTCATACAGAGTAAATTA	5760

QY 5761 AGGGTCATTTGTCGAAGGAAACCTTGTAAGAGTCCGCACTGAACCAACCGGGGC 5820
DB 5761 AGGGTCATTTGTCGAAGGAAACCTTGTAAGAGTCCGCACTGAACCAACCGGGGC 5820
QY 5821 CCCTCCACCTCCCGCAG 5837
DB 5821 CCCTCCACCTCCCGCAG 5837

RESULT 11
US-10-017-216-3
Sequence 3, Application US/10017216
Publication No. US20020160483A1
GENERAL INFORMATION:
APPLICANT: KABELLER-LIBERMANN, Rosana
TITLE OF INVENTION: Kinase and Uses Therefor
FILE REFERENCE: 10147-5701
CURRENT APPLICATION NUMBER: US/10/017,216
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: US 60/242,429
PRIOR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 6159
TYPE: DNA
ORGANISM: Homo sapiens
US-10-017-216-3

Query Match 91.8%; Score 5661.4; DB 13; Length 6159;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

QY 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCTTTGATGCTGTGCTGTAACCAATT 60
DB 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCTTTGATGCTGTGCTGTAACCAATT 60
QY 61 GCCACCGGGGCTCCAGAGTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAA 120
DB 61 GCCACCGGGGCTCCAGAGTGAATCTGTTCTCCAGGGGAAACCAACCTTTATGACTCAA 120
QY 121 CACGAGATGTCTCTCTTTCCCGAGAGGATATTAGATGCCCTTTGTTCTTTGAA 180
DB 121 CACGAGATGTCTCTCTTTCCCGAGAGGATATTAGATGCCCTTTGTTCTTTGAA 180
QY 181 GAAATGACGATGCTGCTGTGATGAAGATTAAAGCACTGTGACAACTTTGTCCGGAATAT 240
DB 181 GAAATGACGATGCTGCTGTGATGAAGATTAAAGCACTGTGACAACTTTGTCCGGAATAT 240
QY 241 TCCGACACCATAGTGTGATTAAGAGAGCTCCAGCTTCGCGAAGAGCTTGAAGTACA 300
DB 241 TCCGACACCATAGTGTGATTAAGAGAGCTCCAGCTTCGCGAAGAGCTTGAAGTACA 300
QY 301 AGTCTTGAAGTTGTGCTGCTGTAAGTGAAGTGAAGAGAAACCAACCGGG 360
DB 301 AGTCTTGAAGTTGTGCTGCTGTAAGTGAAGTGAAGAGAAACCAACCGGG 360
QY 361 GACATCTATGCTATGAAGATGATGAAGAGGCTTTATTTGCGCCAGAGCAGGTTTCA 420
DB 361 GACATCTATGCTATGAAGATGATGAAGAGGCTTTATTTGCGCCAGAGCAGGTTTCA 420
QY 421 TTTTGTGAGGAAGCGGAAATTTATCTGGAAGCAACAGCCGTGATCCCAATTA 480
DB 421 TTTTGTGAGGAAGCGGAAATTTATCTGGAAGCAACAGCCGTGATCCCAATTA 480
QY 481 CAGATGCTTTGAGCAAAATCACTTTATCTGATGAGGAATCAAGCTTGAAGGG 540
DB 481 CAGATGCTTTGAGCAAAATCACTTTATCTGATGAGGAATCAAGCTTGAAGGG 540
QY 541 GACTTGCTGTCATTTGAAATGATGAGAGCAGTTAGTGAACCTGATACAGTTT 600
DB 541 GACTTGCTGTCATTTGAAATGATGAGAGCAGTTAGTGAACCTGATACAGTTT 600

DB 541 GACTTGCTGTCATTTGAAATGATGAGAGCAGTTAGTGAACCTGATACAGTTT 600
QY 601 TACCTAGCTGAGTGAATTTGCTGTTCACAGGCTTCATCTGATGAGATACGTGATCGA 660
DB 601 TACCTAGCTGAGTGAATTTGCTGTTCACAGGCTTCATCTGATGAGATACGTGATCGA 660
QY 661 GACATCAAGCTTGAAGAACTTCTGTTGACCCGACAGGAAACATCAAGCTGTGAGATTTT 720
DB 661 GACATCAAGCTTGAAGAACTTCTGTTGACCCGACAGGAAACATCAAGCTGTGAGATTTT 720
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DB 721 GATCTGCGCGGAAATGAATTCAAACAGATGATGATCCAAATCCCGATTTGGAGC 780
QY 781 CCAGATTTACATGAGCTCCTGTAAGTCTGATGATGAACGGGATGAGAAAGGACCTTAC 840
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DB 1021 TTGTTGTGCGGCAAGAAAGAGACTGAAGTGAAGTCTTTGCTGCTTCTTCTTC 1080
QY 1081 TCTTAAATTAATCTGGAACCAATTCGTAATCTCTCCCGCTTCTGCTTCCACCTCAAG 1140
DB 1081 TCTTAAATTAATCTGGAACCAATTCGTAATCTCTCCCGCTTCTGCTTCCACCTCAAG 1140
QY 1141 TCTGACATGACACTTCAATTTTGAATGAACAGAGAAATTCGTGGTTTCACTCTCT 1200
DB 1141 TCTGACATGACACTTCAATTTTGAATGAACAGAGAAATTCGTGGTTTCACTCTCT 1200
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DB 1501 TCCCTCTGAGAGAGGACTTGTACTACATCAAGATGAGTGAAGTGAAGTGAAGTGAAGT 1560
QY 1561 TTGAGAGCAAGCAGATGAGAGTGTCCAGAGAGTGAAGCAAGCACTGACAGTTTCTCAT 1620
DB 1561 TTGAGAGCAAGCAGATGAGAGTGTCCAGAGAGTGAAGCAAGCACTGACAGTTTCTCAT 1620
QY 1621 GATATCAGAGAGCAGAGCCGGAAGCTTCAAGAAATCAAGAGCAGAGTACAGGCTCAA 1680
DB 1621 GATATCAGAGAGCAGAGCCGGAAGCTTCAAGAAATCAAGAGCAGAGTACAGGCTCAA 1680

Qy	1681	GTGGAAGAAATGAGCTGATGATGATCACTGTTGGAAAGAGATCTTGTCTTCAGCAAGAAAG	1740
Db	1681	GTGGAAAGAAATGAGTTGATGATGATCACTGTTGGAAAGAGATCTTGTCTTCAGCAAGAAAG	1740
Qy	1741	CGAGAGTATCTTAACGAATCTGAGCTGAGAGATCTTCGGCTTCTCTCTGAAAGATTCAAG	1800
Db	1741	CGAGAGTATCTTAACGAATCTGAGCTGAGAGATCTTCGGCTTCTCTCTGAAAGATTCAAG	1800
Qy	1801	CGAAAAACGACAGAAATGTCAGCATTAACCTGTTGAAGGCTTAAGAGTCAAGGAAAGCTCGAA	1860
Db	1801	CGAAAAACGACAGAAATGTCAGCATTAACCTGTTGAAGGCTTAAGAGTCAAGGAAAGCTCGAA	1860
Qy	1861	GTGGAGGAATATGTCGAAACTGAGGAAGATTAATGCTGAGCAGCAGCTCAAAATTCCAGAG	1920
Db	1861	GTGGAGGAATATGTCGAAACTGAGGAAGATTAATGCTGAGCAGCAGCTCAAAATTCCAGAG	1920
Qy	1921	CTCCAAAGAGAACTGAGGAAGGCTGTAAAGCCAGACCGAGGCCACCGAGCTGCTGCAG	1980
Db	1921	CTCCAAAGAGAACTGAGGAAGGCTGTAAAGCCAGACCGAGGCCACCGAGCTGCTGCAG	1980
Qy	1981	AATATCCGCCAGGCAAGAGCGAGCCGAGAGGAGCTGAGAAAGCTGCAGAACCGAGAG	2040
Db	1945	-----GCAAGAGAGCGAGCCGAGAGGAGACTGAGAAAGCTGCAGAACCGAGAG	1992
Qy	2041	GATTCTTCTGAAGGCGATCAGAAAGAGCTGTGAGAAAGCTGAGAAAGCCGCCATTTCTGTG	2100
Db	1993	GATTCTTCTGAAGGCGATCAGAAAGAGCTGTGAGAAAGCTGAGAAAGCCGCCATTTCTGTG	2052
Qy	2101	GAGAACAAAGTTAAAGACTAGAGACCATGAGCCGTAGAGAAACAGACTGAAGATGAC	2160
Db	2053	GAGAACAAAGTTAAAGACTAGAGACCATGAGCCGTAGAGAAACAGACTGAAGATGAC	2112
Qy	2161	ATCCAGACAAAAATCCCAACAGATCCAGCAGATGCGCTGATAAATTTCTGAGCTCGAAGAG	2220
Db	2113	ATCCAGACAAAAATCCCAACAGATCCAGCAGATGCGCTGATAAATTTCTGAGCTCGAAGAG	2172
Qy	2221	AAACATCCGAGAGGCCCAAGTCTCAGCCCGACACTTAAGAGTGCACCTGAACAGAAAGAG	2280
Db	2173	AAACATCCGAGAGGCCCAAGTCTCAGCCCGACACTTAAGAGTGCACCTGAACAGAAAGAG	2232
Qy	2281	CAGCACTATGAGAAAAGATTAAAGTGTGGAACAATCAGATTAAAGAAAGACTGTGCTGAC	2340
Db	2233	CAGCACTATGAGAAAAGATTAAAGTGTGGAACAATCAGATTAAAGAAAGACTGTGCTGAC	2292
Qy	2341	AAGGAGACACTGAGAAACATGATGCAAGAGACACAGAGAGAGAGGCCCATGAGAAAGGCCAA	2400
Db	2293	AAGGAGACACTGAGAAACATGATGCAAGAGACACAGAGAGAGAGGCCCATGAGAAAGGCCAA	2352
Qy	2401	ATTCTCAGCGAACAGAAAGCGCATGATCAATGCTATGATTCCAAGATCAGATCCCTGGAA	2460
Db	2353	ATTCTCAGCGAACAGAAAGCGCATGATCAATGCTATGATTCCAAGATCAGATCCCTGGAA	2412
Qy	2461	CAGAGAGATTGTGGAACTGTCTGAAGCCCAATTAACCTTGACAGCAAAATAGCAGTCTTTTACC	2520
Db	2413	CAGAGAGATTGTGGAACTGTCTGAAGCCCAATTAACCTTGACAGCAAAATAGCAGTCTTTTACC	2472
Qy	2521	CAAAAGAACATGAAAGGCCCAAGAGAGATGATTTCTGAACCTCAGGCAACAGAAATTTTAC	2580
Db	2473	CAAAAGAACATGAAAGGCCCAAGAGAGATGATTTCTGAACCTCAGGCAACAGAAATTTTAC	2532
Qy	2581	CTGAGACACAGGCTGGAGAGTTGAGGCCCAAGAACCGAAAACTGAGAGACAGCTGAG	2640
Db	2533	CTGAGACACAGGCTGGAGAGTTGAGGCCCAAGAACCGAAAACTGAGAGACAGCTGAG	2592
Qy	2641	AAAGATCCAGCCCAAGAACCAAGTGAACAAGATGGCTGCTGGAACCTGAGACACAAGTTG	2700
Db	2593	AAAGATCCAGCCCAAGAACCAAGTGAACAAGATGGCTGCTGGAACCTGAGACACAAGTTG	2652
Qy	2701	CGGAGGCTCACTTAGAGCAGAGAGCAGAAACTGAGAGCTCAAGGCGCAGGCTCAGAG	2760
Db	2653	CGGAGGCTCACTTAGAGCAGAGAGCAGAAACTGAGAGCTCAAGGCGCAGGCTCAGAG	2712

3793 GGTTTATTATAGTCGACGAGAACCCCTGCTTACCCACACAGGTTCTCTGCACTAC 3852
3856 AATGAGCTGAAGCTGGCCCTTGAGAGAGAGAAAGCTGCTGTGAGAGCTAAGAGAAC 3915
3853 AATGAGCTGAAGCTGGCCCTTGAGAGAGAGAAAGCTGCTGTGAGAGCTAAGAGAAC 3912
3916 CTTCAGAGAACCCGCAATGAGCTCCGGTCCGGCCGGAGAGAGAGTCCCAACCGAAGCA 3975
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4216 TGTCTGATACCGGCACTTTGAGCGCAGGACATCCAAATGTCGCAATGTCAAGTATG 4275
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4516 GACAGTGAAGCAGAGAGAGTGAACAGAGCCGGTGAAGAGATTTGAGCTGTGCCCTTCC 4575
4513 GACAGTGAAGCAGAGAGAGTGAACAGAGCCGGTGAAGAGATTTGAGCTGTGCCCTTCC 4572
4576 GACGGGAGATGATATTTCAATGAGTCCGTTGCTTCCGAACTCCGAAATTAACAGCCAAA 4635
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4636 GCAGATGTCCATATCATATGAAATCTCACCCGACACACACTGTGCGCGGG 4695
4633 GCA----- 4635
4696 AGAACCCTCTAATTGAGCTCCAGCTTCCCTGACAAACAGCGCTGGGTACACGCTTAA 4755
4636 ----- 4635
4756 GAATCAATTGTGCGAGGTGGGAGATTCTAGGAGAAAGCAGAAAGCTGATGCTAACTG 4815
4636 ----- 4662
4816 CTTCGAAATCTCTGCTGAAACTGGAAGGTGATGACGCTTAGACATGAACCTGACGCTG 4875
4663 CTTCGAAATCTCTGCTGAAACTGGAAGGTGATGACGCTTAGACATGAACCTGACGCTG 4722
4876 CCCTTCAGTGAACAGAGTGTGTTGATGGGACACGAGAGAGGCTCTACGCTTGAATGTC 4935

4723 CCCTTCAGTGAACAGAGTGTGTTGATGGGACACGAGAGAGGCTCTACGCTTGAATGTC 4782
4936 TTGAAAAATCTCCCTAACCCATGTCCTCCAGAGAAATTGAGACAGTCTTCCAAATTTATATATC 4995
4783 TTGAAAAATCTCCCTAACCCATGTCCTCCAGAGAAATTGAGACAGTCTTCCAAATTTATATATC 4842
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5116 CCAACATTTTGAAGCTGTCAAGAGCTGCCCATTTGTTGGGCGAGCAAGATTGAAGAC 5175
4963 CCAACATTTTGAAGCTGTCAAGAGCTGCCCATTTGTTGGGCGAGCAAGATTGAAGAC 5022
5176 GGGCTCTGCAATCTGTGAGAGCATGCCAGCAAGTGTCTATTCCTCGGCTCAACAGAAAC 5235
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5416 GCGCTCTTCCAAACGCTTCCCTGCTCATGATGATGAGTGAACAGCGAGGACGAGAG 5475
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5476 GAGTACTTGTGTGTTTCAACGAATTTGAGAGTTCGTGATTTCTTAACGAAGAGCTATG 5535
5263 GAGTACTTGTGTGTTTCAACGAATTTGAGAGTTCGTGATTTCTTAACGAAGAGCTATG 5382
5536 GCGACAGACATCTCAAGTGAAGTCCGTTACCTTTGGCTTTGGCTTACAGAGAACCTGAT 5595
5383 GCGACAGACATCTCAAGTGAAGTCCGTTACCTTTGGCTTTGGCTTACAGAGAACCTGAT 5442
5596 CTGTTGTGACCCACTTCAACCTCACTGAGAGTAAATTGAGATTCAGGACGCTCTCAACA 5655
5443 CTGTTGTGACCCACTTCAACCTCACTGAGAGTAAATTGAGATTCAGGACGCTCTCAACA 5582
5656 GGGACCCCTGCGAGGCTACTGAGACATCCCGAACCCGCGCTTACTGCGGCTTGCATT 5715
5503 GGGACCCCTGCGAGGCTACTGAGACATCCCGAACCCGCGCTTACTGCGGCTTGCATT 5552
5716 TCTCTAGAGAGCATTTAATTGAGGCTCTCTCAATACAGAGTAAATTAAGGCTCATTTGCTGC 5775
5663 TCTCTAGAGAGCATTTAATTGAGGCTCTCTCAATACAGAGTAAATTAAGGCTCATTTGCTGC 5622
5776 AAGGAAACCTCTGAGAGAGTCCGAGCATGAACACACGCGGCGCTTCAACCTCCGCG 5835
5623 AAGGAAACCTCTGAGAGAGTCCGAGCATGAACACACGCGGCGCTTCAACCTCCGCG 5682
5836 AGCAGCCCAACAGAGGCGCCACCACTGACATCAACAGACATCAACAGCGGCTGCGC 5895
5883 AGCAGCCCAACAGAGGCGCCACCACTGACATCAACAGAGCAATCAACAGCGGCTGCGC 5742
5896 TCCAGCCGAGCGCGCCGAGAGGCTCCAGCCACCGGAGAGCCCAAGACACCCCAACCGC 5955
5743 TCCAGCCGAGCGCGCGCCGAGAGGCTCCAGCCACCGGAGAGCCCAACACCCCAACCGC 5802
5956 TACCGGAGAGGCGGAGACCGAGCTGCGAGAGGACAAAGTCTCTGCGCGCGCTTGAAGGA 6015
5803 TACCGGAGAGGCGGAGACCGAGCTGCGAGAGGACAAAGTCTCTGCGCGCGCTTGAAGGA 5862

QY 6016 GAGAAATCCCCCGGCGGATCTAGCAACGCGGAGAGAGCGGCTCCCCCGGAGGCTGTTT 6075
DB 5863 GAGAAATCCCCCGGCGGATCTAGCAACGCGGAGAGAGCGGCTCCCCCGGAGGCTGTTT 5922
QY 6076 GAAGACGACGACGAGGCGGCTCTGCGGAGCGGAGGACCCCGCTGTCTCCAGGTG 6135
DB 5923 GAAGACGACGACGAGGCGGCTCTGCGGAGCGGAGGACCCCGCTGTCTCCAGGTG 5982
QY 6136 AACAAAGTCTGGAGCAAGCTCTT 6158
DB 5983 AACAAAGGAGAGGCGAGAGTGC 6005

RESULT 12
US-10-325-430-11
; Sequence 11, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Siles-Santiago, Immaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; FILE REFERENCE: 32838, 336 and 52908
; CURRENT APPLICATION NUMBER: US/10/325,430
; PRIOR FILING DATE: 2002-12-19
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6162
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(6162)
US-10-325-430-11

Query Match Best Local Similarity 91.8%; Score 5661.4; DB 16; Length 6162;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

QY 1 ATGTTGAAGTTCAATATATGAGCGCGAATCTTTGATGCTGCTGTAACCAT 60
DB 1 ATGTTGAAGTTCAATATATGAGCGCGAATCTTTGATGCTGCTGTAACCAT 60
QY 61 GCCAGCGGCGCTCCAGGCTGAATCTGTTCTTCAGAGGGAACCAACCTTTATGACTCA 120
DB 61 GCCAGCGGCGCTCCAGGCTGAATCTGTTCTTCAGAGGGAACCAACCTTTATGACTCA 120
QY 121 CAGCAGATGTCCTCTTTCCCGAAGAGGATTTAGATGCTCTTTGTTCTTTGAA 180
DB 121 CAGCAGATGTCCTCTTTCCCGAAGAGGATTTAGATGCTCTTTGTTCTTTGAA 180
QY 121 CAGCAGATGTCCTCTTTCCCGAAGAGGATTTAGATGCTCTTTGTTCTTTGAA 180
DB 181 GAATGAGTCAAGCTGCTCTGATGAAGATTAAAGCACTGAGCAACTTTGCGGAATAT 240
QY 181 GAATGAGTCAAGCTGCTCTGATGAAGATTAAAGCACTGAGCAACTTTGCGGAATAT 240
DB 181 GAATGAGTCAAGCTGCTCTGATGAAGATTAAAGCACTGAGCAACTTTGCGGAATAT 240
QY 241 TCCGACACCATAGCTGATGTTACAGAGCTCAAGCTTCGCGAAGAGACTTCGAGTCA 300
DB 241 TCCGACACCATAGCTGATGTTACAGAGCTCAAGCTTCGCGAAGAGACTTCGAGTCA 300
QY 301 AGCTCTTGAGTGTGCTGCTGTTGCTGAAGTGCAGGTGTAAAGAGAAACCAACCGGG 360
DB 301 AGCTCTTGAGTGTGCTGCTGTTGCTGAAGTGCAGGTGTAAAGAGAAACCAACCGGG 360
QY 361 GACATCTATGCTATGAAGATGTAAGAAAGAGGCTTTATGSCCAAGAGAGGTTCA 420
DB 361 GACATCTATGCTATGAAGATGTAAGAAAGAGGCTTTATGSCCAAGAGAGGTTCA 420

QY 421 TTTTGTGAGAGAGCGGAAATATATATCTCGAAGCAAAAGCCCTGATCCCCAATTA 480
DB 421 TTTTGTGAGAGAGCGGAAATATATATCTCGAAGCAAAAGCCCTGATCCCCAATTA 480
QY 481 CAGTAAGCTTTTCAAGGCAAAATATCATCTTTATCTGCTCATGAAATTCAGCCCTGAGGG 540
DB 481 CAGTAAGCTTTTCAAGGCAAAATATCATCTTTATCTGCTCATGAAATTCAGCCCTGAGGG 540
QY 541 GACTTGCTGCTCACTTTTGAATAGATATGAGGACCAAGTATGATGAAACCTGATACAGTTT 600
DB 541 GACTTGCTGCTCACTTTTGAATAGATATGAGGACCAAGTATGATGAAACCTGATACAGTTT 600
QY 601 TACCTAGTCAAGCTGATTTTGGCTGTTACAGGCTTCATGATGGAATACGTGATCGA 660
DB 601 TACCTAGTCAAGCTGATTTTGGCTGTTACAGGCTTCATGATGGAATACGTGATCGA 660
QY 661 GACATCAAGCTGAGAAACATCTGCTGTTGACCGGACAGGACACATCAAGCTGAGATTTT 720
DB 661 GACATCAAGCTGAGAAACATCTGCTGTTGACCGGACAGGACACATCAAGCTGAGATTTT 720
QY 721 GATCTGCGCGAAATGAAATTCAAACAAGATGTAATGCAAACTCCGATTTGGGACC 780
DB 721 GATCTGCGCGCGAAATGAAATTCAAACAAGATGTAATGCAAACTCCGATTTGGGACC 780
QY 781 CCAATTTAATGAGCTGCTGTAAGTGTGACTGTGATGAACGGGATGGAAGGACCTTAC 840
DB 781 CCAATTTAATGAGCTGCTGTAAGTGTGACTGTGATGAACGGGATGGAAGGACCTTAC 840
QY 841 GGCCTGAGCTGTAAGCTGCTGTAAGTGTGACTGTGATGAACGGGATGGAAGGACCTTAC 900
DB 841 GGCCTGAGCTGTAAGCTGCTGTAAGTGTGACTGTGATGAACGGGATGGAAGGACCTTAC 900
QY 901 TCCCCCTTCGAGAGGAACTCTGCGAAGCACTTCAATTAACATTTGAAATTTCCAGCG 960
DB 901 TCCCCCTTCGAGAGGAACTCTGCGAAGCACTTCAATTAACATTTGAAATTTCCAGCG 960
QY 961 TTTTGAATTTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1020
DB 961 TTTTGAATTTTCCAGATGACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1020
QY 1021 TTTTGTGAGGCGCAAGAAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1080
DB 1021 TTTTGTGAGGCGCAAGAAAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1080
QY 1081 TCTAAATTTGATGAGCAACATCTGTAATCTCTCTCCCTTGTTCACCTCAAG 1140
DB 1081 TCTAAATTTGATGAGCAACATCTGTAATCTCTCTCCCTTGTTCACCTCAAG 1140
QY 1141 TCTGACATGACACCTTCAATTTTGAATGAACCAAGAAATTCGTGGTTTCATCTCT 1200
DB 1141 TCTGACATGACACCTTCAATTTTGAATGAACCAAGAAATTCGTGGTTTCATCTCT 1200
QY 1201 CCGTGCAGCTGAGGCTCTGAGGCTTCTGAGTGAAGATGCTGCTGCTGCTGCTGCT 1260
DB 1201 CCGTGCAGCTGAGGCTCTGAGGCTTCTGAGTGAAGATGCTGCTGCTGCTGCTGCT 1260
QY 1261 TACAGCAAGGCACTGAGGATCTTGTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1320
DB 1261 TACAGCAAGGCACTGAGGATCTTGTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAG 1320
QY 1321 CCGTGCAGGCTGAGTGAAGGAAATCTTCAATCAAAAGCAAGAGCTCAAGAC 1380
DB 1321 CCGTGCAGGCTGAGTGAAGGAAATCTTCAATCAAAAGCAAGAGCTCAAGAC 1380
QY 1381 TCTCAAGCAAGTGTCAAGATGAGCAAGAAATGACCCGCTTACATCGAGAGTGTCA 1440
DB 1381 TCTCAAGCAAGTGTCAAGATGAGCAAGAAATGACCCGCTTACATCGAGAGTGTCA 1440
QY 1441 GAGGTGAGGCTGCTGCTTATGATGAGAGAGGCTGAGAGGCTGAGAGCTGAGAG 1500
DB 1441 GAGGTGAGGCTGCTGCTTATGATGAGAGAGGCTGAGAGGCTGAGAGCTGAGAG 1500
QY 1501 TCCCTCTGAGAGGAGCCTTGTCTATCAATCAAGATGAGTGAAGGAGAGT 1560

Db 1501 TCCCTCTGAGAGGACCTTGTCTACTTACATCAAGAAATGCACTTACCTTAAAGCCAAAGT 1560
 Qy 1561 TTGAGACGACGACGATGAGGTGTCCAGAGAGATGACAAAGCACTGACGCTTCTTCAT 1620
 Db 1561 TTGAGACGACGACGATGAGGTGTCCAGAGAGATGACAAAGCACTGACGCTTCTTCAT 1620
 Qy 1621 GATATCAGAGACGAGCCGGAAGCTCCAGAAATCAAAGACGAGGATCACGAGCTCAA 1680
 Db 1621 GATATCAGAGACGAGCCGGAAGCTCCAGAAATCAAAGACGAGGATCACGAGCTCAA 1680
 Qy 1681 GTGGAAGAAATGAGGTGATGATGAATCAGTTGGAAGAGATCTTGTCTGACAGAGAGA 1740
 Db 1681 GTGGAAGAAATGAGGTGATGATGAATCAGTTGGAAGAGATCTTGTCTGACAGAGAGA 1740
 Qy 1741 CGGAGTATCTCTACGATCTGAGCTGAGAGAGTCTGAGCTTGTCTGTAAGAAATTCAG 1800
 Db 1741 CGGAGTATCTCTACGATCTGAGCTGAGAGAGTCTGAGCTTGTCTGTAAGAAATTCAG 1800
 Qy 1801 CGGAAAGCGACAGAAATGTCAGCATAACTGTTGAAGCTTAAGATCAAGGGAAGCTGAA 1860
 Db 1801 CGGAAAGCGACAGAAATGTCAGCATAACTGTTGAAGCTTAAGATCAAGGGAAGCTGAA 1860
 Qy 1861 GTGGAAGAAATGAGGTGATGATGAATCAGTTGGAAGAGATCTTGTCTGACAGAGAGA 1920
 Db 1861 GTGGAAGAAATGAGGTGATGATGAATCAGTTGGAAGAGATCTTGTCTGACAGAGAGA 1920
 Qy 1921 CTCGAGAGAACTGAGAGAGGCTGTAAAGCCAGACGAGAGCCAGAGCTGCTGAG 1980
 Db 1921 CTCGAGAGAACTGAGAGAGGCTGTAAAGCCAGACGAGAGCCAGAGCTGCTGAG 1980
 Qy 1981 AATATCCGCGAGCAAGAGAGAGCCGAGAGAGGAGCTGAGAGAGCTGAGAGAGCCGAGAG 2040
 Db 1945 -----GCAAGAGAGCGAGCCGAGAGGAGGAGCTGAGAGAGCTGAGAGAGCCGAGAG 1992
 Qy 2041 GATTCTTCTGAGAGCATCAGAAAGAGCTGTGAGAGCTGAGAGAGCCGCTTCTCTG 2100
 Db 1993 GATTCTTCTGAGAGCATCAGAAAGAGCTGTGAGAGCTGAGAGAGCCGCTTCTCTG 2052
 Qy 2101 GAGAAACAAGGTAAAGAGACTAGAGACCATGAGAGCTGAGAGAGAAACAAGTGAAGATGAC 2160
 Db 2053 GAGAAACAAGGTAAAGAGACTAGAGACCATGAGAGCTGAGAGAGAAACAAGTGAAGATGAC 2112
 Qy 2161 ATCCAGACAAAAATCCAAACAGATCCAGACAGATGAGCTGATAAATTTCTGAGCTCGAAGAG 2220
 Db 2113 ATCCAGACAAAAATCCAAACAGATCCAGACAGATGAGCTGATAAATTTCTGAGCTCGAAGAG 2172
 Qy 2221 AAAATCTGGGAGGCCCAAGTCTCAGCCAGACACTAGAAGTGCCTGAAACAGAAAGAG 2280
 Db 2173 AAAATCTGGGAGGCCCAAGTCTCAGCCAGACACTAGAAGTGCCTGAAACAGAAAGAG 2232
 Qy 2281 CACACATATGAGAGAAAGATTTAAAGTGTGAGCAATCAGATTAAGAAAGAAAGCTGAGTAC 2340
 Db 2233 CACACATATGAGAGAAAGATTTAAAGTGTGAGCAATCAGATTAAGAAAGAAAGCTGAGTAC 2292
 Qy 2341 AAGGAGACATGAGAGACATGATGACAGACAGAGAGAGGAGCCATGAGAGAGGAGGAGAA 2400
 Db 2293 AAGGAGACATGAGAGACATGATGACAGACAGAGAGAGGAGCCATGAGAGAGGAGGAGAA 2352
 Qy 2401 ATTCTCAGCAACGAGAGGAGGATGATCAATGATGATTCAGAGATTCAGATTCCTGAGAA 2460
 Db 2353 ATTCTCAGCAACGAGAGGAGGATGATCAATGATGATTCAGAGATTCAGATTCCTGAGAA 2412
 Qy 2461 CAGAGATTTGTGAGATCTGTGAGAGCAATTAACCTTCAGCAAAATACAGCTTTTAAACC 2520
 Db 2413 CAGAGATTTGTGAGATCTGTGAGAGCAATTAACCTTCAGCAAAATACAGCTTTTAAACC 2472
 Qy 2521 CAAAGGAACTGAAGGAGCCAGAGAGATGATTTCTGAATCAGGCAACGAAATTTTAC 2580
 Db 2473 CAAAGGAACTGAAGGAGCCAGAGAGATGATTTCTGAATCAGGCAACGAAATTTTAC 2532
 Qy 2581 CTGAGACACAGGCTGGAGAGTTGAGAGCCAGAGAACGAAAACTGAGAGAGCAGCTGAG 2640

Db 2533 CTGAGACACAGGCTGGGAAGTTGAGAGGCCAGAACCGAAAACTGAGAGAGCAGCTGAG 2592
 Qy 2641 AAGATACGCCACCAAGACCAAGTGAACAGAAATCGGCTGTGGAACCTGAGACAAAGTTG 2700
 Db 2593 AAGATACGCCACCAAGACCAAGTGAACAGAAATCGGCTGTGGAACCTGAGACAAAGTTG 2652
 Qy 2701 CGGAGGTCAGTGTAGAGCAGAGAGCAGAACTGGAGTCAAGGCCAGCTCACAGAG 2760
 Db 2653 CGGAGGTCAGTGTAGAGCAGAGAGCAGAACTGGAGTCAAGGCCAGCTCACAGAG 2712
 Qy 2761 CTACAGCTCTCCCTGAGAGAGCCGAGTCAAGTGTGACAGCCCTGACAGCTGACCGGCG 2820
 Db 2713 CTACAGCTCTCCCTGAGAGAGCCGAGTCAAGTGTGACAGCCCTGACAGCTGACCGGCG 2772
 Qy 2821 GCCCTGAGAGCCAGCTTCCAGAGCCGAGACAGAGCTGGAAGAGACACAGCAAGAACT 2880
 Db 2773 GCCCTGAGAGCCAGCTTCCAGAGCCGAGACAGAGCTGGAAGAGACACAGCAAGAACT 2832
 Qy 2881 GAAAGAGATCCAGGACCTCAGGCACTAGAGATGAAATCCAGGCGAAATTTGATGCT 2940
 Db 2833 GAAAGAGATCCAGGACCTCAGGCACTAGAGATGAAATCCAGGCGAAATTTGATGCT 2892
 Qy 2941 CTTGCTTAACGCTGTACTGTATCAAGACCTGAGAGAGCAGCTAAACAGCTGACCGAG 3000
 Db 2893 CTTGCTTAACGCTGTACTGTATCAAGACCTGAGAGAGCAGCTAAACAGCTGACCGAG 2952
 Qy 3001 GACAAAGCTGAATCTCAACAAACAACTTCTACTTCTCCAAACAACTGATGAGCTTCT 3060
 Db 2953 GACAAAGCTGAATCTCAACAAACAACTTCTACTTCTCCAAACAACTGATGAGCTTCT 3012
 Qy 3061 GGGCGCAACGACAGATTTGTAACAATGCGAAGTGAAGTGAACCAATTCGCGCGAGATC 3120
 Db 3013 GGGCGCAACGACAGATTTGTAACAATGCGAAGTGAAGTGAACCAATTCGCGCGAGATC 3072
 Qy 3121 ACGGAACGAGATGAGAGCTTACAGCGAAGCAACAAAGTGAAGCTGAGAGACCAAG 3180
 Db 3073 ACGGAACGAGATGAGAGCTTACAGCGAAGCAACAAAGTGAAGCTGAGAGACCAAG 3132
 Qy 3181 TGCAACATGCTGAGAGAAACAGTCAATGATTTGAGAGCCCTTAACAGATGAGCTGAGAA 3240
 Db 3133 TGCAACATGCTGAGAGAAACAGTCAATGATTTGAGAGCCCTTAACAGATGAGCTGAGAA 3192
 Qy 3241 AAGAGCGAGTGGAGAGCTTGAAGAGCGCTTGGAGTATGAGAAATCCAGTTGAG 3300
 Db 3193 AAGAGCGAGTGGAGAGCGCTTGAAGAGCGCTTGGAGTATGAGAAATCCAGTTGAG 3252
 Qy 3301 TGTGGGTTGAGAGCTGAGAGAGATGCTGAGAACCGAGAAACAGAGCAGGCGAGAGCC 3360
 Db 3253 TGTGGGTTGAGAGCTGAGAGAGATGCTGAGAACCGAGAAACAGAGCAGGCGAGAGCC 3312
 Qy 3361 GATCAGCGATCAACGAGCTGCGCAGGTGCTGAGAGTGGAGTGAAGAGAGCAAGAGCT 3420
 Db 3313 GATCAGCGATCAACGAGCTGCGCAGGTGCTGAGAGTGGAGTGAAGAGAGCAAGAGCT 3372
 Qy 3421 GAGATTCGCTCTGAGCAGAGCTCTCAAGAGCAAGAGCTGAAGGCCAGAGCTTCT 3480
 Db 3373 GAGATTCGCTCTGAGCAGAGCTCTCAAGAGCAAGAGCTGAAGGCCAGAGCTTCT 3432
 Qy 3481 GACAGCTCAATGACCTGGAAGAGCAATGCTATGTTGAATGATGCTCCAGAGCTTA 3540
 Db 3433 GACAGCTCAATGACCTGGAAGAGCAATGCTATGTTGAATGATGCTCCAGAGCTTA 3492
 Qy 3541 CAGCAGAGCTGAGACTGAACGAGAGCTCAACAGAGGCTTCTGGAAGAGCAAGGCCAA 3600
 Db 3493 CAGCAGAGCTGAGACTGAACGAGAGCTCAACAGAGGCTTCTGGAAGAGCAAGGCCAA 3552
 Qy 3601 TTACAGCAGAGATGAGCTGAGAGAAATCAATTTCCGCTGACTCAAGAGCTGCA 3660
 Db 3553 TTACAGCAGAGATGAGCTGAGAGAAATCAATTTCCGCTGACTCAAGAGCTGCA 3612
 Qy 3661 GAAAGCTTAGATGGGCTGATCTTACAGAGACAGAAAGAGTGAATTTGAGATCAGCTG 3720
 Db 3613 GAAAGCTTAGATGGGCTGATCTTACAGAGACAGAAAGAGTGAATTTGAGATCAGCTG 3672

Db 5683 AGACAGCCCAACAGAGGAGGAGCCACCACTACAGAGACATCAACAGCCGCTGGCC 5742
Qy 5896 TCCAGCCCAAGCCGCGCCGAGAGCCCAAGCCCAAGAGCCCAAGCCCAAGCCG 5955
Db 5743 TCCAGCCCAAGCCGCGCCGAGAGCCCAAGCCCAAGAGCCCAAGCCCAAGCCG 5802
Qy 5956 TACCGGAGAGGAGGAGCCGAGCTGCGAGGAGCAAGTCTTCTGCGCCGCCCTGAGAGCA 6015
Db 5803 TACCGGAGAGGAGGAGCCGAGCTGCGAGGAGCAAGTCTTCTGCGCCGCCCTGAGAGCA 5862
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Db 5863 GAGAACTCCCGCGCGGAGATCTCAGACAGCGGAGAGAGGAGTCCCGCGAGAGCTGTTT 5922
Qy 6076 GAGAGACAGAGAGGAGGAGGAGCTGCGCGAGAGCCGAGAGAGCCCGCTGCTCCAGAGTG 6135
Db 5923 GAGAGACAGAGAGGAGGAGGAGCTGCGCGAGAGCCGAGAGAGCCCGCTGCTCCAGAGTG 5982
Qy 6136 AACAGAGCTGGAGCCAGTCTTC 6158
Db 5983 AACAGAGGAGAGAGGAGAGTGC 6005

RESULT 13
US-10-017-216-1
; Sequence 1, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KABELLER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prod
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017,216
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-017-216-1

Query Match 91.8%; Score 5661.4; DB 13; Length 6574;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

Qy 1 ATGTTGAAGTTCAAAATATGAGAGCGGAAATCTTTGGATGCTGCTGCTGAACCAT 60
Db 19 ATGTTGAAGTTCAAAATATGAGAGCGGAAATCTTTGGATGCTGCTGCTGAACCAT 78
Qy 61 GCCAGCCGAGGCTCCAGGCTGAATCTGTTCTTCAAGGAGAAACCACTTTATGACTCA 120
Db 79 GCCAGCCGAGGCTCCAGGCTGAATCTGTTCTTCAAGGAGAAACCACTTTATGACTCA 138
Qy 121 CAGCAATGCTCTCTTTTCCCGAAGAGATATGATGCTCTTTGTTCTTTTGA 180
Db 139 CAGCAATGCTCTCTTTTCCCGAAGAGATATGATGCTCTTTGTTCTTTTGA 198
Qy 181 GAATGAGTCAGCTCTCTGATGAGATTAAGACAGTGAACAATTGTCCGGAAGTAT 240
Db 199 GAATGAGTCAGCTCTCTGATGAGATTAAGACAGTGAACAATTGTGTCCGGAAGTAT 258
Qy 241 TCCGACACCATAGCTAGTGAATTAAGAGCTCCAGCTTCCGCAAGAGACTTCGAAGTCA 300
Db 259 TCCGACACCATAGCTAGTGAATTAAGAGCTCCAGCTTCCGCAAGAGACTTCGAAGTCA 318
Qy 301 AGCTTGTAGTGTGTGTCACTTTGCTGAAGTGAAGTGTGAAGAGAAAGCAACCGGG 360
Db 319 AGCTTGTAGTGTGTGTCACTTTGCTGAAGTGAAGTGTGAAGAGAAAGCAACCGGG 378

Qy 361 GACATCTATGCTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCCAAGAGCAAGTTTCA 420
Db 379 GACATCTATGCTATGAAAGTGAAGAAAGAGGCTTTATTTGGCCCAAGAGCAAGTTTCA 438
Qy 421 TTTTGTGAGAGAGAGGAGAAATATATATCTGAGAGCAAGCCGAGATCCCCAATTA 480
Db 439 TTTTGTGAGAGAGAGGAGAAATATATATCTGAGAGCAAGCCGAGATCCCCAATTA 498
Qy 481 CAGTATGCTTTTCAGAGCAAAAATCACTTTATCTGATCAATGAAATATCAAGCTGAGAGG 540
Db 499 CAGTATGCTTTTCAGAGCAAAAATCACTTTATCTGATGAGAGAAATATCAAGCTGAGAGG 558
Qy 541 GACTTGTCTCACTTTTGAATATATATGAGAGCAAGTATGATGAAACCTGATACACTT 600
Db 559 GACTTGTCTCACTTTTGAATATATATGAGAGCAAGTATGATGAAACCTGATACACTT 618
Qy 601 TACCTAGCTGAGCTGATTTTGGCTGTCAAGGCTTCATCTGATGAGGATACGTCATCA 660
Db 619 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGGCTTCATCTGATGAGGATACGTCATCA 678
Qy 661 GACATCAAGCTGAGAGCAATCTCTGTTGACCGCAGACACATCAAGCTGTGATTTT 720
Db 679 GACATCAAGCTGAGAGCAATCTCTGTTGACCGCAGACACATCAAGCTGTGATTTT 728
Qy 721 GATCTGCGCGCAAAATGAATTCAAACAGATGCTGAATGCCAACTCCGATTTGGAGC 780
Db 739 GATCTGCGCGCAAAATGAATTCAAACAGATGCTGAATGCCAACTCCGATTTGGAGC 798
Qy 781 CCAATTAACAGCTCTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 799 CCAATTAACAGCTCTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 858
Qy 841 GGCCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 859 GGCCTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 918
Qy 901 TCCCTCTGCGAGAGGAACTCTGCGAGAACTTCAATTAATTAATTAATTAATTAATTAAT 960
Db 919 TCCCTCTGCGAGAGGAACTCTGCGAGAACTTCAATTAATTAATTAATTAATTAATTAAT 978
Qy 961 TTTTGAATTTTCCAAATGACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 979 TTTTGAATTTTCCAAATGACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1038
Qy 1021 TTGTTGCGGCGCAG 1080
Db 1039 TTGTTGCGGCGCAG 1098
Qy 1081 TCTAAATTTGATGAGAAACATTCGTAACTCTCTCCCTCTCTCTCTCTCTCTCTCTCTCA 1140
Db 1099 TCTAAATTTGATGAGAAACATTCGTAACTCTCTCTCCCTCTCTCTCTCTCTCTCTCTCA 1158
Qy 1141 TCTGAGATGACACTTCCAAATTTTGAATGAACAGAGAAATTCGTGAGTTTCACTCT 1200
Db 1159 TCTGAGATGACACTTCCAAATTTTGAATGAACAGAGAAATTCGTGAGTTTCACTCT 1218
Qy 1201 CCGTGCAGCTGAGCCCTCAGGCTTCTGCGGAGAGAACTGCGGTTTGTGGGATTTTCG 1260
Db 1219 CCGTGCAGCTGAGCCCTCAGGCTTCTGCGGAGAGAACTGCGGTTTGTGGGATTTTCG 1278
Qy 1261 TACAGCAAGGCACTGGGAGATCTTGGATGATCTGAGTCTGTGTGTGTGTGTGTGTGTGT 1320
Db 1279 TACAGCAAGGCACTGGGAGATCTTGGATGATCTGAGTCTGTGTGTGTGTGTGTGTGTGT 1338
Qy 1321 CCTGCGCAAGACTGCTCATGGAAGAACTTCTCATGAAGCAAGAGCTGACAAAG 1380
Db 1339 CCTGCGCAAGACTGCTCATGGAAGAACTTCTCATGAAGCAAGAGCTGACAAAG 1398
Qy 1381 TCTCAGAGCAAGTGTCAAAAGATGAGAGAGAAATGACCCGTTTAACTCGAGAGTGTCA 1440
Db 1399 TCTCAGAGCAAGTGTCAAAAGATGAGAGAGAAATGACCCGTTTAACTCGAGAGTGTCA 1458
Qy 1441 GAGTGAAGGCTGTGCTTATGTCAGAAAGAGTGAAGGCTTCTGAGACTCAGAGA 1500

1459 GAGGTGAGGCTGTGCTTAAAGTGAAGAGGCTGAAGGCTCTGAGACTCAAGAGA 1518
1501 TCCCTCTGAGACAGACCTTGTCTAAGTCAAGATGACAGTAAAGCGAAGT 1560
1519 TCCCTCTGAGACAGACCTTGTCTAAGTCAAGATGACAGTAAAGCGAAGT 1578
1561 TTGGAGAACACGAGATGAGAGTGTCTCCAGAGAGATCAAGACATCTGACCTTCAT 1620
1579 TTGGAGAACACGAGATGAGAGTGTCTCCAGAGAGATCAAGACATCTGACCTTCAT 1638
1621 GATATCAGAGACAGAGCCGAGAGCTCAAGAAATCAAGAGCAGAGTACAGGCTCAA 1680
1639 GATATCAGAGACAGAGCCGAGAGCTCAAGAAATCAAGAGCAGAGTACAGGCTCAA 1698
1681 GTGGAGAAATGAGGTTGATGATGAATCAAGTTGAGAGAGATCTTGTCTCAGCAAGAGA 1740
1699 GTGGAGAAATGAGGTTGATGATGAATCAAGTTGAGAGAGATCTTGTCTCAGCAAGAGA 1758
1741 CGGAGTATCTTAACGAATCTGAGCTGAGAGAGTCTTGCGCTTGTCTGTAAGAAATTCAG 1800
1759 CGGAGTATCTTAACGAATCTGAGCTGAGAGAGTCTTGCGCTTGTCTGTAAGAAATTCAG 1818
1801 CGGAAAGCAGACAGATGTCAGCATTAACGTGTAAGGCTAAAGATCAAGGGAAGCTGAA 1860
1819 CGGAAAGCAGACAGATGTCAGCATTAACGTGTAAGGCTAAAGATCAAGGGAAGCTGAA 1878
1861 GTGGAGAAATGAGGTTGATGATGAATCAAGTTGAGAGAGATCTTGTCTCAGCAAGAGA 1920
1879 GTGGAGAAATGAGGTTGATGATGAATCAAGTTGAGAGAGATCTTGTCTCAGCAAGAGA 1938
1921 CTCGAGAGAAATGAGAGAGGCTGTAAAGCCAGACCGAGGCTCAGAGCTGCTCAG 1980
1939 CTCGAGAGAAATGAGAGAGGCTGTAAAGCCAGAGCTGCTCAGAGCTGCTCAG 1962
1981 AATATCCGCGCAAGAGCGAGCGAGAGGAGCTGAGAAAGCTGCAAGACGAGAG 2040
1963 -----CGAAAGAGCGAGCGAGAGGAGCTGAGAAAGCTGCAAGACGAGAG 2010
2041 GATTTCTTGAAGGATCAGAAAGAAAGCTGTGGAAGCTGAGAGAGCGCGCATTTCTCTG 2100
2011 GATTTCTTGAAGGATCAGAAAGAAAGCTGTGGAAGCTGAGAGAGCGCGCATTTCTCTG 2070
2101 GAGAACAGATTAAGAGATTAAGAGACATGAGAGCTGAGAGAAACAGACTGAAGATGAC 2160
2071 GAGAACAGATTAAGAGATTAAGAGACATGAGAGCTGAGAGAAACAGACTGAAGATGAC 2130
2161 ATCCAGACAAATATCCCAAGATCCAGAGATGAGCTGATTAATTTGAGAGCTCGAAGAG 2220
2131 ATCCAGACAAATATCCCAAGATCCAGAGATGAGCTGATTAATTTGAGAGCTCGAAGAG 2190
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2191 AAACATCGGAGGCGCCAAATCTCAAGCCAGACCTTAAGAGTCACTGAAGAGAG 2250
2281 CAGCATATGAGAGAAAGATTAAGTGTGAGCAATCAGATTAAGAAAGAGCTGCTGAC 2340
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2761 CTACAGCTCTCCCTGAGAGCGCGAGTCAAGTTGACAGCCCTGAGAGCTGACGAGGCG 2820
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RESULT 14
US-10-325-430-10
; Sequence 10, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; TITLE OF INVENTION: 32838, 336 and 52908
; FILE REFERENCE: MP101-294PRM
; CURRENT APPLICATION NUMBER: US/10/325,430
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-325-430-10

Query Match 91.8%; Score 5661.4; DB 16; Length 6574;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

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Qy 1921 CTCGAAGAGAACTGAGAGAGGCTGTAAAGCCAGCAGCAGAGCCAGAGCTGCTGAG'1980
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Qy 2821 GCCCTGAGAGCCAGGCTTCGACGAGGCGAAGACAGAGCTGGAAGAGACCAAGAGAACT 2880
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RESULT 15
US-10-757-262-51
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; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheci, Venkateswarlu
; APPLICANT: Sliou-Santiago, Inmaculada
; APPLICANT: Eliasof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
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; TITLE OF INVENTION: 55053
; FILE REFERENCE: MP103-007P1RNONMIN
; CURRENT APPLICATION NUMBER: US/10757, 262
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; PRIOR APPLICATION NUMBER: US 60/457, 901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468, 775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471, 614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478, 742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488, 529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491, 156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499, 594

; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506, 332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 6574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)...(6180)
US-10-757-262-51

Query Match 91.8%; Score 5661.4; DB 18; Length 6574;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

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(without alignments)
19571.828 Million cell updates/sec

Title: US-10-791-666-1
Perfect score: 6165
Sequence: 1 atgctgaattcaataatg9.....gggaccagcttcagratataa 6165

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_esc1:*
2: gb_esc2:*
3: gb_hrc:*
4: gb_esc3:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	913.6	14.8	1011	5	BQ070955 AGENCOURT
2	822.6	13.3	879	5	BQ228524 AGENCOURT
3	814	13.2	956	5	BQ071141 AGENCOURT
4	810.2	13.1	830	5	BU181633 AGENCOURT
5	750.6	12.2	849	4	BI253509 602973370
6	732.8	11.9	855	5	BK342268 BX342268
7	732	11.9	757	7	CN281134 170004237
8	705.6	11.4	958	3	BC031156 Mus muscu
9	698.2	11.3	843	4	BG912161 602812833
10	649.4	10.5	653	7	CN295302 170006001
11	629.2	10.2	652	2	BF905370 IL3-MT026
12	628.8	10.2	640	5	BQ807302 NISC_K01
13	620.4	10.1	716	7	CK636398 UI-M-HNO
14	603.4	9.8	881	4	BG976452 602846269
15	602.6	9.8	698	5	BP146990 BP146990
16	599	9.7	891	4	BI558919 603240959
17	591.4	9.6	746	6	CA749280 UI-M-FV0
18	588.6	9.5	681	2	AM605350 QV3-DT004
19	581.6	9.4	968	5	BU138506 603132657
20	575.2	9.3	1078	5	BU139267 603132236
21	574.4	9.3	698	6	CD348416 UI-M-FV0
22	573.6	9.3	647	7	CF744580 UI-M-GV0
23	570.4	9.2	730	7	CF723360 UI-M-GV0
24	566.4	9.2	1085	5	BM904785 AGENCOURT

25	557.4	9.0	647	2	BB207065	BB207065
26	557.2	9.0	675	7	CF735558	CF735558 UI-M-HB0
27	538	8.7	566	5	BK481181	BK481181 DKE2686P
28	515.4	8.4	839	7	CN225795	CN225795 WLA078D10
29	511.8	8.3	775	5	BU105833	BU105833 603005490
30	511	8.3	804	5	BU236617	BU236617 603411670
31	508.6	8.2	547	7	CF744826	CF744826 UI-M-GV0
32	498.2	8.1	719	5	BU339218	BU339218 603515216
33	497.4	8.1	563	7	CN536028	CN536028 UI-M-HS0
34	495.6	8.0	933	5	BU232508	BU232508 603408272
35	494.6	8.0	532	7	CR735660	CR735660 CR735660
36	491.6	8.0	875	5	BK723780	BK723780 BX723780
37	489.6	7.9	525	7	CR735680	CR735680 CR735680
38	489.6	7.9	596	7	CF540358	CF540358 UI-M-GV0
39	488	7.9	657	5	BQ831488	BQ831488 IL612149
40	481	7.8	820	5	BQ941506	BQ941506 AGENCOURT
41	479.6	7.8	922	7	CR746615	CR746615 CR746615
42	460.8	7.5	798	5	BX888120	BX888120 BX888120
43	457.6	7.4	789	7	CO798747	CO798747 AGENCOURT
44	451.4	7.3	459	5	BU429033	BU429033 UI-M-HB0
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ALIGNMENTS

RESULT 1
LOCUS BQ070955 1011 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6855647 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5923441
5' mRNA sequence.
ACCESSION BQ070955
VERSION BQ070955.1 GI:19900001
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
1 (bases 1 to 1011)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINT at:
http://image.llnl.gov
Plate: LINC2091 row: p column: 02
High quality sequence drop: 634.
Location/Qualifiers
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/clone="IMAGE:5923441"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 47"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

QY 4369 ATGAACTCCCGAGTCTCCAGACCAAGAGCCCAAGCAAGCTTGGACTCTGAAAGGATG 4428
 DB 4421 ATGAACTCCCGAGTCTCCAGACCAAGAGCCCAAGCAAGCTTGGACTCTGAAAGGATG 4480
 QY 4429 ATGAAAGTGGCCGGAATACAAAGAGAGCAGCAAGGCTGGAGCAAGAAATCATTTGC 4488
 DB 4481 ATGAAAGTGGCCGGAATACAAAGAGAGCAGCAAGGCTGGAGCAAGAAATCATTTGC 540
 QY 4489 CTGAGAGGATCAAAAGTCTCATTTATGACAAATGAAGCCAGAGAGCTGGACAGAGCCG 4548
 DB 541 CTGAGAGGATCAAAAGTCTCATTTATGACAAATGAAGCCAGAGAGCTGGACAGAGCCG 600
 QY 4549 GTGGAAGAAATTGAGCTGTGCTCTTCCGAGCGGAGATGATCTAATCAATGCTGCTTGGT 4608
 DB 601 GTGGAAGAAATTGAGCTGTGCTCTTCCGAGCGGAGATGATCTAATCAATGCTGCTTGGT 660
 QY 4609 GCTTCGGAATCGCAATACAGCAAGAGAGATGTCCTACATCTAGTAAGATGAATCT 4668
 DB 661 GCTTCGGAATCGCAATACAGCAAGAGAGATGTCCTACATCTAGTAAGATGAATCT 720
 QY 4669 CACCCGACACCACTGCT-GGCCCGGAGAACTCTTACTTCTAGCTCCAGCTTCCG 4727
 DB 721 CACCCGACACCACTGCTGCTGGGCCCGGAGAACTCTTACTTCTAGCTCCAGCTTCCG 780
 QY 4728 TGACAAACAGCGCTGGGTCAACGCTTAAGATGATGTCAGAGT-GGGAGATTTCTA 4786
 DB 781 TGACAAACAGCGCTGGGTCAACGCTTGAATCATGTTGTCGAGGTGGGAGAGTTTCTA 840
 QY 4787 GGGAAAAGCAAGAGTGTCTAACTGC 4816
 DB 841 GGGAAAAGCAAGAGTGTCTTGGCCG 870

RESULT 3
 B0071141
 LOCUS B0071141 956 bp mRNA linear EST 02-APR-2002
 DEFINITION AGENCOUNT 6853098 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5927502
 5', mRNA sequence..
 B0071141
 ACCESSION B0071141.1 GI:19900187
 VERSION EST.
 KEYWORDS Homo sapiens
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 956)
 NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.jnl.gov
 Plate: L10M2102 row: 1 column: 07
 High quality sequence scop: 650.
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 /db_xref="taxon:9606"
 /clone="IMAGE:5927502"
 /issue_type="neuroblastoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_47"
 /note="Organ: brain; Vector: pOTB7, Site_1: XhoI, Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

Query Match 13.2%; Score 814; DB 5; Length 956;
 Best Local Similarity 97.0%; Pred. No. 2.9e-202;
 Matches 873; Conservative 0; Mismatches 20; Indels 7; Gaps 4;

ORIGIN
 QY 2701 CCGAGAGTCACTTACAGACAGAGAGCAAACTGAGCTCAAGCGCCAGCTCACAG 2760
 DB 1 CCGAGAGTCACTTACAGACAGAGAGCAAACTGAGCTCAAGCGCCAGCTCACAG 60
 QY 2761 CTACAGCTCTCCCTGAGAGGCGGATCAAGCTTGAACGCTTGAAGCTGACCGGCG 2820
 DB 61 CTACAGCTCTCCCTGAGAGGCGGATCAAGCTTGAACGCTTGAAGCTGACCGGCG 120
 QY 2821 GCCCTGAGAGCAGCTTGCAGAGCGGAGACAGAGCTGAAAGACACAGAGAACT 2880
 DB 121 GCCCTGAGAGCAGCTTGCAGAGCGGAGACAGAGCTGAAAGACACAGAGAACT 180
 QY 2881 GAAAGAGATCCAGGCACTACGCGACATAGATGAATCCAGCGCAATTGATGCT 2940
 DB 181 GAAAGAGATCCAGGCACTACGCGACATAGATGAATCCAGCGCAATTGATGCT 240
 QY 2941 CTTCTTACAGCTTACTTATACAGACCTGAGAGACAGTAAACAGCTGACCGAG 3000
 DB 241 CTTCTTACAGCTTACTTATACAGACCTGAGAGACAGTAAACAGCTGACCGAG 300
 QY 3001 GACAAAGCTGAATCAACAAACAACTCTACTTGTCCAAACAACTGATGAGCTTCT 3060
 DB 301 GACAAAGCTGAATCAACAAACAACTCTACTTGTCCAAACAACTGATGAGCTTCT 360
 QY 3061 GCGGCCCAACGAGAGATTGTACAACTGCGAGTGAAGTGAACATCTCCGCGGAGATC 3120
 DB 361 GCGGCCCAACGAGAGATTGTACAACTGCGAGTGAAGTGAACATCTCCGCGGAGATC 420
 QY 3121 ACGGAACGAGATGAGTACCTTACCGCCGAAAGCAATGAGGCTTGAAGACACG 3180
 DB 421 ACGGAACGAGATGAGTACCTTACCGCCGAAAGCAATGAGGCTTGAAGACACG 480
 QY 3181 TGCACATCTGAGAGAAAGGTCATGATTTGAGGCGCTTAAAGATGAGCTGATGAA 3240
 DB 481 TGCACATCTGAGAGAAAGGTCATGATTTGAGGCGCTTAAAGATGAGCTGATGAA 540
 QY 3241 AAAGAGCGCAGATGGAGGCTGAGAGAGCTCTGAGTGAATGAGATCCAGTTTGA 3300
 DB 541 AAAGAGCGCAGATGGAGGCTGAGAGAGCTCTGAGTGAATGAGATCCAGTTTGA 600
 QY 3301 TGTGGGTTGAGAGTGTGAGATGCTGACACCGAGAAACAGAGCGGCGAGAGCC 3360
 DB 601 TGTGGGTTGAGAGTGTGAGATGCTGACACCGAGAAACAGAGCGGCGAGAGCC 660
 QY 3361 GATCAGCGGATACCGAGTCTGCCAGAGTGTGAGGCTGCGATGAGAGAGCAAGGCT 3420
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 QY 3421 GAGATTCTGCTCTGAGAGGCTCTCAAGAGAGCAAGAGCTGAGAGGCTCTCTCT 3480
 DB 721 GAGATTCTGCTCTGAGAGGCTCTCAAGAGAGCAAGAGCTGAGAGGCTCTCTCT 780
 QY 3481 GACAACTCATGACCT-GGAGAGAGATCTTATGCTTGA--TGAATGCCGAGAC 3537
 DB 781 GACAACTCATGACCTGAGAGAGATCTTATGCTTGA--TGAATGCCGAGAC 840
 QY 3538 TTAACAGCAA--GCTGAGAGCTGAAC--GAGAGTCAACAGAGGCTTCTGGAAGGA 3593
 DB 841 TTAACAGCAAAGCTGGAAGTGAACGAGAGGCTTCTGGAAGGA 900

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RESULT 4
LOCUS      BU181633                830 bp      mRNA      linear      EST 04-SEP-2002
DEFINITION AGNCOURT_7906225 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6140538
            5', mRNA sequence.
ACCESSION  BU181633
VERSION     BU181633.1  GI:22695617
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1  (bases 1 to 830)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLES     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: L1AM13459 row: e column: 19
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            Average insert size 1.75 kb. Library constructed by Life
            Technologies."

ORIGIN
Query Match      13.1%; Score 810.2; DB 5; Length 830;
Best Local Similarity 99.4%; Pred. No. 2.7e-201;
Matches 823; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY      2435 TGGATTCCAAAGTCAAGTCCCTTGGACACAGAGATTGTGGAACTGTCTGAAAGCCAAATTAAC 2494
DB      1 TGGATTCCAAAGTCAAGTCCCTTGGACACAGAGATTGTGGAACTGTCTGAAAGCCAAATTAAC 60

QY      2495 TTGCAGCAATATAGACAGTCTTTTACCAAGAAACATGAAAGGCCCAAGAGATGATT 2554
DB      61 TTGCAGCAATATAGACAGTCTTTTACCAAGAAACATGAAAGGCCCAAGAGATGATT 120

QY      2555 CTGAACCTCAGGCAAGAAATTTTACCTGGAGACACAGGCTGGAAAGTTGGAGGCCCAAG 2614
DB      121 CTGAACCTCAGGCAAGAAATTTTACCTGGAGACACAGGCTGGAAAGTTGGAGGCCCAAG 180

QY      2615 ACCGAAATCTGAGAGGACGCTGGAGAAATCGACCAACCAACACACAGTGAAGAATTC 2674
DB      181 ACCGAAATCTGAGAGGACGCTGGAGAAATCGACCAACCAACACACAGTGAAGAATTC 240

QY      2675 GGCTGTGGAACTGAGAGCAAGATTGGGGAGGTCTGTAGAGACAGAGAGCAGAAAC 2734
DB      241 GGCTGTGGAACTGAGAGCAAGATTGGGGAGGTCTGTAGAGACAGAGAGCAGAAAC 300

QY      2735 TGGAGCTCAAGCCGCACTCAAGAGTCAAGCTCTCCCTGACAGAGCGGAGTCAAGT 2794
DB      301 TGGAGCTCAAGCCGCACTCAAGAGTCAAGCTCTCCCTGACAGAGCGGAGTCAAGT 360

QY      2795 TGAACAGCCCTGACAGGCTGACAGGCGGCGCTTGGAGAGCCAGTTCCGACAGGCAAGACAG 2854
DB      361 TGAACAGCCCTGACAGGCTGACAGGCGGCGCTTGGAGAGCCAGTTCCGACAGGCAAGACAG 420

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QY      2855 AGCTGAAAGAGACCAACAGAGAAAGCTGAAGAGAGATCCAGGCACTCATGGCATAAGAG 2914
DB      421 AGCTGAAAGAGACCAACAGAGAAAGCTGAAGAGAGATCCAGGCACTCATGGCATAAGAG 480

QY      2915 ATGAAATTCAGGCGCAATTTGATGCTTCCTGTAACAGGCTGATCTGTAATCACAGACTGG 2974
DB      481 ATGAAATTCAGGCGCAATTTGATGCTTCCTGTAACAGGCTGATCTGTAATCACAGACTGG 540

QY      2975 AGAGAGCTTAACACAGCTGACCGAGGACCAAGCTGTAACCAACCAAACTTCTACT 3034
DB      541 AGAGAGCTTAACACAGCTGACCGAGGACCAAGCTGTAACCAACCAAACTTCTACT 600

QY      3035 TGTCCAAACACTCGATGAGGCTTGTGCGCCCAAGACAGAGTTGTACAACTGCGAAGT 3094
DB      601 TGTCCAAACACTCGATGAGGCTTGTGCGCCCAAGACAGAGTTGTACAACTGCGAAGT 660

QY      3095 AAGTGACCATCTCCGCGCGGAGATCACGGAACGAGAGTGAAGCTTACAGCCAGAAC 3154
DB      661 AAGTGACCATCTCCGCGCGGAGATCACGGAACGAGAGTGAAGCTTACAGCCAGAAC 720

QY      3155 AAACAGTAGAGGCTCTGAAGACCAAGTGCACCATGCTGGAGGAACAGTCAATGATTT 3213
DB      721 AAACAGTAGAGGCTCTGAAGACCAAGTGCACCATGCTGGAGGAACAGTCAATGATTT 780

QY      3214 GAGGCCCTTAACGATGAGCTGTGTAAGAAAAGCGGCACTGGAGGCC 3261
DB      781 GAGGCCCTTAACGATGAGCTGTGTAAGAAAAGCGGCACTGGAGGCC 828

RESULT 5
LOCUS      BI253509                849 bp      mRNA      linear      EST 17-JUL-2001
DEFINITION 602973370F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5112737 5',
            mRNA sequence.
ACCESSION  BI253509
VERSION     BI253509.1  GI:14805003
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1  (bases 1 to 849)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/.
TITLES     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-remail.nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
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            Technologies."

ORIGIN

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Query Match 12.2%; Score 750.6; DB 4; Length 849;
 Best Local Similarity 98.5%; Pred. No. 1.4e-185;
 Matches 789; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

4812 ACTGCTTGAAACTCCCTGCTGAACTGGAAGGTGATGACCGCTCTAGACATGATGAC 4871
 3 AGCGCTGGAAACTCCCTGCTGAACTGGAAGGTGATGACCGCTCTAGACATGATGAC 62

4872 GCTGCTCTTCACTGATGACCAAGTGTGTTGGTGGCACCAGGAAGGCTCTACGCTTGA 4931
 63 GCTGCTCTTCACTGATGACCAAGTGTGTTGGTGGCACCAGGAAGGCTCTACGCTTGA 122

4932 TGTCTTGAAAACTCCCTAACCATGCTCCAGGAATGAGAGCTCTTCAAAATTTATAT 4991
 123 TGTCTTGAAAACTCCCTAACCATGCTCCAGGAATGAGAGCTCTTCAAAATTTATAT 182

4992 TATCAAGACCTGAGAGCTACTATCATATAGACAGGAAGAGCGGCACTGTCTTGT 5051
 183 TATCAAGACCTGAGAGCTACTATCATATAGACAGGAAGAGCGGCACTGTCTTGT 242

5052 GGAAGTGAAGAAAGTGAAGAGTCCCTGCGCCAGTCCCACTGCTGCGCCAGCCGACAT 5111
 243 GGAAGTGAAGAAAGTGAAGAGTCCCTGCGCCAGTCCCACTGCTGCGCCAGCCGACAT 302

5112 CTCACCCCACTTTTGAAGCTGTCAAGGGCTGCCCTTGTGGGGCAGCGAAATTTGA 5171
 303 CTCACCCCACTTTTGAAGCTGTGTCAAGGGCTGCCCTTGTGGGGCAGCGAAATTTGA 362

5172 GAAGGGCTCTGCTGATGTGACAGCAGTCCCAAGCAAGTGTCTCTCGCTACCAAGA 5231
 363 GAAGGGCTCTGCTGATGTGACAGCAGTCCCAAGCAAGTGTCTCTCGCTACCAAGA 422

5232 AAACCTCAGCAATATCTGATCCGGAAGAGATAGAGACCTGAGACCTGAGCTGTAT 5291
 423 AAACCTCAGCAATATCTGATCCGGAAGAGATAGAGACCTGAGACCTGAGCTGTAT 482

5292 CCACCTTCAACATTTATAGATATCTCTATTGGAACCAATTAATTCTAGAAATGACATGAA 5351
 483 CCACCTTCAACATTTATAGATATCTCTATTGGAACCAATTAATTCTAGAAATGACATGAA 542

5352 GCAAGTACAGCTCGAGGAATTCCTGGAATAAGATGACATTCCTTGGGCACTGTGTAT 5411
 543 GCAAGTACAGCTCGAGGAATTCCTGGAATAAGATGACATTCCTTGGGCACTGTGTAT 602

5412 TGCAGCTCTTTCACACAGCTTCCTGTCTCAATCTGTCAGTGAACAGCGCAGGACAGG 5471
 603 TGCAGCTCTTTCACACAGCTTCCTGTCTCAATCTGTCAGTGAACAGCGCAGGACAGG 662

5472 AAGAGATATCTGCTGTGTTTCCAGAAATTTGAGAGTGTCTGATTTCTTACGAAAGAGC 5531
 663 AAGAGATATCTGCTGTGTTTCCAGAAATTTGAGAGTGTCTGATTTCTTACGAAAGAGC 722

5532 T-AGCGCAGCAGACGATCTCAAGTGAAGTGCCTTACCTTGGCCTTGGCTTACAGAAAC 5590
 723 TAAAGCGCAGCAGACGATCTCAAGTGAAGTGCCTTACCTTGGCCTTGGCTTACAGAAAC 780

5591 CCTATCTGTTTGTGACCCACT 5611
 781 CCTATCTGTTTGTGACCCACT 801

RESULT 6
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 ACCESSION BX342268
 VERSION BX342268.2 GI:46268625
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 855)
 AUTHORS Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 2, 2003 this sequence version replaced gi:30334095.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 6533.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0DK011920&pic=6533.r.

FEATURES
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 11.9%; Score 732.8; DB 5; Length 855;
 Best Local Similarity 99.6%; Pred. No. 6.6e-181;
 Matches 745; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

5418 CTCCTTCAACAGCTTCCTGCTCTCAATCTGACGTGAACAGCGCAGCGAGAGAGA 5477
 1 CTCCTTCAACAGCTTCCTGCTCTCAATCTGACGTGAACAGCGCAGCGAGAGAGA 60

5478 GTACTTGTCTGTCTTCCAGGAATTTGAGATGTTCTGTGATTTCTTACGGAAGAGTACCG 5537
 61 GTACTTGTCTGTCTTCCAGGAATTTGAGATGTTCTGTGATTTCTTACGGAAGAGTACCG 120

5538 CACAGACATCTCAAGTGAAGTGTCTTACCTTGTGCTTGTGCTTACAGAAACCTATCT 5597
 121 CACAGACATCTCAAGTGAAGTGTCTTACCTTGTGCTTGTGCTTACAGAAACCTATCT 180

5598 GTTGTGAACCACTTCACTCACTGAAATTAATGATCCAGGACGCTCTCTCAGCAG 5657
 181 GTTGTGAACCACTTCACTCACTGAAATTAATGATCCAGGACGCTCTCTCAGCAG 240

5658 GACCCCTGCGGAGGTACTGTGATATCCGAAACCGCGCTACCTGTGCGCATTTTC 5717
 241 GACCCCTGCGGAGGTACTGTGATATCCGAAACCGCGCTACCTGTGCGCATTTTC 300

5718 CTCAGAGGATTTTACTTGGAGTCTCTCATPACCAAGATTAATTAAGGGTCAATTGCTGCA 5777
 301 CTCAGAGGATTTTACTTGGAGTCTCTCATPACCAAGATTAATTAAGGGTCAATTGCTGCA 360

5778 GGGAAACCTCGTGAAGAGTCCGGAATGAACCAACCGGGCCGCTCCACCTCCGCGAG 5837
 361 GGGAAACCTCGTGAAGAGTCCGGAATGAACCAACCGGGCCGCTCCACCTCCGCGAG 420

5838 CAGCCCAACAAAGCAGGCGCCACCAAGTGAAGAGCATATCACCAGCGGTGCTTC 5897
 421 CAGCCCAACAAAGCAGGCGCCACCAAGTGAAGAGCATATCACCAGCGGTGCTTC 480

5898 CAGCCCAAGCGCGCCGAGGCGCCAGCAGCAGCGGAGGAGCAACACCCACCGCTTA 5957
 481 CAGCCCAAGCGCGCCGAGGCGCCAGCAGCAGCGGAGGAGCAACACCCACCGCTTA 539

5958 CCGCAGAGGGCGGAGCCGAGCTGCGGAGGAGCAAGTCTCTGTGCTGCGCCCTTGGAGCGAGA 6017

Dd		540	CCGGAGGCGGCACACCAGCTGCGCAGGGAACAATCTTCTTG6CCGCCCTTCGAGCCAGA	599
Oy		6018	GAAGTCCCCCGCGGATACTCAGACCGCGAGAGAGCGATCCCCCGCAGGCTTTTGA	60777
Dd		600	GAAGTCCCCCGCGGATGCTCAGACGCGGAGAGAGCGGTCCCCCGGAGAGCTTTTGA	659
Oy		6078	AGACAGCAGCAGCGGGGCGCGCTGCTTGGCGGAGCCGTGAGAACCCCCGTGTCCCAAGTGA	6137
Dd		660	AGACAGCAGCAGCGGGGCGCGCTGCTTGGCGGAGCCGTGAGAACCCCCTGTCTCCAGTGA	719
Oy		6138	C AAGTCTGGAGCACCACTTCAGATAA	6165
Dd		720	C AAGTCTGGAGCACCACTTCAGATAA	747
RESULT 7				
LOCUS	CN281134		757 bp	mRNA linear EST 16-MAY-2004
DEFINITION	17000423750642 GRN EB Homo sapiens cDNA 5', mRNA sequence.			
ACCESSION	CN281134			
VERSION	CN281134.1		GI:47297548	
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 757) Brandenberger R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Pang,R., Guebler,K., Rao,M.S., Mandalam,R., Leboweki,J and Stanton,L.W.			
TITLE	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation			
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)			
COMMENT	Contact: Brandenberger R Regenerative Medicine Genon Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel.: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@genon.com Insert Length: 757 Std Error: 0.00. Location/Qualifiers 1..757			
FEATURES	source			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/tissue_type="embryonic stem cells, embryoid bodies derived from H1, H7 and H9 cells"			
	/clone_id="GRN_EB"			
	/note="Oligo dt primed, full-length enriched cDNA library from embryoid body outgrowths derived from hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions."			
ORIGIN				
Query Match	11.9%; Score 732; DB 7; Length 757;			
Best Local Similarity	99.7%; Pred.No.1e-180;			
Matches	754; Conservative 0; Mismatches 0; Indels 2; Gaps 2;			
Oy	1551 AAAGGAAAGTTTGGAGCAAGCAGGATGAGGTGTCCTCCAGAGGATGCAAAAGCACTGCA	1610		
Dd	3 AAAGGAAAGTTTGGAGCAAGCAGGATGAGGTGTCCTCCAGAGGATGCAAAAGCACTGCA	62		
Oy	1611 GCTTTCATATTATTCAGAGCAGAGCGGAAAGCTCCAAAGAAATCAAAGAGCAGAGTA	1670		
Dd	63 GCTTTCATATTATTCAGAGCAGAGCGGAAAGCTCCAAAGAAATCAAAGAGCAGAGTA	122		
Oy	1671 CCAGGCTCAAGTGAAGAAATGAGGTTTATGATCATGTTGGAAGAGATCTTGTCTC	1730		
Dd	123 CCAAGGCTCAAGTGAAGAAATGAGGTTTATGATCATGTTGGAAGAGATCTTGTCTC	182		
Oy	1731 AGCAAGAAAGCAGAGTATCTCTACGAATCTGAGCTGAGAGAGTCTCGGCTTCTGCTGA	1790		

Dd		183	AGCAAGAAGACGAGTATCTCTACGAATCGACTGAGAGAGTCCTGGCTTGCTGTGA	242
Oy		1791	AGAA TTCA GCGGA AACC GA CAG ATTC AG CAT AA CT GTT GAA GGC TTA AG AT CA AG	1650
Dd		243	AGAA TTC AAG GCG GA ACC GA CAG ATTC AG CAT AA CT GTT GAA GGC TTA AG AT CA AG	302
Oy		1651	GA ACC CTG AAT GTG GGA AAT ATG TG AAA CTG GGA AAG AT CA ATG CTC AG CA GC CT CA A	1910
Dd		303	GAA CCT GGA AT GTG GGA AAT ATG TG AAA CTG GGA AAG AT CA ATG CTC AG CA GC CT CA A	362
Oy		1911	AAT TCAGA GAG CTC CA - GAG AAA CTG GAG AAG GCT GTT AAA AGC AG CA CGA CGG CA CG	1969
Dd		363	AAT TCAGA GAG CTC CA AGA AACTG GAG AAG GCT GTT AAA AGC AG CA CGA CGG CA CG	422
Oy		1970	AG CTG CTG CAG AAT ATTC CC GCA AGC AA AGA GCG AGC CGA GAG GAG CTG GAG AAG GTG C	2029
Dd		423	AG CTG CTG CAG AAT ATTC CC GCA AGC AA AGA GCG AGC CGA GAG GAG CTG GAG AAG GTG C	482
Oy		2030	AGA ACC GA GAG ATTTCTTTCG AAG GCA TC A GAA A GAA AGC GTG GAA GCTG A GAA AC GCC	2089
Dd		483	AGA ACC GA GAG ATTTCTTTCG AAG GCA TC A GAA A GAA AGC GTG GAA GCTG A GAA AC GCC	542
Oy		2090	GCC ATTCTCTG GAA CA AAG GTA AA GAG ACTAG A GCA CAT GAG AGC GTT GAG AAA CA GAC	2149
Dd		543	GCC ATTCTCTG GAA CA AAG GTA AA GAG ACTAG A GCA CAT GAG AGC GTT GAG AAA CA GAC	602
Oy		2150	TGA AGATG A CATC CAG ACAA AATCCCA CAG ATCCAG CAG ATG C TGA TAAA TTCTGG	2209
Dd		603	TGA AGATG A CATC CAG ACAA AATCCCA CAG ATCCAG CAG ATG C TGA TAAA TTCTGG	662
Oy		2210	AG CTCG AAG AACA ATCG GGA GGCCCA AG CTC CAG CCAG CCA CTTA GAG TGA GCA CTTGA	2269
Dd		663	AG CTCG AAG AACA ATCG GGA GGCCCA AG CTC CAG CCAG CCA CTTA GAG TGA GCA CTTGA	721
Oy		2270	AACAGAAA GAG CAG CACTATG A GGA AAA GATTAA G 2305	
Dd		722	AACAGAAA GAG CAG CACTATG A GGA AAA GATTAA G 757	
RESULT 8				
LOCUS	BC031156	958 bp	mRNA	linear HTC 04-MAR-2003
DEFINITION	Mus musculus, similar to citron, clone IMAGE:4976752, mRNA.			
ACCESSION	BC031156			
VERSION	BC031156.1	GI:21411076		
KEYWORDS	HTC.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.			
TITLE	1 (bases 1 to 958)			
JOURNAL	Strausberg, R. Direct Submission Submitted (03-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA			
REMARK				
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: gcgaps-remail.nih.gov Tissue Procurement: Jeffrey Green M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-sbgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov			

Series: IRAX Plate: 59 Row: J Column: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis

FEATURES
This clone has the following problem: retained intron.

source

1. 958
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4976752"
/tissue_type="Mammary tumor, C3(1)-Tag model. Infiltrating ductal carcinoma. 5 month old virgin mouse."
/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 11.4%; Score 705.6; DB 3; Length 958;
Best Local Similarity 89.1%; Pred. No. 1e-173;
Matches 775; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

5302 AATTACGATCTCTCTGTAAGCAATTAATTTAGCAATTCAGATGAGAGTACAG 5361
40 AAGAAAGCACTCTCATGTGGACCAACAAATTTATGATGCATGAAAGCATACAG 99
5362 CTCGAGAAATTCCTGTAAGATGACATTCCTTGGACCTCTGTGTTTGGCCCTC 5421
100 CTGATGAGAGTCTCTGCAAGAAAGACATTCCTTGGACCTCTGTGTTTGGCCCTC 159
5422 TCCACAGCTTCCCTGTCTCAATGTGACAGTGAACAGCGGACGAGGAGAGTAC 5481
160 TCCACAGCTTCCCTGTCTCAATGTGACAGGCGGACGAGGAGAGTAC 219
5482 TTGCTGTGTTTCCAGAAATTTGAGTGTCTGATTTCTTACGAAAGAGTACCCGCA 5541
220 CTGCTGTGTTTCCAGAAATTTGAGTGTCTGATTTCTTACGAAAGAGTACCCGCA 279
5542 GACGATCTCAAGTGAAGTGCCTTACCTTGGACCTTGGACCTTGGACCTTGGAC 5601
280 GATGATCTTAAGTGAAGTGCCTTACCTTGGACCTTGGACCTTGGACCTTGGAC 339
5602 GTGACCTCACTCACTCACTCGAAGTAAATTGAGATCCAGGACGCTCTTACGAGGAG 5661
340 GTGACCTCACTCACTCACTCGAAGTAAATTGAGATCCAGGACGCTCTTACGAGGAG 399
5662 CCTGCCGAGCGGATCTGAGATCCCGAACCCGCGTACCTGGGCTTGCATTTCTCA 5721
400 CCTGCCGAGCGGATCTGAGATCCCGAACCCGCGTACCTGGGCTTGCATTTCTCC 459
5722 GGAGGATTTAATCTGAGTCTCTCATACAGATTAATTAAGGATCTTTGCTGCAAGG 5781
460 GGAGGATTTAATCTGAGTCTCTCATACAGATTAATTAAGGATCTTTGCTGCAAGG 519
5782 AACCTGTGAAGAGTCCGAGCATGAACACACCGGAGCCCGTCACTTCCGACAGC 5841
520 AACCTGTGAAGAGTCCGAGCATGAACACACCGGAGCCCGTCACTTCCGACAGC 579
5842 CCCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5901
580 CCCAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 639
5902 CCAGGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5959
640 CCAGGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 699
5960 ----GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6015
700 GACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 759
6016 GAGAGTCCCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6075

Db 760 GAGAGTCCCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 819
Qy 6076 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6135
Db 820 GAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 879
Qy 6136 AACAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6165
Db 880 AACAGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 909

RESULT 9

BG912161 843 bp mRNA 1linear EST 05-JUN-2001
LOCUS 602812833F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:494657
DEFINITION 5', mRNA sequence.

ACCESSION BG912161 GI:14292637
VERSION BG912161.1

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 843)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph. D.
Email: gcrabbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10890 row: a column: 10
High quality sequence scop: 778.

FEATURES

source
1. 843
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:494657"
/tissue_type="anaplastic oligodendroglioma with 1p/19q loss"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Brn67"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NCI; Site 2: Salt; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Query Match 11.3%; Score 698.2; DB 4; Length 843;
Best Local Similarity 93.3%; Pred. No. 8.5e-172;
Matches 785; Conservative 0; Mismatches 48; Indels 8; Gaps 5;

4669 CACCGGACACCACTGCTGCGCCGAGAGAACCTTACTTGTAGCTCCAGCTTCCT 4728
2 CAGGGTCCACCACTGCTGCGCCGAGAGAACCTTACTTGTAGCTCCAGCTTCCT 61
4729 GACAAAGCGCTGGGTCACCGCTTAGAATGATGTCGAGAGGAGGAGGAGGAGG 4788
62 GACAAAGCGCTGGGTCACCGCTTAGAATGATGTCGAGAGGAGGAGGAGGAGGAGG 121
4789 GAAAAAGCAGAGTGAATCTGCTTGAATCTCCCTGCTGAATCTGGAAGGTGAT 4848
122 GAAAAAGCAGAGTGAATCTGCTTGAATCTCCCTGCTGAATCTGGAAGGTGAT 181
Qy 4849 GACGCTTGAATGAATGACGCTGCTTCACTGAGTACAGAGTGTGTGGGACCC 4908
Db 182 GACGCTTGAATGAATGACGCTGCTTCACTGAGTACAGAGTGTGTGGGACCC 241

QY 4909 GAGGAGGGCTCTACGCCCTGGAATGCTTTGAAAAAACTCCCTAACCCATGTCCAGGAATT 4968
| | | | |
DB 242 GAGGAGAGGGCTCTACGCCCTGGAATGCTTTGAAAAAACTCCCTAACCCATGTCCAGGAATT 301
| | | | |
QY 4969 GAGGAGCTTTTCCAAATTTATATATATCAAGAGACTTGAGAGAGTACTATGATAGAGA 5028
| | | | |
DB 302 GAGGAGAGTCTTCCAAATTTATATATATCAAGAGACTTGAGAGAGTACTATGATAGAGA 361
| | | | |
QY 5029 GAAGAGCGGGCACTGTGCTTGTGACGTGAGAGAAAGTAAACAGTCCCTGGCCAGTCC 5088
| | | | |
DB 362 GAAGAGCGGGCACTGTGCTTGTGACGTGAGAGAAAGTAAACAGTCCCTGGCCAGTCC 421
| | | | |
QY 5089 CACCTGCTGCTCCAGCCGCAACATTCACCCCAATTTTGAAGCTGTCAAAGGCTGCCAC 5148
| | | | |
DB 422 CACCTGCTGCTCCAGCCGCAACATTCACCCCAATTTTGAAGCTGTCAAAGGCTGCCAC 481
| | | | |
QY 5149 TTGTTTGGGGGAGGCAAGTTGAGAAACGGGCTCTGATCTGTGACGCCATGCCAGCAAA 5208
| | | | |
DB 482 TTGTTTGGGGGAGGCAAGTTGAGAAACGGGCTCTGATCTGTGACGCCATGCCAGCAAA 541
| | | | |
QY 5209 GTGCTCATCTCCGCTACAGCAAGAAACCTCAGCAATATCTGATCCGAAAAGATAGAG 5268
| | | | |
DB 542 GTGCTCATCTCCGCTACAGCAAGAAACCTCAGCAATATCTGATCCGAAAAGATAGAG 601
| | | | |
QY 5269 ACCTCAGAGCCCTGCACTGTATCCACTTCACCAATTACAGTATCTCAAT--GGAACAA 5327
| | | | |
DB 602 ACCTCAGAGCCCTGCACTGTATCCACTTCACCAATTACAGTATCTCAATGGGAACAA 661
| | | | |
QY 5328 TAAATTTCTACG-AAATCAGATGAA-GCAGTACAGCTGAGAGAAAT--CTGAGATMAA 5383
| | | | |
DB 662 TAAATTTCTACGAAATTCAGATGAAAGCAGTACACCTCAGAGAAATTTCTGATTAACA 721
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QY 5384 ATGACCATCTCTTGACACCTGCTGTG---TTTGCCGCTCTTCCAAAGCTTCCCTGTCT 5440
| | | | |
DB 722 ATGACCATCTCTTGACACCTGCTGTG---TTTGCCGCTCTTCCAAAGCTTCCCTGTCT 781
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QY 5441 CATCTGTGAGGTGAACAGCGCAGGCGCAGAGAGATCTGTGTGTTTCCAGGAAT 5500
| | | | |
DB 782 AATCTGTGAGGTGAACAGGCGCAGGCGCAGAGAGATCTGTGTGTTTCCAGGAAT 841
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QY 5501 T 5501
| | | | |
DB 842 T 842
| | | | |
RESULT 10
CN295302 653 bp mRNA linear EST 16-MAY-2004
LOCUS DEFINITION 17000600183004 GRN_PRENBU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN295302
VERSION CN295302.1 GI:47311716
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 653)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murgu, J., Fisk, G., J.,
Li, Y., Xu, C., Pang, R., Guejler, K., Rao, M. S., Mandalam, R.,
Lebkowski, J. and Stanton, L. W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
TITLE
JOURNAL
COMMENT
Contact: Brandenberger R
Regenerative Medicine
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@regeron.com
Insert Length: 653 Std Error: 0.00.
Location/Qualifiers

source
1. .653
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/mol_type="mRNA"
/db_xref="taxon:9606"
/issue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_lib="GRN_PRENBU"
/note="Oligo dt primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic and mitogens."

Query Match 10.5%; Score 649.4; DB 7; Length 653;
Best Local Similarity 99.8%; Pred. No. 5; Se-159;
Matches 650; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2017 CTGGAAGGCTGCACAAACCGAGAGATTTCTTGAAGGATCAGAAAGAGCTGTGGA 2076
| | | | |
DB 3 CGGAGAAAGCTGCACAAACCGAGAGATTTCTTGAAGGATCAGAAAGAGCTGTGGA 62
| | | | |
QY 2077 GCTGAGGAACCGCCGCAATTTCTGTGAGAACAGGTAAAGACTAGAGCCATGAGCGT 2136
| | | | |
DB 63 GCTGAGGAACCGCCGCAATTTCTGTGAGAACAGGTAAAGACTAGAGCCATGAGCGT 122
| | | | |
QY 2137 AGAGAAAACAGCTGAGAGTACATCCAGACAAAATCCCAACAGATCCAGAGATGGCT 2196
| | | | |
DB 123 AGAGAAAACAGCTGAGAGTACATCCAGACAAAATCCCAACAGATCCAGAGATGGCT 182
| | | | |
QY 2197 GATTAATTTCTGAGAGCTGCAGAGAAACATCGGGAGGCCCAAGCTCAGCCGACAGCTA 2256
| | | | |
DB 183 GATTAATTTCTGAGAGCTGCAGAGAAACATCGGGAGGCCCAAGCTCAGCCGACAGCTA 242
| | | | |
QY 2257 GAAGTGCACTTGAAAACAGAAAGAGAGAGAGCTATGAGAAAAGATTAAAGTGTGACAAT 2316
| | | | |
DB 243 GAAGTGCACTTGAAAACAGAAAGAGAGAGAGAGCTATGAGAAAAGATTAAAGTGTGACAAT 302
| | | | |
QY 2317 CAGATTAAGAAAG 2376
| | | | |
DB 303 CAGATTAAGAAAG 362
| | | | |
QY 2377 GAGGAGGCCCATGAGAGAGGCGAAATTTCTCAGCGAAACAGAGGCGATGATCATGCTATG 2436
| | | | |
DB 363 GAGGAGGCCCATGAGAGAGGCGAAATTTCTCAGCGAAACAGAGGCGATGATCATGCTATG 422
| | | | |
QY 2437 GATTCAGAGATCAGATCCCTGTGAGACAGAGATTTGGAATCTGTGAAGCCATTAACCT 2496
| | | | |
DB 423 GATTCAGAGATCAGATCCCTGTGAGACAGAGATTTGGAATCTGTGAAGCCATTAACCT 482
| | | | |
QY 2497 GAGGCAATAGCAGATCTTTTAAACCAAGAGAAACATGAGAGGCCCAAGAGAGATTTCT 2556
| | | | |
DB 483 GAGGCAATAGCAGATCTTTTAAACCAAGAGAAACATGAGAGGCCCAAGAGAGATTTCT 542
| | | | |
QY 2557 GAATCAGGCAACAGAAATTTTAACTGTGAGACACAGGCTGGAGGTGAGGCCCAAGAC 2616
| | | | |
DB 543 GAATCAGGCAACAGAAATTTTAACTGTGAGACACAGGCTGGAGGTGAGGCCCAAGAC 602
| | | | |
QY 2617 CGAAAACTGAGAGAGAGCTGTGAGAGAGATCAGCCACCAAGACAGAGTAC 2667
| | | | |
DB 603 CGAAAACTGAGAGAGAGCTGTGAGAGAGATCAGCCACCAAGACAGAGTAC 653
| | | | |
RESULT 11
BP905370/c 652 bp mRNA linear EST 18-JAN-2001
LOCUS DEFINITION IL3-MT0267-261200-410-H07 MT0267 Homo sapiens cDNA, mRNA sequence.
ACCESSION BP905370
VERSION BP905370.1 GI:12296829
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 652)
 AUTHORS Dae Neco, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.G.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?fl=IL3&f2=IL3-WT0267-261200-410-H07&t3=2000-12-26&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 624.
 Location/Qualifiers
 1..652
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_1fb="WT0267"
 /note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Query Match 10.2%; Score 629.2; DB 2; Length 652;
 Best Local Similarity 98.0%; Pred. No. 1.1e-153;
 Matches 637; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

2525 GGAACATGAAGGCCCAAGAGATGATTCTGAATCTGAGGACAGCAAGAAATTTTACTCGG 2584
 652 GGAACATGAAGGCCCAAGAGATGATTCTGAATCTGAGGACAGCAAGAAATTTTACTCGG 593
 2585 AGACACAGGCTGGAGATTGAGGCCAGAACCGAAACTGAGAGAGAGCTGGAGAGAA 2644
 592 AACACAGGCTGGAGATTGAGGCCCAACCGAAACTGAGAGAGAGCTGGAGAGAA 533
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 ACCESSION BQ807302 GI:22031511
 VERSION BQ807302.1 GI:22031511
 KEYWORDS EST.
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.
 1 (bases 1 to 640)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-rmail.nih.gov
 CDNA Library Preparation:
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC)
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
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 VERSION BG976452.1 GI:14364089
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 881)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph. D.
 Email: cgaab-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
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 http://image.llnl.gov
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 /note="Organ: mammary; Vector: pCMV-SportE; Site: 1; Salt;
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 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

ORIGIN
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 DB 878 AA 879

RESULT 15
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 ACCESSION BP146990
 VERSION BP146990.1 GI:40396461
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
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 Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 1 (bases 1 to 698)
 Uenishi, H., Eguchi, T., Suzuki, K., Sawazaki, T., Toki, D., Shinkai, H.,
 Okumura, N., Hamada, N. and Awata, T.
 PEDS (pig EST Data Explorer): construction of a database for ESTs
 derived from porcine full-length cDNA libraries
 Nucleic Acids Res. 32 (1), D484-D488 (2004)
 CONTACT: Hirohide Uenishi
 Animal Genome Laboratory, Genome Research Department
 National Institute of Agrobiological Sciences
 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: +81-29-838-8627
 Fax: +81-29-838-8627
 Email: huenishi@affrc.go.jp
 EST project with full-length enriched cDNA libraries carried out in
 Animal Genome Research Program (Japan) by National Institute of
 Agrobiological Sciences and STRAF-Institute
 Single pass sequencing of clones derived from oligo-capped cDNA
 library
 Vector sequences were eliminated by RepeatMasker version 2002/07/13
 and crossmatch version 0.990319
 Low quality bases were trimmed based on the quality values.

FEATURES
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Job time : 12000 secs

PT similar to animal kinases, useful for drug screening, diagnosis, in gene
PT therapy of disorders and diseases e.g. cancer and pharmacogenomic
PT applications.

PS Claim 1; Page 37-39; 50pp; English.

XX The invention relates to a novel human protein that shares structural
CC similarity with animal kinases, including serine-threonine kinases,
CC particularly Cdkron rho-interacting kinases. The proteins of the
CC invention have mitogenic and cytoskeletal activity. The polynucleotides may
CC have a use in gene therapy. The encoded novel polypeptides are useful for
CC generating antibodies, as reagents in diagnostic assays, for identifying
CC other cellular gene products related to NHP and as reagents in assays for
CC screening for compounds that are useful in the treatment of mental,
CC biological or medical disorders and diseases including cancer. The
CC sequence encodes a novel human kinase of the invention

XX Sequence 6165 BP; 1735 A; 1550 C; 1679 G; 1201 T; 0 U; 0 Other;

Query Match 100.0%; Score 6165; DB 6; Length 6165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3421 GAGATTCGCTCTGACAGAGGCTCTCAAGAGACAGAGCTGAAGGCCGAGAGGCTCTCT 3480
QY 3481 GACAGCTCAATGACTGAGAGAGAGAGACATGCTATGCTTGAATGAATGCCGAAAGCTTA 3540
DB 3481 GACAGCTCAATGACTGAGAGAGAGAGACATGCTATGCTTGAATGAATGCCGAAAGCTTA 3540
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DB 3541 CAGAGAGGCTGAGAGACTGAACGAGAGGCTCAACAGAGGCTTGAAGAGCAAGCCAA 3600
QY 3601 TTAACAGCAGAGATGACCTGAGAAAAATCACTTTTCGCTGACTCAAGACTGCA 3660
DB 3601 TTAACAGCAGAGATGACCTGAGAAAAATCACTTTTCGCTGACTCAAGACTGCA 3660
QY 3661 GAAAGCTTAGATCGGCTGATTTAATGAGACAGAAAGAAAGTGAAGTATCACTG 3720
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QY 3781 CAAACCAAACTCAATGATTTTCTGCAAGCCAAATGAGCAACCTGCTAATAAAGAAAAAG 3840
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DB 3961 GCCCAGCGCAAGAGCAGACCCACACCAATCCAGCCAGGCAAGGCGAGAGCAGAG 4020
QY 4021 ATGCGCATGTCGCGCATGTCGCTGCGCAGAGACCAAGCCCAAGTGCATGAGCTGCTG 4080

ID AAD3864 standard; cDNA; 6298 BP.
 XX AAD3864;
 AC
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Human kinase (PKIN) -21 cDNA.
 XX
 KM Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis;
 KM acquired immune deficiency syndrome; AIDS; Addison's disease; allergy;
 KM asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis;
 KM development; hepatitis; cardiovascular; hypertension; drug screening;
 KM myocardial infarction; Goodpasture's syndrome; lipid disorder; growth;
 KM fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;
 KM hypercholesterolemia; obesity; gene therapy; cytostatic; anti-HIV;
 KM neuroprotective; hepatotropic; hypotensive; cardiac; nephrotropic;
 KM hyperlipidaemia; enzyme; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 55..6219
 FT /tag= a
 FT /product= "Human kinase (PKIN) -21"
 XX
 PN MO200233099-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 20-OCT-2001; 2001MO-US047728.
 XX
 PR 20-OCT-2000; 2000US-0242410P.
 PR 27-OCT-2000; 2000US-0244068P.
 PR 03-NOV-2000; 2000US-0245708P.
 PR 09-NOV-2000; 2000US-0247672P.
 PR 16-NOV-2000; 2000US-0249565P.
 PR 22-NOV-2000; 2000US-0252730P.
 PR 01-DEC-2000; 2000US-0250807P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Gururajan R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arivian C;
 PI Yao MG, Ramm Kumar J, Ding L, Tang YT, Hafalia AJA, Nguyen DB;
 PI Gandhi AR, Lu Y, Yue H, Burford N, Bandman O, Tribouley CM, Lal PG;
 PI Reclison SA, Lu DM, Borowsky ML, Thornton M, Swannaker A;
 PI Thangavelu K, Khan FA, Ison CH;
 XX
 DR WPI; 2002-454603/48.
 DR P-PSDB; AAE24150.
 XX
 PT New human kinase polypeptide, for diagnosing, preventing and treating
 PT cancer, immune system disorders, growth and development disorders,
 PT cardiovascular disorders and lipid disorders.
 XX
 PS Claim 5; Page 207-209; 210pp; English.
 XX
 CC The invention relates human kinases (PKIN) and their corresponding
 CC nucleic acid sequences. PKIN and its DNA are useful for diagnosing,
 CC treating and preventing cancer, an immune system disorder (e.g., acquired
 CC immune deficiency syndrome (AIDS), Addison's disease, allergy, asthma,
 CC atherosclerosis, multiple sclerosis, psoriasis), disorders affecting
 CC growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis),
 CC cardiovascular disorder (e.g., hypertension, myocardial infarction,
 CC Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver,
 CC Gaucher's disease, Niemann-Pick's disease, hypercholesterolemia,
 CC hyperlipidaemia, obesity), and for assessing the effects of exogenous
 CC compounds. Anti-PKIN antibody is useful in a diagnostic test for a
 CC condition or a disease associated with the expression of PKIN in a
 CC biological sample. A composition comprising PKIN or an agonist or
 CC antagonist of PKIN is useful for treating a disease or condition
 CC associated with decreased or increased expression of functional PKIN.
 CC PKIN is useful in a number of drug screening techniques and to analyse
 CC the proteome of a tissue or cell type. PKIN DNA is useful for creating

CC knockin humanised animals or transgenic animals to model human diseases,
 CC and in somatic or germ-line gene therapy. The present sequence is human
 CC PKIN cDNA
 XX
 SQ Sequence 6298 BP; 1772 A; 1585 C; 1720 G; 1221 T; 0 U; 0 Other;
 Query Match 99.9%; Score 6161.8; DB 6; Length 6298;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 6163; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ATGTGAAGTCAAAATATGAGAGCGGGAATCCTTGGATGCTGCTGTAACCAT 60
 DB ATTTGAAGTTCAAAATATGAGAGCGGGAATCCTTGGATGCTGCTGTAACCAT 114
 QY GCCAGCGGGGCTCCAGAGCTGAATCTGTTCTTCAGGGGAAACACCCCTTATGACTCAA 120
 DB GCCAGCGGGGCTCCAGAGCTGAATCTGTTCTTCAGGGGAAACACCCCTTATGACTCAA 174
 QY 121 CAGCAGATGTCCTCTCTTCCGAGAAAGGATATTAATGATGCCCTTCTTCTTGA 180
 DB CAGCAGATGTCCTCTCTTCCGAGAAAGGATATTAATGATGCCCTTCTTCTTGA 234
 QY 181 GAATGACGTACGCTGCTGATGAATTAAGCAGTGAGCACTTTCGGGAAGTAT 240
 DB GAATGACGTACGCTGCTGATGAATTAAGCAGTGAGCACTTTCGGGAAGTAT 294
 QY 235 GAATGACGTACGCTGCTGATGAATTAAGCAGTGAGCACTTTCGGGAAGTAT 294
 DB 241 TCCGACACATAGCTGATGATTAAGAGAGCTCCAGCTTCGGCAAGAGCTTCGAGTACA 300
 DB 295 TCCGACACATAGCTGATGATTAAGAGAGCTCCAGCTTCGGCAAGAGCTTCGAGTACA 354
 QY 301 AGTCTTGAGTGTGTGCTCACTTGTCTGAAGTCAAGTGTGAAGAGAAAGCAACCGGG 360
 DB AGTCTTGAGTGTGTGCTCACTTGTCTGAAGTCAAGTGTGAAGAGAAAGCAACCGGG 414
 QY 355 AGTCTTGAGTGTGTGCTCACTTGTCTGAAGTCAAGTGTGAAGAGAAAGCAACCGGG 414
 DB 361 GACATCTAGCTTGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 415 GACATCTAGCTTGAAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
 QY 421 TTTTGGAGGAAG 480
 DB 475 TTTTGGAGGAAG 534
 QY 481 CAGTATGCTTTGAG 540
 DB 535 CAGTATGCTTTGAG 594
 QY 541 GACTTGCTGCTCACTTTGGAATAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 DB 595 GACTTGCTGCTCACTTTGGAATAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 654
 QY 601 TACCTAGCTGAGCTGATTTTGGCTGTTACAGAGCTTCATCTGATGGGATACGTCAG 660
 DB 655 TACCTAGCTGAGCTGATTTTGGCTGTTACAGAGCTTCATCTGATGGGATACGTCAG 714
 QY 661 GACATCAAGCTGAGAAATTCCTGTTGACCGAGACAGACATCAAGCTGTGATTTT 720
 DB 715 GACATCAAGCTGAGAAATTCCTGTTGACCGAGACAGACATCAAGCTGTGATTTT 774
 QY 721 GATCTGCGCGGAAATGAATTAACACAGATGTAATCCAAATCCCGATTTGGAGAC 780
 DB 775 GATCTGCGCGGAAATGAATTAACACAGATGTAATCCAAATCCCGATTTGGAGAC 834
 QY 781 CGAATTAACAGCTGCTGTAAGTGAATGATGTAAGAGAGAGAGAGAGAGAGAGAG 840
 DB 835 CGAATTAACAGCTGCTGTAAGTGAATGATGTAAGAGAGAGAGAGAGAGAGAGAG 894
 QY 841 GGCCTGAGCTGATCTGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 DB 895 GGCCTGAGCTGATCTGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 954
 QY 901 TCCCTGCTGAG 960
 DB 955 TCCCTGCTGAG 1014

QY 961 TTTTGAATTTTCAGATGACCCCAAGTGACGTACTTTTGATCTGATTTCAAAGC 1020
Db 1015 TTTTGAATTTTCAGATGACCCCAAGTGACGTACTTTTGATCTGATTTCAAAGC 1074
QY 1021 TTGTGTGCGGCGCAAGAAAGAGAGACTGAAAGTTTGAGAGTCTTTGCTGCACTCTTCTC 1080
Db 1075 TTGTGTGCGGCGCAAGAAAGAGAGACTGAAAGTTTGAGAGTCTTTGCTGCACTCTTCTC 1134
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Db 1135 TCTAAATTTGACTGGAACAACATTCGTAACTCTCCGCCCTTCGTTCCACCTCAAG 1194
QY 1141 TCTGAGATGACACTCTCAATTTTGATGAACCAAGAAAGAAATTTGTTGGTTTCACTCT 1200
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Db 1435 TCTCAGGACAAGTGTCACAAGATGAGCAGAGAAATGACCCGGTTTACCTGGAGAGTCTCA 1494
QY 1441 GAGGTGAGGCTGTGCTTACTCAAGAGAGTGAAGCTGAAGGCTCTGAGACTCAGAGA 1500
Db 1495 GAGGTGAGGCTGTGCTTACTCAAGAGAGTGAAGCTGAAGGCTCTGAGACTCAGAGA 1554
QY 1501 TCCCTCTGAGAGCAAGCTTTTGTCTACTCATCAAGAAATGACGTAGCTTAAAGCGAAGT 1560
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DB 5395 ATGACATGAAGACGATACAGCTGAGAAATTCCTGGATAGATGACCATTCCTGGCA 5454
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DB 5455 CTTGCTGTGTTTGGCGCTCTTCAACAGCTTCCCTGCTCAATCGAGAGTGAACAGC 5514
QY 5461 GCAGGGCAGGAGAGAGTACTTGCTGTGTTTCCAGAAATTTGGAGTGTTCGTGAATCT 5520
DB 5515 GCAGGGCAGGAGAGAGTACTTGCTGTGTTTCCAGAAATTTGGAGTGTTCGTGAATCT 5574
QY 5521 TAGGGAAGAGTGGCGGACAGAGATCTCAAGAGAGTGGCTTACTTTGGCTTTGGCC 5580
DB 5575 TAGGGAAGAGTGGCGGACAGAGATCTCAAGAGAGTGGCTTACTTTGGCTTTGGCC 5634
QY 5581 TAGAGAAACCCATCTGTTTGTGACCACTTCAACTCACTCGAAGTAAATTGAGATCAG 5640
DB 5635 TAGAGAAACCCATCTGTTTGTGACCACTTCAACTCACTCGAAGTAAATTGAGATCAG 5694
QY 5641 GCACGCTCTTCAAGAGGAGCCCTGCGGAGCGTACCTGACATCCCGAACCCGCGCTAC 5700
DB 5695 GCACGCTCTTCAAGAGGAGCCCTGCGGAGCGTACCTGACATCCCGAACCCGCGCTAC 5754
QY 5701 CTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5760
DB 5755 CTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5814
QY 5761 AGGGTCAATTTGCTGCAAGAGGAAACCTGCTGAGAGAGTCCGGCACTGAAACCAACCGGGGC 5820
DB 5815 AGGGTCAATTTGCTGCAAGAGGAAACCTGCTGAGAGAGTCCGGCACTGAAACCAACCGGGGC 5874
QY 5821 CGCTCCACCTCCCGCAGAGAGCCCAACAGAGAGGAGCCCAACGTAACAGAGACATC 5880
DB 5875 CGCTCCACCTCCCGCAGAGAGCCCAACAGAGAGGAGCCCAACGTAACAGAGACATC 5934
QY 5881 ACCAAGCGGTGGCTTCCAGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5940
DB 5935 ACCAAGCGGTGGCTTCCAGCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5994
QY 5941 AGCAGACCCCAACCGCTACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6000
DB 5995 AGCAGACCCCAACCGCTACCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6054
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DB 6055 CGCCCTCTGAGAGGAGAGAGTCCCGCGCGAGTACTGACAGCAGCGAGAGCGGCTCC 6114
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DB 6115 CCGGCGAGGCTGTTTGAAGACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6174
QY 6121 CCGCTGTCCAGGTGAACAGAGTCTGAGGACCAAGTCTTCAGTATTA 6165
DB 6175 CCGCTGTCCAGGTGAACAGAGTCTGAGGACCAAGTCTTCAGTATTA 6219

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KW obesity; comorbidities; cancer; anorexia; cachexia; bulimia;
KM central nervous system disorder; chronic obstructive pulmonary disease;
XX diabetes; pain; gene; ds.
OS Homo sapiens.
PH Key Location/Qualifiers
FT CDS 1..6165
/*tag= a
/*product= "Human CR1K protein"
PN W02003004523-A1.
XX
PD 16-JAN-2003.
XX
PF 28-JUN-2002; 2002W0-EP007156.
XX
PR 02-JUL-2001; 2001US-0301841P.
PR 11-DEC-2001; 2001US-0338651P.
PR 25-APR-2002; 2002US-0375014P.
XX
PA (FARB ) BAYER AG.
XX
PI Zhu Z;
XX
XX WPI; 2003-221576/21.
DR P-PSDB; A0026959.
XX
PT New human citron rho/rac-interacting kinase (CR1K) polypeptide and
PT polynucleotide, useful in preventing, ameliorating or treating diseases
PT associated with human CR1K dysfunction, e.g. obesity, diabetes or
PT Alzheimer's disease.
XX
PS Example 1; Fig 1; 237bp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a human
XX citron rho/rac-interacting kinase polypeptide. The isolated
XX polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
XX specification. The human citron rho/rac-interacting kinase (CR1K)
XX polypeptide and polynucleotide are useful in preventing, ameliorating, or
XX treating diseases associated with human CR1K dysfunction such as obesity
XX and obesity-associated comorbidities (e.g. hypertension, coronary artery
XX disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
XX cancer including endometrial, breast, prostate and colon cancer),
XX anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
XX disorders, anxiety disorders, Parkinson's disease or Alzheimer's
XX disease), chronic obstructive pulmonary disease, or diabetes. These can
XX also be used to treat pain associated with the disorders. The human CR1K
XX polypeptide is also useful in diagnostic assays or in genetic testing.
XX The expression vector or the reagent is useful in preparing a medicament
XX for modulating the activity of a human CR1K in a disease, e.g. obesity, a
XX central nervous system disorder, or chronic obstructive pulmonary
XX disease. The fusion protein is useful for generating antibodies against a
XX CR1K polypeptide and for use in various assay systems. The methods are
XX useful in producing and detecting the polynucleotide and polypeptide and
XX in screening for agents that modulate the activity of the human CR1K
XX polypeptide. This polynucleotide sequence represents a DNA sequence
XX encoding a human CR1K protein of the invention

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SQ Sequence 6165 BP; 1735 A; 1549 C; 1680 G; 1201 T; 0 U; 0 Other;
Query Match 99.9%; Score 6160.2; DB 9; Length 6165;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6162; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ATGTTGAAGTTCAAATATGAGACCGGGAATCTTTGATGCTGCTGCTGAACCATTT 60
DB 1 ATGTTGAAGTTCAAATATGAGACCGGGAATCTTTGATGCTGCTGCTGAACCATTT 60
QY 61 GCCAGCCGGGCGCTCAGGCTGATGTTCTTCCAGGGGAAACCACTTATGACTCAA 120
DB 61 GCCAGCCGGGCGCTCAGGCTGATGTTCTTCCAGGGGAAACCACTTATGACTCAA 120

```

QY 121 CACAGATGTCCTCTCTTTCCCGAAGAGATATAGATGCTCTTTGTTCTTTGAA 180
DB 121 CACAGATGTCCTCTCTTTCCCGAAGAGATATAGATGCTCTTTGTTCTTTGAA 180
QY 181 GAATGCACTGAGCTGCTGTGATGAAGATTAGACAGTGACAACTTTGTCCGGAAGTAT 240
DB 181 GAATGCACTGAGCTGCTGTGATGAAGATTAGACAGTGACAACTTTGTCCGGAAGTAT 240
QY 241 TCCGACACCATAGCTGATTACAGAGCTCAGCTTCGCGAAGAGACTTCGAACTGAGA 300
DB 241 TCCGACACCATAGCTGATTACAGAGCTCAGCTTCGCGAAGAGACTTCGAACTGAGA 300
QY 301 AGCTCTGTAGCTGTGTGCTCACTTTGCTGAAGTGAAGTGTGAAGAGAAAGCACTCGGG 360
DB 301 AGCTCTGTAGCTGTGTGCTCACTTTGCTGAAGTGAAGTGTGAAGAGAAAGCACTCGGG 360
QY 361 GACATCATGCTTATGAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 GACATCATGCTTATGAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 TTTTGTGAGAGAGCGGAACTATTTATCTGAAAGCAAGAGCGCTGGAATCCCGCAATTA 480
DB 421 TTTTGTGAGAGAGCGGAACTATTTATCTGAAAGCAAGAGCGCTGGAATCCCGCAATTA 480
QY 481 CAGTATGCTTTTCAAGCAAAATCACCTTTATCTGTAATGCAATGCAAGCTGAGAGG 540
DB 481 CAGTATGCTTTTCAAGCAAAATCACCTTTATCTGTAATGCAATGCAAGCTGAGAGG 540
QY 541 GACTGTGTGCACTTTGAAATGATGAGAGACAGTGAATGAAACCTGATACGTTT 600
DB 541 GACTGTGTGCACTTTGAAATGATGAGAGACAGTGAATGAAACCTGATACGTTT 600
QY 601 TACCTAGCTAGCTGATTTTGCTGTTCAAGAGCTTATGATGGAATGCTGATACGA 660
DB 601 TACCTAGCTAGCTGATTTTGCTGTTCAAGAGCTTATGATGGAATGCTGATACGA 660
QY 661 GACATCAAGCTGAGAACTTCTGTTGACCGCACAGAGACATCAAGCTGTGTGATTTT 720
DB 661 GACATCAAGCTGAGAACTTCTGTTGACCGCACAGAGACATCAAGCTGTGTGATTTT 720
QY 721 GATCTGCTGCTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAA 780
DB 721 GATCTGCTGCTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAA 780
QY 781 CCAATTAATCAATGCTCTGAAAGTCTGATGTAAGTGAAGAGAGAGAGAGAGAGAG 840
DB 781 CCAATTAATCAATGCTCTGAAAGTCTGATGTAAGTGAAGAGAGAGAGAGAGAGAG 840
QY 841 GGCCTGAGCTGTGACTGTGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAG 900
DB 841 GGCCTGAGCTGTGACTGTGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAG 900
QY 901 TCCCTGCTGCTGAG 960
DB 901 TCCCTGCTGCTGAG 960
QY 961 TTTTGTGAAATTTTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 961 TTTTGTGAAATTTTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 TTTGTGTGCGCGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 TTTGTGTGCGCGCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 TCTTAAATTTGATGAG 1140
DB 1081 TCTTAAATTTGATGAG 1140
QY 1141 TCTGAGATGAG 1200
DB 1141 TCTGAGATGAG 1200
QY 1201 CCGTGCAAGCTGAG 1260

DB 1201 CCGTGCAAGCTGAG 1260
QY 1261 TACAG 1320
DB 1261 TACAG 1320
QY 1321 CTTGCAAG 1380
DB 1321 CTTGCAAG 1380
QY 1381 TCTCAG 1440
DB 1381 TCTCAG 1440
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QY 1561 TTTGAG 1620
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QY 1681 GTGGAAGAAATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1740
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QY 1801 CGGAAAG 1860
DB 1801 CGGAAAG 1860
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DB 1921 CTCGAAG 1980
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DB 1981 AATATCCGAG 2040
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QY 2161 ATCCAG 2220
DB 2161 ATCCAG 2220
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DB 2221 AAACATCGAG 2280
QY 2281 CAGCACTAG 2340

Dh 2281 CAGCACTATGAGAAAATTAAAGTTGTGGACAATCAGATAAAGAAAGACTGGCTGAC 2340
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Db 2341 AAGGAGCACTGGGAACATGATTCAGAGACACAGAGAGAGGCCCATGAGAGGGCCAA 2400
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Db 2401 ATTCTCAGCGAACAGAGGGCGATGATCAATGCTATGATTCAGAGATCAGATCCCTGAA 2460
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Qy 2521 CAAAGGAACATGAAGGCCCAAGAAAGATGATTTCTAAGCTCAGGCAACAGAAATTTTAC 2580
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Qy 2821 GCCCTGAGAGCCAGCTTCCGCAAGGCGAAGACAGAGCTGGAGAGACACAGCAGAACT 2880
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Qy 2881 GAAAGAGAGATCCAGGCACTCAGGCAATGAGATGAATTCAGCGCAAAATTTGATGCT 2940
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Db 3901 GAGCTGAGAAAGCCCTTCAGAAAGCCCGCATGAGCTCCGGTCCGCGGAGAGAACT 3960
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 Db 4741 TGGGTCAACCGCTTGAATGATGTGTGAGAGTGGAGAGTTCTTAGGAAAAAGCAGAA 4800
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 Db 4801 GCTGATCTAACTGCTTGGAACTCCCTGCTGAACTGGAAGGTGATGACCTGTAGAC 4860
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 Db 5341 ATGACATGAAAGCAGTACAGCTGAGAGAAATTCCTGATGAAGATGACATTCCTGGCA 5400
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 Db 5401 CTTGCTGTGTTTGGCGCTCTTCCAAAGCTTCCCTGTCTCAATCTGACAGTGAACAGC 5460
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 Db 5521 TACGGAAGAGCTAGCCGACAGAGATCTCAAGTGAAGTGTGCTTACCTTTGGCC 5580
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Db 5581 TACAGAAACCTTATCTGTGTTGTGACCACTTCAACTCACTCGAAGTATTGATTCAG 5640
 QY 5641 GCAGCTCTCAGCAGGAGACCCCTGCGAGCGTACTGACATCTCCGAACCCGCGTAC 5700
 Db 5641 GCAGCTCTCAGCAGGAGACCCCTGCGAGCGTACTGACATCTCCGAACCCGCGTAC 5700
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 Db 5701 CTGGGCGCTGCTTCTTCTTCAAGAGCATTTACTTGGCGTCTCATACAGATTAATTA 5760
 QY 5761 AGGTCAATTTGTCTGCAAGGGAACCTGTGAAGAGTCCGCACTGAACACACCGGGGC 5820
 Db 5761 AGGTCAATTTGTCTGCAAGGGAACCTGTGAAGAGTCCGCACTGAACACACCGGGGC 5820
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 Db 5821 CCGTCACTCTCCGACAGCCCAAGAGAGAGCCCAAGAGTCAAGAGTCAAGAGTCAATC 5880
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 Db 5881 ACCAAGCGGTGCTTCAAGCCAGCGCCCGGAGAGCCCAAGAGTCAAGAGTCAATC 5940
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 Db 5941 AGCAGACCCCAAGCGCTACCGCGAGAGGCGGACCGAGTGTGCGAGGCAAGTCTTCTGCG 6000
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 Db 6001 CGCGCCCTGAGAGAGAGAGTCCCGCGCGGATCTACAGACAGCGGAGAGAGCGTCC 6060
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 Db 6061 CCGCGAGAGGCTGTTTGAAGAAGAGAGGAGCGGCGTGTGCGGAGCGGTGAGAGCC 6120
 QY 6121 CCGGTGTCCAGGTGAACAAGGTGTGAGACCAAGTCTTCAATATA 6165
 Db 6121 CCGGTGTCCAGGTGAACAAGGTGTGAGACCAAGTCTTCAATATA 6165

RESULT 4
 AAL55215
 ID AAL55215 standard; DNA, 8603 BP.
 XX
 AC AAL55215;
 XX
 DT 01-MAY-2003 (first entry)
 XX
 DE Human CR1K related DNA sequence, SEQ ID No 4.
 XX
 KW Anorectic; hypotensive; cardiac; antihypertensive; cerebroprotective;
 KW antiagout; osteopathic; antirheumatic; cytoleptic; antidepressant;
 KW immunomodulator; antineuritic; tranquilizer; antiparkinsonian; nootropic;
 KW neuroprotective; antiinflammatory; antidiabetic; analgesic;
 KW human c12ron rho/rac-interacting kinase; enzyme; CR1K; ameliorating;
 KW obesity; comorbidity; cancer; anorexia; cachexia; bulimia;
 KW central nervous system disorder; chronic obstructive pulmonary disease;
 KW diabetes; pain; ds.
 XX
 OS Homo sapiens.
 PN WO200304523-A1.
 PD 16-JAN-2003.
 XX
 PF 28-JUN-2002; 2002WO-EP007156.
 XX
 PR 02-JUL-2001; 2001US-0301841P.
 PR 11-DEC-2001; 2001US-038651P.
 PR 25-APR-2002; 2002US-0375014P.
 XX
 PA (FARB) BAYER AG.

PI Zhu Z;
XX
XX WPI: 2003-221576/21.
XX
XX New human citron rho/rac-interacting kinase (CRIK) polypeptide and
PT polynucleotide, useful in preventing, ameliorating or treating diseases
PT associated with human CRIK dysfunction, e.g. obesity, diabetes or
PT Alzheimer's disease.
XX
XX
XX Disclosure; Fig 4; 237p; English.

XX
XX The invention relates to an isolated polynucleotide encoding a human
CC citron rho/rac-interacting kinase polypeptide. The isolated
CC polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
CC specification. The human citron rho/rac-interacting kinase (CRIK)
CC polypeptide and polynucleotide are useful in preventing, ameliorating, or
CC treating diseases associated with human CRIK dysfunction such as obesity
CC and obesity-associated comorbidities (e.g. hypertension, coronary artery
CC disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
CC cancer including endometrial, breast, prostate and colon cancer),
CC anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
CC disorders, anxiety disorders, Parkinson's disease or Alzheimer's
CC disease), chronic obstructive pulmonary disease, or diabetes. These can
CC also be used to treat pain associated with the disorders. The human CRIK
CC polypeptide is also useful in diagnostic assays or in genetic testing.
CC The expression vector or the reagent is useful in preparing a medicament
CC for modulating the activity of a human CRIK in a disease, e.g. obesity, a
CC central nervous system disorder, or chronic obstructive pulmonary
CC disease. The fusion protein is useful for generating antibodies against a
CC CRIK polypeptide and for use in various assay systems. The methods are
CC useful in producing and detecting the polynucleotide and polypeptide and
CC in screening for agents that modulate the activity of the human CRIK
CC polypeptide. This polynucleotide sequence represents a DNA sequence
CC relating to the human CRIK protein of the invention
XX
XX

Sequence 8603 BP; 2305 A; 2206 C; 2215 G; 1877 T; 0 U; 0 Other;

Query Match 99.9%; Score 6160.2; DB 9; Length 8603;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 6162; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OY	3841	GTTCCTCTGCAGTACAAATGAGCTGGAAGCTGGCCCTGGAGAGAGAAAAGCTCGCTGTCA	3900
Db	3841	GTTCCTCTGCAGTACAAATGAGCTGGAAGCTGGCCCTGGAGAGAGAAAAGCTCGCTGTCA	3900
OY	3901	GAGCTAGAGAAAGCCCTTCAGAAAGCCGCATCGAGCTCCGCTCCGCCGGAGGAGACT	3960
Db	3901	GAGCTAGAGAAAGCCCTTCAGAAAGCCGCATCGAGCTCCGCTCCGCCGGAGGAGACT	3960
OY	3961	GCCCCCGGAAAGCAACGACCAACCCATCAAGCCAGCCACCGGAGGACGAG	4020
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OY	4021	ATCGCATATCCGCATCGTGGGCTCCGACAGGACCAAGCCCATGAGCATGAGCCTGTG	4080
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RESULT 5
ADJ96544 ID ADJ96544 standard; DNA; 8656 BP.
AC ADJ96544;
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XX Human citron Rho-interacting kinase CRK DNA Seg1.
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XX
XX WPI; 2004-122753/12.
XX P-PSDB; ADJ96610.
XX
XX New nucleic acid molecule encoding a kinase polypeptide, useful for
XX preparing a composition for treating diseases or disorders, e.g., cancer,
XX or neurological, immunological or inflammatory disorders.
XX
XX Example 1; SEQ ID NO 1; 366bp; English.

XX This invention relates to a novel isolated, enriched or purified nucleic
CC acid molecule that encodes a kinase polypeptide. Specifically, it relates
CC to human tyrosine and serine/threonine protein kinases (PK's and STK's),
CC as well as protein kinase-like enzymes. The present invention describes
CC screening methods to identify agonists, antagonists and antibodies that
CC can be used to modulate the activity or function of the mammalian kinase
CC enzymes. As such, these compositions can be used for gene therapy
CC purposes to treat diseases or disorders including cancer, immune-related
CC diseases, cardiovascular disease, brain or neuronal associated disease,
CC metabolic and inflammatory disorders. Accordingly, they exhibit
CC cytostatic, neuroprotective, immunomodulator and antiinflammatory
CC activities. This polynucleotide sequence is a human kinase DNA sequence
CC of the invention.
XX
XX Sequence 8656 BP; 2314 A; 2219 C; 2239 G; 1884 T; 0 U; 0 Other;

Query Match 99.7%; Score 6144; DB 12; Length 8656;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6160; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 1 ATGTGAAGTCAAAATATGAGGCGGAAATCCTTGGATGCTGCTGTAACCAT 60
Db 51 ATGTGAAGTCAAAATATGAGGCGGAAATCCTTGGATGCTGCTGTAACCAT 110
QY 61 GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCTTATGACTCAA 120
Db 111 GCCAGCCGGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCTTATGACTCAA 170
QY 121 CAGCAGATGCTCTCTTCCGAGAGAGGATATAGATCCCTCTTGTCTCTTTGAA 180
Db 171 CAGCAGATGCTCTCTTCCGAGAGAGGATATAGATCCCTCTTGTCTCTTTGAA 230
QY 181 GAATGACATGAGCTCTCTGATGAAGATTAACAGTGAACAATTGCGGAA---G 237
Db 231 GAATGACATGAGCTCTCTGATGAAGATTAACAGTGAACAATTGCGGAAATG 290
QY 238 TATTCGACACATAGCTGATTAACAGAGCTCCAGCTTCGGCAAGACTTCGAATG 297
Db 291 TATTCGACACATAGCTGATTAACAGAGCTCCAGCTTCGGCAAGACTTCGAATG 350
QY 298 AGAAGTCTGATGATGCTGCTCACTTCTGAAAGTGAAGTGAAGAAAGCAACC 357
Db 351 AGAAGTCTGATGATGCTGCTCACTTCTGAAAGTGAAGTGAAGAAAGCAACC 410
QY 358 GGGGACATCATGCTATGAAAGATGAAGAAAGCTTATTTGGCCGAGACAGGT 417
Db 411 GGGGACATCATGCTATGAAAGATGAAGAAAGCTTATTTGGCCGAGACAGGT 470
QY 418 TCAATTTTGAAGAGAGCGAATATTTATCTGAAGCAAGCCCGTGGATCCCAA 477
Db 471 TCAATTTTGAAGAGAGCGAATATTTATCTGAAGCAAGCCCGTGGATCCCAA 530
QY 478 TTAAGATAGCTTTGAGAGCAAAATACCTTATCTGATGAAATACGCTGGA 537
Db 531 TTAAGATAGCTTTGAGAGCAAAATACCTTATCTGATGAAATACGCTGGA 590
QY 538 GGGGACTTGTGCTCACTTTGAATAGATGAAGCAAGTGAATGAATCACTGATCAG 597
Db 591 GGGGACTTGTGCTCACTTTGAATAGATGAAGCAAGTGAATGAATCACTGATCAG 650
QY 598 TTTTACCTAGCTAGCTGATTTTGGCTGTCACAGCGTTTATCTGATGAGATAGTGCAT 657
Db 651 TTTTACCTAGCTAGCTGATTTTGGCTGTCACAGCGTTTATCTGATGAGATAGTGCAT 710
QY 658 CGAGACATCAAGCTGAGAAATCTCTGTTGACCGGACAGACATCAAGCTGTGGAT 717
Db 711 CGAGACATCAAGCTGAGAAATCTCTGTTGACCGGACAGACATCAAGCTGTGGAT 770
QY 718 TTTGATCTGCGCGGAAATGAATTTCAACAAATGATGAAATCCCAATCTCCGATTTGG 777
Db 771 TTTGATCTGCGCGGAAATGAATTTCAACAAATGATGAAATCCCAATCTCCGATTTGG 830

QY	778	ACCACGATTACATGGCTCTCTGAAGTCTGACTGTGATGAACGGGGATGAAAGGACCC	837
Db	831	ACCCAGATTACATGGCTCTCTGAAGTCTGACTGTGATGAACGGGGATGAAAGGACCC	890
QY	838	TACGGCTTGACCTGTGACCTGTGTAGTGGGGGTGAATTGCCATGAGATGATTAATGGG	897
Db	891	TACGGCTTGACCTGTGACCTGTGTAGTGGGGGTGAATTGCCATGAGATGATTAATGGG	950
QY	898	AGATCCCCCTTCGACAGAGGAAACCTTCGCAGAAACCTTCATATACATTAATGATTTCCAG	957
Db	951	AGATCCCCCTTCGACAGAGGAAACCTTCGCAGAAACCTTCATATACATTAATGATTTCCAG	1011
QY	958	CGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAATCTTCTTGATCTGATTCAA	1011
Db	1011	CGGTTTTTGAATTTCCAGATGACCCCAAGTGAAGTGAATCTTCTTGATCTGATTCAA	1077
QY	1018	AGCTTGTTGTGGGCGACAGAAAGACTGAAGTTTGAAGGCTTTGCTGGCAATCCTTTC	1077
Db	1071	AGCTTGTTGTGGGCGACAGAAAGACTGAAGTTTGAAGGCTTTGCTGGCAATCCTTTC	1130
QY	1078	TTCTCTAAATTTGACTGACCAACAATTCGTAATCTCCCTCCCTCGTTGCTTCCACCTCC	1133
Db	1131	TTCTCTAAATTTGACTGACCAACAATTCGTAATCTCCCTCCCTCGTTGCTTCCACCTCC	1199
QY	1138	AAGTCTGACATGATGACCTCCATTTTGTATGAACAGAGAGAAATTCGTGGTTTCATCC	1199
Db	1191	AAGTCTGACATGATGACCTCCATTTTGTATGAACAGAGAGAAATTCGTGGTTTCATCC	1255
QY	1198	TCTCCGTCGACGTGAGGCCCTCAGGCTTCTCGGGTGAAGATCAGCCGTTGTGGGGTTT	1255
Db	1251	TCTCCGTCGACGTGAGGCCCTCAGGCTTCTCGGGTGAAGATCAGCCGTTGTGGGGTTT	1310
QY	1258	TCGTACAGCAAGCACTGGGGATTCCTTGGTAGATCTGATCTGTGTGTGTGGGTCTGAC	1317
Db	1311	TCGTACAGCAAGCACTGGGGATTCCTTGGTAGATCTGATCTGTGTGTGTGGGTCTGAC	1376
QY	1318	TCCCTTCGCAAGACTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTACAA	1377
Db	1371	TCCCTTCGCAAGACTAGCTCCATGGAAGAACTTCTCATCAAAAGCAAGAGCTACAA	1430
QY	1378	GACTCTCAGCAAGGTGTCACAAGATGAGAGAGAAATGACCCGGTTACATCGAGATG	1433
Db	1431	GACTCTCAGCAAGGTGTCACAAGATGAGAGAGAAATGACCCGGTTACATCGAGATG	1490
QY	1438	TCAGAGGTGAGGCTGTGCTTATGTCAGAGAGAGGTGAGACTGAAAGCCTCTGAGACTAG	1497
Db	1491	TCAGAGGTGAGGCTGTGCTTATGTCAGAGAGAGGTGAGACTGAAAGCCTCTGAGACTAG	1556
QY	1498	AGATCCCTCTTGAGAGAGACCTTGTCTACCTACATCACAGATGACGTATTAAGGGA	1557
Db	1551	AGATCCCTCTTGAGAGAGACCTTGTCTACCTACATCACAGATGACGTATTAAGGGA	1610
QY	1558	AGTTTGAAGCAAGACCGATGGAAGTGTCCAGAGAGATGACAAAGCACTGCACTTCTC	1617
Db	1611	AGTTTGAAGCAAGACCGATGGAAGTGTCCAGAGAGATGACAAAGCACTGCACTTCTC	1670
QY	1618	CATGATATTCAGAGAGCAGAGCCGGAAGCTCCAAAGAAATCAAGAGCAGAGATACAGGCT	1677
Db	1671	CATGATATTCAGAGAGCAGAGCCGGAAGCTCCAAAGAAATCAAGAGCAGAGATACAGGCT	1730
QY	1678	CAAGTGAAGAAATGAGGTTGATGATGAATCAGTTGGAAGAGATCTTGTCTCAGCAAG	1737
Db	1731	CAAGTGAAGAAATGAGGTTGATGATGAATCAGTTGGAAGAGATCTTGTCTCAGCAAG	1790
QY	1738	AGACGGAGTGAATCTCTACGAATCTGAGCTGAGAGATCTCGGCTTGTGCTGAAAGATTC	1797
Db	1791	AGACGGAGTGAATCTCTACGAATCTGAGCTGAGAGATCTCGGCTTGTGCTGAAAGATTC	1850
QY	1798	AAAGCGAAAGCGACAGATGTCAACATTAATGTTGAAGCTTAAGATCAAGGGAAGCCT	1857
Db	1851	AAAGCGAAAGCGACAGATGTCAACATTAATGTTGAAGCTTAAGATCAAGGGAAGCCT	1910
QY	1858	GAAGTGGAGAAATATGCGAAATCGAGAAAGATCAATGCTGAGCAGAGCTCAAAATTCAG	1917

Db	1911	GAAGTGGGGAATATGTCGAAACTGGAGAAATCAATGTGACAGACGCTCAAAATTCC	197
Qy	1918	GAGCTCCAGAGAAACTGGAGAAAGCTGTAAAAGCAGACGAGAGGCCACCGAGCTGCG	197
Db	1971	GAGCTCCAGAGAAATCGAGAAAGCTGTAAAAGCAGACGAGAGGCCACCGAGCTGCG	203
Qy	1978	CAGAAATATCCGCGCAGGCAAAAGAGCGAGCGCAGAGAGGAGCTGGAAAGCTGCAAGACGA	203
Db	2031	CAGAAATATCCGCGCAGGCAAAAGAGCGAGCGCAGAGAGGAGCTGGAAAGCTGCAAGACGA	209
Qy	2038	GAGGATTCCTTCTGAAAGCATCAAAAAGAACTGTGGAAAGCTGAGGAAAGCCGCCATTC	209
Db	2091	GAGGATTCCTTCTGAAAGCATCAAAAAGAAAGCTGTGGAAAGCTGAGGAAAGCCGCCATTC	215
Qy	2098	CTGGAGAACAAAGGTAAAGACTAAGACCAATGAGCCGTAGGAAACACACTGAAGAT	215
Db	2151	CTGGAGAACAAAGGTAAAGAGACTAAGACCAATGAGCCGTAGGAAACACACTGAAGAT	221
Qy	2158	GACATCCAGACAAAATCCCAACAGATCCAGCAGATGAGGTGATTAATTCGAGGCTCGAA	221
Db	2211	GACATCCAGACAAAATCCCAACAGATCCAGCAGATGAGGTGATTAATTCGAGGCTCGAA	227
Qy	2218	GAGAAACATCGGAGAGCCCAAGTCTCAGCCCGACCTTGAAGTGACACTTGAACAGAAA	227
Db	2271	GAGAAACATCGGAGAGCCCAAGTCTCAGCCCGACCTTGAAGTGACACTTGAACAGAAA	233
Qy	2278	GAGCAGCAGCTATGAGGAAAGATTAAAGTGTGGCAATTCAGATTAAGAAAGACCTGGCT	233
Db	2331	GAGCAGCAGCTATGAGGAAAGATTAAAGTGTGGCAATTCAGATTAAGAAAGACCTGGCT	239
Qy	2338	GACAAAGAGACACTGGAGAACATGATGACAGACACGAGAGAGAGGCCCATATGAGAGGCG	239
Db	2391	GACAAAGAGACACTGGAGAACATGATGACAGACACGAGAGAGAGGCCCATATGAGAGGCG	245
Qy	2398	AAAATTCCTCAGGGAACAGAGGCCATGATCAATGCTATGATTCAGATCAATGATCCCTG	245
Db	2451	AAAATTCCTCAGGGAACAGAGGCCATGATCAATGCTATGATTCAGATCAATGATCCCTG	251
Qy	2458	GAAAGAGAGATTGGGAACTGTCTGGAABCCCAATTAACCTTGACGAAATATGACAGTCTTTT	251
Db	2511	GAAAGAGAGATTGGGAACTGTCTGGAABCCCAATTAACCTTGACGAAATATGACAGTCTTTT	257
Qy	2518	AACCCAAAGAAATGAAAGGCCCAAGAAAGATGATTTTGAACCTCAGGCAACAGAAATTT	257
Db	2571	AACCCAAAGAAATGAAAGGCCCAAGAAAGATGATTTTGAACCTCAGGCAACAGAAATTT	263
Qy	2578	TACCTGAGACACAGGCTGGGAAGTTGAGGCCCAAGAACCGAAAACTGGAGAGCAGCTG	263
Db	2631	TACCTGAGACACAGGCTGGGAAGTTGAGGCCCAAGAACCGAAAACTGGAGAGCAGCTG	269
Qy	2638	GAGAAAGATCAACCCACCAAGAACCAACATGACAAAGAAATCGGCTGTGGAACTGGAAACAAAG	269
Db	2691	GAGAAAGATCAACCCACCAAGAACCAACATGACAAAGAAATCGGCTGTGGAACTGGAAACAAAG	275
Qy	2698	TTGCGGAGAGTCACTGTAGAGCACGAGAGCAGAACTGAGAGCTCAAGCGCCAGCTCACA	275
Db	2751	TTGCGGAGAGTCACTGTAGAGCACGAGAGCAGAACTGAGAGCTCAAGCGCCAGCTCACA	281
Qy	2758	GAGCTACAGCTCTCTCTGACAGAGCGCGAGTCAACAGTTGACAGCCCTGACAGCTGCACG	281
Db	2811	GAGCTACAGCTCTCTCTGACAGAGCGCGAGTCAACAGTTGACAGCCCTGACAGCTGCACG	287
Qy	2818	GCGGCGCTTGGAGACACCACTTCGCGCAGGCCAAGACAAAGCTGGAAAGACCAACAGCAGAA	287
Db	2871	GCGGCGCTTGGAGACACCACTTCGCGCAGGCCAAGACAAAGCTGGAAAGACCAACAGCAGAA	293
Qy	2878	GCTAAGAGAGATCCAGGCACTCAGCGCACATAGAGATGAATCCAGCGCAATTTGAT	293
Db	2931	GCTAAGAGAGATCCAGGCACTCAGCGCACATAGAGATGAATCCAGCGCAATTTGAT	299
Qy	2938	GCTTCTGTAAACAGCTTACTGTATATCAGACCTTGAGAGAGAGCTTAAACAGTCAACC	299

Db	2991	GCTCTTGTAACAGCTGTACTGTATATCAACAAGCTGGAGGAGCAGCTAAACCACTGACC	3050
Oy	2998	GAGGACCAACGCTGAACTCAACAACCAAACTTCTACTGTGCCAAACAACCTGATGAGGCT	3057
Db	3051	GAGGACCAACGCTGAACTCAACAACCAAACTTCTACTGTGCCAAACAACCTGATGAGGCT	3110
Oy	3058	TCTGGCCGCAACGACGAGATTGTACACTGGAAAGTGAATGAGACATCTCCGCCGGAG	3117
Db	3111	TCTGGCCGCAACGACGAGATTGTACACTGGAAAGTGAATGAGACATCTCCGCCGGAG	3170
Oy	3118	ATCACGGAACGAGAGATGACGCTTACACGACGAAAGCAAAAGATGGAGGCTCTGAAGAC	3177
Db	3171	ATCACGGAACGAGAGATGACGCTTACACGACGAAAGCAAAAGATGGAGGCTCTGAAGAC	3230
Oy	3178	ACGTGCAACATGCTGGAGAAACAGTTCATGGAATTTGGAGGCCCTTAAACGATGAGCTGTA	3237
Db	3231	ACGTGCAACATGCTGGAGAAACAGTTCATGGAATTTGGAGGCCCTTAAACGATGAGCTGTA	3290
Oy	3238	GAAAAAGAGCGGCACTGGGAGGCTTGGAGAGCGTCTTGGGTGATGAGAAATCCAGTTT	3297
Db	3291	GAAAAAGAGCGGCACTGGGAGGCTTGGAGAGCGTCTTGGGTGATGAGAAATCCAGTTT	3350
Oy	3298	GAGTGTCCGGTTCAGAGACTGCAAGATGCTGACACCGGAGAAACAGAGAGGGCCGAG	3357
Db	3351	GAGTGTCCGGTTCAGAGACTGCAAGATGCTGACACCGGAGAAACAGAGAGGGCCGAG	3410
Oy	3358	GCCGATCAGCGGATCAACCGAGTCTTCGACGAGTGGTGGAGCTGGGACGTGAAGSACACAG	3417
Db	3411	GCCGATCAGCGGATCAACCGAGTCTTCGACGAGTGGTGGAGCTGGGACGTGAAGSACACAG	3470
Oy	3418	GCTGAGATTCTCGCTCTGCAGACGGCTCTCAAAAGCAGAACTGAAAGGCCGAGACCTC	3477
Db	3471	GCTGAGATTCTCGCTCTGCAGACGGCTCTCAAAAGCAGAACTGAAAGGCCGAGACCTC	3530
Oy	3478	TCTGCAAGCTCCATGACCTGGAAGAAAGATGCTATGCTTGAATGAATGCCCGAAGC	3537
Db	3531	TCTGCAAGCTCCATGACCTGGAAGAAAGATGCTATGCTTGAATGAATGCCCGAAGC	3590
Oy	3538	TTACAGCAGAAAGCTGGAGACTGAACGAGAGCTCAACAGAGGCTTCTGGAAGACAAGCC	3597
Db	3591	TTACAGCAGAAAGCTGGAGACTGAACGAGAGCTCAACAGAGGCTTCTGGAAGACAAGCC	3650
Oy	3658	CAGAAGCTCTAGATCGGGCTGATTTACTGAAGACAGAAAGATGACTTGGAGATACAG	3717
Db	3711	CAGAAGCTCTAGATCGGGCTGATTTACTGAAGACAGAAAGATGACTTGGAGATACAG	3770
Oy	3718	CTGGAAAACATTCAGGTTCTCTATTTCTCATGAAAAAGTGAATGGAGGACATATTTCT	3777
Db	3771	CTGGAAAACATTCAGGTTCTCTATTTCTCATGAAAAAGTGAATGGAGGACATATTTCT	3830
Oy	3778	CAACAAACCAAACTCATTGATTTTTCTGCAAGCCAAATGGAACAACTGTAAAAAGAA	3837
Db	3831	CAACAAACCAAACTCATTGATTTTTCTGCAAGCCAAATGGAACAACTGTAAAAAGAA	3890
Oy	3838	AAAGTTCTCTGCACTACATAGAGCTGAAAGTGGCCCTTGGAGAGAGAAAGCTCGCTGT	3897
Db	3891	AAAGTTCTCTGCACTACATAGAGCTGAAAGTGGCCCTTGGAGAGAGAAAGCTCGCTGT	3950
Oy	3898	GCAGAGCTAGAGAAAGCCCTTCAGAAAGACCCGATCGAGCTCCGGTCCGCCCGGAGGAA	3957
Db	3951	GCAGAGCTAGAGAAAGCCCTTCAGAAAGACCCGATCGAGCTCCGGTCCGCCCGGAGGAA	4010
Oy	3958	GCTGCCCAACCGCAAGCAACGAGCCACCAACCCATCAGCGCAACCGCGAGGAG	4017
Db	4011	GCTGCCCAACCGCAAGCAACGAGCCACCAACCCATCAGCGCAACCGCGAGGAG	4070
Oy	4018	CAGATCGCATATGTCGCCATGCTGGCGGTGCGCAGAGCACAGGCCATGCTAGAGCTTG	4077
Db	4071	CAGATCGCATATGTCGCCATGCTGGCGGTGCGCAGAGCACAGGCCATGCTAGAGCTTG	4130

QY	4078	CTGGCCCCGCATCCAGCCGCGAAGAAAGAGCTTTCACTCCAGAGGAATTTAGTCGGCGT	4137
Db	4131	CTGGCCCCGCATCCAGCCGCGAAGAAAGAGTCTTCAACTCCAGAGGAATTTAGTCGGCGT	4190
QY	4138	CTTAAGGAACGATGATCACAACATTTCTCAACGATTAAGATGATGAACTGAACATGCCA	4197
Db	4191	CTTAAGGAACGATGATCACAACATTTCTCAACGATTAAGATGAACTGAACATGCCA	4250
QY	4198	GCCACAAAGTGTGCTGTGTCTGTGATACCTGTGACCTTTGACGCGCAGGCATCCAAATGT	4257
Db	4251	GCCACAAAGTGTGCTGTGTCTGTGATACCTGTGACCTTTGACGCGCAGGCATCCAAATGT	4310
QY	4258	CTCGAATGTCAAGTATGTGTCAACCCCAAGTCTCCAGTCTTCAGCCACTCGCGC	4317
Db	4311	CTCGAATGTCAAGTATGTGTCAACCCCAAGTCTTCAGCTGTTCAGCCACTCGCGC	4370
QY	4318	TTGGCTGTCTGAATATGGCCACACATTCACCCGAGGCTTGTGCGGTACAAATGAATCC	4377
Db	4371	TTGGCTGTCTGAATATGGCCACACATTCACCCGAGGCTTGTGCGGTACAAATGAATCC	4430
QY	4378	CCAGGTCTCCAGACCAAGAGGCCACAGCAGACTTGTGACCTTGAAAGGTGATGAAGTGTG	4437
Db	4431	CCAGGTCTCCAGACCAAGAGGCCACAGCAGACTTGTGACCTTGAAAGGTGATGAAGTGTG	4490
QY	4438	CCCAAGAAATACAAACGAGGACAGCAAGGCTGGGACAGGAAGTACATTTGTCTTGAGGGA	4497
Db	4491	CCCAAGAAATACAAACGAGGACAGCAAGGCTGGGACAGGAAGTACATTTGTCTTGAGGGA	4550
QY	4498	TCAAAAGTCTCATTTATATGACATGAGCCACAGAAAGCTGTGACAGAGGCCGTGTGAAGAA	4557
Db	4551	TCAAAAGTCTCATTTATATGACATGAGCCACAGAAAGCTGTGACAGAGGCCGTGTGAAGAA	4610
QY	4558	TTTGAAGTGTGCTTCCCGACCGGGATGTATCTATTATGAGTGCCTGTGGTCTTCCGAA	4617
Db	4611	TTTGAAGTGTGCTTCCCGACCGGGATGTATCTATTATGAGTGCCTGTGGTCTTCCGAA	4670
QY	4618	CTCGCAAAATACAGCCAAAGACAGATGTCCCATACATCTAGAATGGAATCTCACCCGCAC	4677
Db	4671	CTCGCAAAATACAGCCAAAGACAGATGTCCCATACATCTAGAATGGAATCTCACCCGCAC	4730
QY	4678	ACCACCTGTGGCCCGGGAGAAACCTCTATCTTGTGATGCTCCAGCTTCCCTGACAAACAG	4737
Db	4731	ACCACCTGTGGCCCGGGAGAAACCTCTATCTTGTGATGCTCCAGCTTCCCTGACAAACAG	4790
QY	4738	CGCTGGGTCAACGCTTGAATCAGTGTGCGAGGTGGAGAGTTCTAGGGAAAAAGCA	4797
Db	4791	CGCTGGGTCAACGCTTGAATCAGTGTGCGAGGTGGAGAGTTCTAGGGAAAAAGCA	4850
QY	4798	GAAAGTGAATGTAAACCTGCTTGAAACTCCCTGCTGAACCTGGAAAGTGTGACCGTCTA	4857
Db	4851	GAAAGTGAATGTAAACCTGCTTGAAACTCCCTGCTGAACCTGGAAAGTGTGACCGTCTA	4910
QY	4858	GACATGAACCTGACGCTGCCCTTCAAGTGCACAGTGTGTTGGTGGGCAACCGAGAAAGG	4917
Db	4911	GACATGAACCTGACGCTGCCCTTCAAGTGCACAGTGTGTTGGTGGGCAACCGAGAAAGG	4970
QY	4918	CTCTACGCCCTGAATGTCTTGA AAAAATCCCTTAACCCATGTCACAGAAATTTGAGCAGTC	4977
Db	4971	CTCTACGCCCTGAATGTCTTGA AAAAATCCCTTAACCCATGTCACAGAAATTTGAGCAGTC	5030
QY	4978	TTCCAAATTTATATTAATCAAGACCTGGAAGCTTACTATGATAGCAGAGGAAGAGCGG	5037
Db	5031	TTCCAAATTTATATTAATTAACAAGACCTGGAAGCTTACTATGATAGCAGAGGAAGAGCGG	5090
QY	5038	GCACTGTGTCTTTGTGACGTGAAGAAAGTGAACAGTCCCTGTGCCAGTCCACTGTGCT	5097
Db	5091	GCACTGTGTCTTTGTGACGTGAAGAAAGTGAACAGTCCCTGTGCCAGTCCACTGTGCT	5150
QY	5098	GCCGACCCCGGACATCTCACCCCAATTTTGAAGCTGTCAAGGGCTGCCACTTGTGTTGG	5157
Db	5151	GCCGACCCCGGACATCTCACCCCAATTTTGAAGCTGTCAAGGGCTGCCACTTGTGTTGG	5210


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QY 5158 GCAGGCAAGATTGAGACGGGCTCTGCACTCTGTGACGACCATCCAGCAAGTGTGATT 5217
Db 5211 GCAGGCAAGATTGAGACGGGCTCTGCACTCTGTGACGACCATCCAGCAAGTGTGATT 5270
QY 5218 CTCGGCTACACGAAAACTCAGCAAACTACTGATCTCCGGAAGAGATAGAGACTCAGAG 5277
Db 5271 CTCGGCTACACGAAAACTCAGCAAACTACTGATCTCCGGAAGAGATAGAGACTCAGAG 5330
QY 5278 CCTCGACGCTGTATCCACTTCAACCAATTACATCTCTCATTTGGAACCAATTAATTTCTAC 5337
Db 5331 CCTCGACGCTGTATCCACTTCAACCAATTACATCTCTCATTTGGAACCAATTAATTTCTAC 5390
QY 5338 GAAATGACATGAAAGAGTACAGCTCAGAGAAATTCCTGATAGAAATGACATTTCTCTTG 5397
Db 5391 GAAATGACATGAAAGAGTACAGCTCAGAGAAATTCCTGATAGAAATGACATTTCTCTTG 5450
QY 5398 GCACTGCTGTGTTTGGCCGCTCTTCCAAAGCTTCCCTGTCTCAATCGTGACAGTGAAC 5457
Db 5451 GCACTGCTGTGTTTGGCCGCTCTTCCAAAGCTTCCCTGTCTCAATCGTGACAGTGAAC 5510
QY 5458 AGCGCAGGGGACGAGAGAGAGTACTTGTGTGTTTCCAGCAATTTGAGTGTCTGAT 5517
Db 5511 AGCGCAGGGGACGAGAGAGAGTACTTGTGTGTTTCCAGCAATTTGAGTGTCTGAT 5570
QY 5518 TCTTACGGAAGAGGTACCGGACAGAGATCTCAAGTGGAGTGGCTTAACCTTTGGCCTTT 5577
Db 5571 TCTTACGGAAGAGGTACCGGACAGAGATCTCAAGTGGAGTGGCTTAACCTTTGGCCTTT 5630
QY 5578 GCCTACAGAGAACCTTATCTGTTTGTGACCACTTCAACTCACTCGAAGTAATTGAGATC 5637
Db 5631 GCCTACAGAGAACCTTATCTGTTTGTGACCACTTCAACTCACTCGAAGTAATTGAGATC 5690
QY 5638 CAGGACGCTCTCTGACAGAGAACCCCTGCCCCAGCGTACTCTGACATCCCGAACCCGCGC 5697
Db 5691 CAGGACGCTCTCTGACAGAGAACCCCTGCCCCAGCGTACTCTGACATCCCGAACCCGCGC 5750
QY 5698 TACCTGGGCGCTGCGCAATTTCTCAGAGAGGATTTACTGCGGTCTCTATACAGAGTAAA 5757
Db 5751 TACCTGGGCGCTGCGCAATTTCTCAGAGAGGATTTACTGCGGTCTCTATACAGAGTAAA 5810
QY 5758 TTAAAGGTCATTTGCTGCAAGGAAAACCTGTGAAAGAGTCCCGCACTGAAACCAACCGG 5817
Db 5811 TTAAAGGTCATTTGCTGCAAGGAAAACCTGTGAAAGAGTCCCGCACTGAAACCAACCGG 5870
QY 5818 GGGCCGTCCACTCTCCGACAGACGCCACACAGAGAGGCCACCACTGTAACAAGAGCAC 5877
Db 5871 GGGCCGTCCACTCTCCGACAGACGCCACACAGAGAGGCCACCACTGTAACAAGAGCAC 5930
QY 5878 ATCACCAGAGGCGTGGCTTCAGCCAGCGCGCGCCGGAAGGCCCAACCCGCGAGAG 5937
Db 5931 ATCACCAGAGGCGTGGCTTCAGCCAGCGCGCGCCGGAAGGCCCAACCCGCGAGAG 5990
QY 5938 CCAAGACACACCCACCGCTTACCGCAGAGGGCGAGCCGAGTGTGCGACAGGCAAGTCTCT 5997
Db 5991 CCAAGACACACCCACCGCTTACCGCAGAGGGCGAGCCGAGTGTGCGACAGGCAAGTCTCT 6050
QY 5998 GGGCGGCGCTGTGAGCGAGAGAAATGTCCTCCGCGCGGATACTCGACACGCGAGAGACCG 6057
Db 6051 GGGCGGCGCTGTGAGCGAGAGAAATGTCCTCCGCGCGGATACTCGACACGCGAGAGACCG 6110
QY 6058 TCCCGCGGAGGCGTGTGTAAGACACACACAGAGGGCGCGCTGTGCTGCGGAGCGGTGAGG 6117
Db 6111 TCCCGCGGAGGCGTGTGTAAGACACACACAGAGGGCGCGCTGTGCTGCGGAGCGGTGAGG 6170
QY 6118 ACCCGCGTGTCCAGGTGAACAAGTCTGAGACCACTTCTTCAGTATATA 6165
Db 6171 ACCCGCGTGTCCAGGTGAACAAGTCTGAGACCACTTCTTCAGTATATA 6218

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RESULT 6
AAL55217
ID AAL55217 standard; DNA; 6156 BP.
XX

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AC AAL55217;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human CR1K related DNA sequence, SEQ ID No 8.
XX
KW Anorectic; hypotensive; cardiast; antilipemic; cerebroprotective;
KW antilipid; osteopathic; antidiabetic; cytosolic; antidepressant;
KW immunomodulator; antitumor; tranquilizer; antiparkinsonian; nootropic;
KW neuroprotective; antiinflammatory; antidiabetic; analgesic;
KW human citron rho/rac-interacting kinase; enzyme; CR1K; ameliorating;
KW obesity; comorbidity; cancer; anorexia; cachexia; bulimia;
KW central nervous system disorder; chronic obstructive pulmonary disease;
KW diabetes; pain; ds.
XX
OS Homo sapiens.
XX
PN WC0200304523-A1.
XX
PD 16-JAN-2003.
XX
PF 28-JUN-2002; 2002MO-EP007156.
XX
PR 02-JUL-2001; 2001JUS-0301841P.
PR 11-DEC-2001; 2001JUS-0338651P.
PR 25-APR-2002; 2002JUS-0375014P.
XX
PA (FARB ) BAYER AG.
XX
PI Zhu Z;
XX
DR WPI; 2003-221576/21.
XX
PT New human citron rho/rac-interacting kinase (CR1K) polypeptide and
PT polynucleotide, useful in preventing, ameliorating or treating diseases
PT associated with human CR1K dysfunction, e.g. obesity, diabetes or
PT Alzheimer's disease.
XX
PS Disclosure; Page 217-222; 237pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a human
XX citron rho/rac-interacting kinase polypeptide. The isolated
XX polynucleotide comprises a 6165 or 6603 base pair sequence, given in the
XX specification. The human citron rho/rac-interacting kinase (CR1K)
XX polypeptide and polynucleotide are useful in preventing, ameliorating, or
XX treating diseases associated with human CR1K dysfunction such as obesity
XX and obesity-associated comorbidities (e.g. hypertension, coronary artery
XX disease, hyperlipidaemia, stroke, gout, osteoarthritis, some types of
XX cancer including endometrial, breast, prostate and colon cancer),
XX anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
XX disorders, anxiety disorders, Parkinson's disease or Alzheimer's
XX disease), chronic obstructive pulmonary disease, or diabetes. These can
XX also be used to treat pain associated with the disorders. The human CR1K
XX polypeptide is also useful in diagnostic assays or in genetic testing.
XX The expression vector or the reagent is useful in preparing a medicament
XX for modulating the activity of a human CR1K in a disease, e.g. obesity, a
XX central nervous system disorder, or chronic obstructive pulmonary
XX disease. The fusion protein is useful for generating antibodies against a
XX CR1K polypeptide and for use in various assay systems. The methods are
XX useful in producing and detecting the polynucleotide and polypeptide and
XX in screening for agents that modulate the activity of the human CR1K
XX polypeptide. This polynucleotide sequence represents a DNA sequence
XX relating to the human CR1K protein of the invention
XX
SQ Sequence 6156 BP; 1732 A; 1548 C; 1679 G; 1197 T; 0 U; 0 Other;
XX
Query Match 99.6%; Score 6142.2; DB 9; Length 6156;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 6147; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ATGTTGAAGTCAAAATATGAGACGGGGAATCCTTTGATGCTGTGCTGACCAACCAATT 60
Db 1 ATGTTGAAGTCAAAATATGAGACGGGGAATCCTTTGATGCTGTGCTGACCAACCAATT 60

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QY 61 GCCAGCCGGGCTTCAGGCTGAATCTGTCTTCCAGGGGAAACACCCTTTATGACTCAA 120
DB 61 GCCAGCCGGGCTTCAGGCTGAATCTGTCTTCCAGGGGAAACACCCTTTATGACTCAA 120
QY 121 CAGAGATGTCCTCTCTTCCCGAGAGGGAATTTAGATGCCCTCTTGTCTCTTGA 180
DB 121 CAGAGATGTCCTCTCTTCCCGAGAGGGAATTTAGATGCCCTCTTGTCTCTTGA 180
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DB 481 CAGTATGCTCTTTCAGGACAAAATCACCTTTATCTGATCATGGAATTCAGCTGAGGG 540
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DB 541 GACTGTGCTCATCTTTGAATGATATGAGAGACAGTTAGTGAAGAACTGATACAGTTT 600
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DB 661 GACATCAAGCTGAGAACTTCTGTTGACCGCAAGAGACATCAAGCTGTGTGATTTT 720
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DB 1741 CGGAGTATCTCAGAAATCTGAGCTGAGAGATCTCGGTTGCTGTGGAAGAAATTCAG 1800
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 DB 6121 CCGCTGTCCAGGTGAACAAAGTCTGGGACCATGC 6155

RESULT 7
 AAS06701
 ID AAS06701 standard; cDNA; 6159 BP.
 XX
 AC AAS06701;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Polynucleotide sequence encoding human protein kinase #1.
 XX
 KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; se.
 XX
 OS Homo sapiens.
 XX
 PN W0200138503-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000MO-US032085.
 XX
 PR 24-NOV-1999; 99US-0167482P.
 XX
 PA (SUGB-) SUGEN INC.
 XX
 PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;

PI Flanagan P, Clary D;
XX WPI: 2001-343950/36.
DR P-PSDB; AA003501.
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections.
XX
PS Example 1; Fig 1; 433p; English.
XX
CC AA06701-AA06757 encode for novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity
XX
SQ Sequence 6159 BP; 1732 A; 1549 C; 1680 G; 1198 T; 0 U; 0 Other;

Query Match 99.4%; Score 6126; DB 4; Length 6159;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 6145; Conservative 0; Mismatches 10; Indels 3; Gaps 1;

QY 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGCTGTAACCAT 60
DB 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCTTTGGATGCTGCTGTAACCAT 60

QY 61 GCCAGCGCGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCCCTTATGACTCAA 120
DB 61 GCCAGCGCGGCTCCAGGCTGAATCTGTTCTTCAGGGGAAACACCCCTTATGACTCAA 120

QY 121 CAGCAATGCTCTCTCTTCCGAGAAAGGATATTAGATGCTCTTGTCTCTTGA 180
DB 121 CAGCAATGCTCTCTCTTCCGAGAAAGGATATTAGATGCTCTTGTCTCTTGA 180

QY 121 CAGCAATGCTCTCTCTTCCGAGAAAGGATATTAGATGCTCTTGTCTCTTGA 180
DB 121 CAGCAATGCTCTCTCTTCCGAGAAAGGATATTAGATGCTCTTGTCTCTTGA 180

QY 181 GAATGAGTCAGGCTGCTCTGATGAAGATTAAAGCAGTGAGCACTTTGCCGGA 237
DB 181 GAATGAGTCAGGCTGCTCTGATGAAGATTAAAGCAGTGAGCACTTTGCCGGA 237

QY 238 TATTCGACACCATAGCTAGTTACAGAGCTTCAGCTTCGCAAGAGCTTCGAAGTC 297
DB 241 TATTCGACACCATAGCTAGTTACAGAGCTTCAGCTTCGCAAGAGCTTCGAAGTC 300

QY 298 AGAAGCTCTTGAGTGTGTGCTCACTTGTCTGAAAGTCAAGTGTAAAGAAAGCAACC 357
DB 301 AGAAGCTCTTGAGTGTGTGCTCACTTGTCTGAAAGTCAAGTGTGTAAAGAAAGCAACC 360

QY 358 GGGGACATCATGCTATGTAAGATGAGAAAGAAAGGCTTTATTTGGCCAGAGCAAGTT 417
DB 361 GGGGACATCATGCTATGTAAGATGAGAAAGAAAGGCTTTATTTGGCCAGAGCAAGTT 420

QY 418 TCATTTTTGAGAAAGCGGAAACATATTATCTCGAAGCAACAAGCCGCTGATCCCCCA 477
DB 421 TCATTTTTGAGAAAGCGGAAACATATTATCTCGAAGCAACAAGCCGCTGATCCCCCA 480

QY 478 TTACAGTATGCTTTTCAGACAAAATCACTTTATCTGCTCATGTAATATCAAGCTGGA 537
DB 481 TTACAGTATGCTTTTCAGACAAAATCACTTTATCTGCTCATGTAATATCAAGCTGGA 540

QY 538 GGGGACTTGCTGCTCTTTGAATGATGAGACCAATTAGTAAAACTGATACG 597
DB 541 GGGGACTTGCTGCTCTTTGAATGATGAGACCAATTAGTAAAACTGATACG 600

DB 541 GGGGACTTGCTGCTCTTTGAATGATGAGACCAATTAGTAAAACTGATACG 600
QY 598 TTTTACCTAGCTAGCTGATTTTGGCTGTTCAAGCGTTCATCTGATGGATAGTGCAT 657
DB 601 TTTTACCTAGCTAGCTGATTTTGGCTGTTCAAGCGTTCATCTGATGGATAGTGCAT 660
QY 658 CGAGATCAAGCTTGAGAACTTCTGTTGACCGCAACAGACATCAAGCTGTGTGAT 717
DB 661 CGAGATCAAGCTTGAGAACTTCTGTTGACCGCAACAGACATCAAGCTGTGTGAT 720
QY 718 TTTGATCTGCGCGAAATGAATTCAACAAGATGGTGAATGCCAACTCCGATTGGG 777
DB 721 TTTGATCTGCGCGAAATGAATTCAACAAGATGGTGAATGCCAACTCCGATTGGG 780
QY 778 ACCCCAGATTACATGAGCTCTGTAAGTCTGATCTGATGAACCGGAGATGAAAAGCAC 837
DB 781 ACCCCAGATTACATGAGCTCTGTAAGTCTGATGAACCGGAGATGAAAAGCAC 840
QY 838 TACGCTGAGCTGTGATCTGTGTGTCAATGAGGCTGATTTGCTATGATGATTTATGG 897
DB 841 TACGCTGAGCTGTGATCTGTGTGTCAATGAGGCTGATTTGCTATGATGATTTATGG 900
QY 898 AGATCCCTGCGCAGAGGGAACCTGCGCAGAACCTTCAATACATTAATGAATTTCCAG 957
DB 901 AGATCCCTGCGCAGAGGGAACCTGCGCAGAACCTTCAATACATTAATGAATTTCCAG 960
QY 958 CGGTTTTGAATTTTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATTTCAA 1017
DB 961 CGGTTTTGAATTTTCCAGATGACCCCAAGTGAAGTGAAGTCTTCTGATCTGATTTCAA 1020
QY 1018 AGCTTTGTGTGGCGCAGAAAGAGACTGAAGTTGAAGTCTTGTGCTGCACTCTTC 1077
DB 1021 AGCTTTGTGTGGCGCAGAAAGAGACTGAAGTTGAAGTCTTGTGCTGCACTCTTC 1080
QY 1078 TTTCTAAATGATCTGGAACCAATGTAATCTGCTCCCTCCCTGCTGCTCCACCTTC 1137
DB 1081 TTTCTAAATGATCTGGAACCAATGTAATCTGCTCCCTCCCTGCTGCTCCACCTTC 1140
QY 1138 AAGTTCAGATGACACTTCAATTTTGTATGAACAGAGAAAGTCTGTGGTTTCATCC 1197
DB 1141 AAGTTCAGATGACACTTCAATTTTGTATGAACAGAGAAAGTCTGTGGTTTCATCC 1200
QY 1198 TCTCGTGCAGCTGAGCCCTCAAGCTTCTGGGTGAAGAACTGCCGTTTGTGGGTTT 1257
DB 1201 TCTCGTGCAGCTGAGCCCTCAAGCTTCTGGGTGAAGAACTGCCGTTTGTGGGTTT 1260
QY 1258 TCGTACAGCAAGGCACTGGGGATTTCTGGTATGATGATGCTGTGTGTGGGTCTGGAC 1317
DB 1261 TCGTACAGCAAGGCACTGGGGATTTCTGGTATGATGATGATGCTGTGTGTGGGTCTGGAC 1320
QY 1318 TCCCTGCGCAAGCTAGCTTCATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTACAA 1377
DB 1321 TCCCTGCGCAAGCTAGCTTCATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTACAA 1380
QY 1378 GACTCTCAGGACAGTGTCACAAGATGAGCAGAAATGACCCGGTTACATGAGAGTG 1437
DB 1381 GACTCTCAGGACAGTGTCACAAGATGAGCAGAAATGACCCGGTTACATGAGAGTG 1440
QY 1438 TCAGAGTGGAGGCTGTGTATGTCAGAAAGAGGTGAGCTGAAGGCTCTGAGACTGAC 1497
DB 1441 TCAGAGTGGAGGCTGTGTATGTCAGAAAGAGGTGAGCTGAAGGCTCTGAGACTGAC 1500
QY 1498 AGATCCCTGCGCAGAGGACCTTCTCATCAATCAAGATGAGTGAAGTAAAGCA 1557
DB 1501 AGATCCCTGCGCAGAGGACCTTCTCATCAATCAAGATGAGTGAAGTAAAGCA 1560
QY 1558 AGTTTGAAGCAAGCAGATGAGGTGTCCAGAGATGACAAAGCACTGAGCTTCTC 1617
DB 1561 AGTTTGAAGCAAGCAGATGAGGTGTCCAGAGATGACAAAGCACTGAGCTTCTC 1620
QY 1618 CATGATATCAGAGACAGACCGGAGCTCCAGAAATCAAAAGACAGAGATACAGGCT 1677
DB 1621 CATGATATCAGAGACAGACCGGAGCTCCAGAAATCAAAAGACAGAGATACAGGCT 1680

QY 1678 CAATGGAGAAATGAGTTGATGATGATCAATCAGTTGGAGAAGAGATCTTGTCTGACAGAA 1737
DB 1681 CAATGGAGAAATGAGTTGATGATGATGATCAATCAGTTGGAGAAGAGATCTTGTCTGACAGAA 1740
QY 1738 AGACGAGTATCTCTCAATCTGAGTCTGAGAGAGTCTGAGTCTGCTGCTGAGAAATTC 1797
DB 1741 AGACGAGTATCTCTCAATCTGAGTCTGAGAGAGTCTGAGTCTGCTGCTGAGAAATTC 1800
QY 1798 AACCGAAGACGACAGAAATCTGACATTAACCTGTTGAAGCTTAAGATCAAGAGAACCT 1857
DB 1801 AACCGAAGACGACAGAAATCTGACATTAACCTGTTGAAGCTTAAGATCAAGAGAACCT 1860
QY 1858 GAAGTGGAGAAATATGCGAAATCTGAGAAATCAATCTGACAGAGCTCAAAATTCAG 1920
DB 1861 GAAGTGGAGAAATATGCGAAATCTGAGAAATCAATCTGACAGAGCTCAAAATTCAG 1920
QY 1918 GAGCTCCAGAGAACTGGAGAGGCTGTAAAGCCGACGAGGCGCACGAGCTGCTG 1977
DB 1921 GAGCTCCAGAGAACTGGAGAGGCTGTAAAGCCGACGAGGCGCACGAGCTGCTG 1980
QY 1978 CAGAAATCCCGCAGGCGAAAGAGCGAGCGAGAGGAGCTGAGAAAGCTGACAGAACCGA 2037
DB 1981 CAGAAATCCCGCAGGCGAAAGAGCGAGCGAGAGGAGCTGAGAAAGCTGACAGAACCGA 2040
QY 2038 GAGGATCTTCTGAAAGCATCAGAAAGAGCTGAGAGCTGAGAAAGCTGAGAAAGCTTCT 2097
DB 2041 GAGGATCTTCTGAAAGCATCAGAAAGAGCTGAGAGCTGAGAAAGCTGAGAAAGCTTCT 2100
QY 2098 CTGAGAGAACAGGTAAGAGATCTAGAGACATGAGAGCTGAGAAAGAACATCTGAAAGAT 2157
DB 2101 CTGAGAGAACAGGTAAGAGATCTAGAGACATGAGAGCTGAGAAAGAACATCTGAAAGAT 2160
QY 2158 GACATCCAGACAAATATCCCAACAGATCCAGACAGTGTGATTAATTTCTGAGCTGAA 2217
DB 2161 GACATCCAGACAAATATCCCAACAGATCCAGACAGTGTGATTAATTTCTGAGCTGAA 2220
QY 2218 GAGAAACATCGGAGGCGCCAAAGTCTCAGCCAGACCTAGAAAGTGCACCTGAAACAGAAA 2277
DB 2221 GAGAAACATCGGAGGCGCCAAAGTCTCAGCCAGACCTAGAAAGTGCACCTGAAACAGAAA 2280
QY 2278 GAGCAGACATATGAGAGAAAGATTAAGTGTGACATCAAGTAAAGAAAGCTGAGCT 2337
DB 2281 GAGCAGACATATGAGAGAAAGATTAAGTGTGACATCAAGTAAAGAAAGCTGAGCT 2340
QY 2338 GACAGAGAGACATGAGAGACATGATGACAGACAGAGAGAGGCGCCATGAGAGGCG 2397
DB 2341 GACAGAGAGACATGAGAGACATGATGACAGAGACAGAGAGAGGCGCCATGAGAGGCG 2400
QY 2398 AAAATTTCTCAGCGAACAAGAGCGAGTATCAATGCTTGAATTCAGAGTCAAGTCCCTG 2457
DB 2401 AAAATTTCTCAGCGAACAAGAGCGAGTATCAATGCTTGAATTCAGAGTCAAGTCCCTG 2460
QY 2458 GAAACAGAGATTTGTGAATCTGTCTGAAGCCAAATTAACCTTGACAGAAATAGCAAGTCTTTT 2517
DB 2461 GAAACAGAGATTTGTGAATCTGTCTGAAGCCAAATTAACCTTGACAGAAATAGCAAGTCTTTT 2520
QY 2518 ACCCAAGAGAACATGAAAGGCGCCAAAGAGATGATTTCTGAATCTCAGGCGAACAGAAATTT 2577
DB 2521 ACCCAAGAGAACATGAAAGGCGCCAAAGAGATGATTTCTGAATCTCAGGCGAACAGAAATTT 2580
QY 2578 TACCTGGAGACACAGGCTGGAGAGTTGAGAGCCAGAAACGAAATCTGAGAGAGAGCTG 2637
DB 2581 TACCTGGAGACACAGGCTGGAGAGTTGAGAGCCAGAAACGAAATCTGAGAGAGAGCTG 2640
QY 2638 GAGAGATCAGCCACCAAGACCAACAGTGAACAGAAATGAGTCTGAGAACTGAGACAAAG 2697
DB 2641 GAGAGATCAGCCACCAAGACCAACAGTGAACAGAAATGAGTCTGAGAACTGAGACAAAG 2700
QY 2698 TTGCGGAGAGCTCAATCTAGAGACAGAGAGACGAAATCTGAGAGCTCAAGGCGCACTACA 2757
DB 2701 TTGCGGAGAGCTCAATCTAGAGACAGAGAGACGAAATCTGAGAGCTCAAGGCGCACTACA 2760

QY 2758 GAGCTACAGCTTCCCTGACAGAGCGCGAGTCAAGTTGACAGCCCTGACAGCTGACAGG 2817
DB 2761 GAGCTACAGCTTCCCTGACAGAGCGCGAGTCAAGTTGACAGCCCTGACAGCTGACAGG 2820
QY 2818 GCGGCCCTGGAGAGCCAGCTTCCGACGCGAGAGACAGAGCTGGAGAGACACAGACAGAA 2877
DB 2821 GCGGCCCTGGAGAGCCAGCTTCCGACGCGAGAGACAGAGCTGGAGAGACACAGACAGAA 2880
QY 2878 GCTGAAGAGAGATCCAGGCACTCAGGCGCATAGAGATGAATTCAGGCGCAATTTGAT 2937
DB 2881 GCTGAAGAGAGATCCAGGCACTCAGGCGCATAGAGATGAATTCAGGCGCAATTTGAT 2940
QY 2938 GCTCTGTGAACGCTGTACTGTATCAAGACCTGAGAGAGAGAGCTTAACCAAGCTGACC 2997
DB 2941 GCTCTGTGAACGCTGTACTGTATCAAGACCTGAGAGAGAGAGCTTAACCAAGCTGACC 3000
QY 2998 GAGGACACGCTGAATCTCAACCAACCAAACTTCTACTGTCCAAACATCTGATGAGCT 3057
DB 3001 GAGGACACGCTGAATCTCAACCAACCAAACTTCTACTGTCCAAACATCTGATGAGCT 3060
QY 3058 TCTGGCGCCACGACGAGATTTGTACAATGCGAAGTGAAGTGAACCATCTCGCGCGAG 3117
DB 3061 TCTGGCGCCACGACGAGATTTGTACAATGCGAAGTGAAGTGAACCATCTCGCGCGAG 3120
QY 3118 ATCAGCGAACGAGAGATGACAGCTTACCAGCCAGAACCAACGATGAGAGCTGAGAAC 3177
DB 3121 ATCAGCGAACGAGAGATGACAGCTTACCAGCCAGAACCAACGATGAGAGCTGAGAAC 3180
QY 3178 AGGTGACCAATGTGAGAGGACAGTCAATGATTTGAGAGCCCTTAACGATGAGCTGCTA 3237
DB 3181 AGGTGACCAATGTGAGAGGACAGTCAATGATTTGAGAGCCCTTAACGATGAGCTGCTA 3240
QY 3238 GAAAGAGCGGAGTGGAGAGGCTGAGAGAGCTGAGAGAGCTGAGAGATCCAGTTT 3297
DB 3241 GAAAGAGCGGAGTGGAGAGGCTGAGAGAGCTGAGAGAGCTGAGAGATCCAGTTT 3300
QY 3298 GAGTGTGGGTTTGAAGCTGACAGAGTGTGAGAACCCAGAAACAGAGAGGCGAGAA 3357
DB 3301 GAGTGTGGGTTTGAAGCTGACAGAGTGTGAGAACCCAGAAACAGAGAGGCGAGAA 3360
QY 3358 GCGGATCAGCGATCAACGAGTCTGCGCAGGTGTGAGAGTGGCAGTGAAGAGACCAAG 3417
DB 3361 GCGGATCAGCGATCAACGAGTCTGCGCAGGTGTGAGAGTGGCAGTGAAGAGACCAAG 3420
QY 3418 GCTGAGATTTCTGCTCTGACAGAGCTCTCAAGAGACAGAGCTGAAAGGCGAGAGCTC 3477
DB 3421 GCTGAGATTTCTGCTCTGACAGAGCTCTCAAGAGACAGAGCTGAAAGGCGAGAGCTC 3480
QY 3478 TCTGACAGCTCAATGACCTGAGAGAGAGACATGCTATGCTTGAATGAATGCCGAAAG 3537
DB 3481 TCTGACAGCTCAATGACCTGAGAGAGAGACATGCTATGCTTGAATGAATGCCGAAAG 3540
QY 3538 TTAACAGCAAGCTGAGAGCTGAACGAGAGCTCAACAGAGGCTTCTGAGAGAGCAAGCC 3597
DB 3541 TTAACAGCAAGCTGAGAGCTGAACGAGAGCTCAACAGAGGCTTCTGAGAGAGCAAGCC 3600
QY 3598 AAATTAACAGAGAGATGAGACCTGAGAGAAATCAATTTTCCGTCTGACTCAAGGACTG 3657
DB 3601 AAATTAACAGAGAGATGAGACCTGAGAGAAATCAATTTTCCGTCTGACTCAAGGACTG 3660
QY 3658 CAAGAGCTCTAGATCGGCTGATCTTAATCTGAAGACAGAAAGAGATGACTTGAAGTACAG 3717
DB 3661 CAAGAGCTCTAGATCGGCTGATCTTAATCTGAAGACAGAAAGAGATGACTTGAAGTACAG 3720
QY 3718 CTGAGAAACATTCAGGTTCTTAATTTCTCATGAAGAGTGAATGAGAGCACTATTTCT 3777
DB 3721 CTGAGAAACATTCAGGTTCTTAATTTCTCATGAAGAGTGAATGAGAGCACTATTTCT 3780
QY 3778 CAACAAACCAATCTCAATGATTTTCTGAAGCCCAAAATGAGACCACTGCTAAGAAAGAA 3837
DB 3781 CAACAAACCAATCTCAATGATTTTCTGAAGCCCAAAATGAGACCACTGCTAAGAAAGAA 3840
QY 3838 AAGTTCTCTGACATGACATGAGCTGAAGCTGCGCTGAGAGAGAGAAAGCTCGCTGT 3897

3841 AAGTTCTCTGCGATGACATGAGCTGAGCTGGCCCTGGAGAGAGAAAGCTCGCT 3900
3898 GCAGAGCTTGAAGAGAGCCCTTCAAGAGACCCGATCGAGCTCCGATCCGCCGGAGAGAA 3957
3901 GCAGAGCTAGAGAGAGCCCTTCAAGAGACCCGATCGAGCTCCGATCCGCCGGAGAGAA 3960
3958 GCGGCCACCCGAG 4017
3961 GCGGCCACCCGAG 4020
4018 CAGATCGCATGATCGCATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 4077
4021 CAGATCGCATGATCGCATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 4080
4078 CTGGCCCGCCATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 4137
4081 CTGGCCCGCCATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 4140
4138 CTTAAGGAG 4197
4141 CTTAAGGAG 4200
4198 GCCACAAAGT 4257
4201 GCCACAAAGT 4260
4258 CTGGAATGTGAGT 4317
4261 CTGGAATGTGAGT 4320
4318 TTGCGCTGTGAATGT 4377
4321 TTGCGCTGTGAATGT 4380
4378 CCAGGTCTCTCAGACCAAG 4437
4381 CCAGGTCTCTCAGACCAAG 4440
4438 CCCAGGAATTAACAAACGAG 4497
4441 CCCAGGAATTAACAAACGAG 4500
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4501 TCAGAAAGTCTCTTATATGACATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4560
4558 TTGAGCTGTGCTTCCGACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4617
4561 TTGAGCTGTGCTTCCGACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4620
4618 CTGCAAAATACAGCCAAAG 4677
4621 CTGCAAAATACAGCCAAAG 4680
4678 ACCACTCTGTGGCCGGAG 4737
4681 ACCACTCTGTGGCCGGAG 4740
4738 CGCTGGGTACCGCCTTAAGATCAGTTGTGCAAGGTGGAGAGAGAGAGAGAGAGAGAGAG 4797
4741 CGCTGGGTACCGCCTTAAGATCAGTTGTGCAAGGTGGAGAGAGAGAGAGAGAGAGAGAG 4800
4798 GAAAGCTGATGCTAACTGCTTGGAAACTCTGCTGAAACTGGAAGGTATGACCGTCTA 4857
4801 GAAAGCTGATGCTAACTGCTTGGAAACTCTGCTGAAACTGGAAGGTATGACCGTCTA 4860
4858 GACATGAACCTGACCGTGTCTTCACTGACCAAGGTGTGTGTGTGTGTGTGTGTGTGTGT 4917
4861 GACATGAACCTGACCGTGTCTTCACTGACCAAGGTGTGTGTGTGTGTGTGTGTGTGTGT 4920
4918 CTCTAGCGCTTGAATGTCTTGAAGAACTCCCTAATCCCATGTGCCAGAAATTGAGCATGTC 4977

4921 CTCTAGCGCTTGAATGTCTTGAAGAACTCCCTAATCCCATGTGCCAGAAATTGAGCATGTC 4980
4978 TTCCAAATTTATATTTATCAAGAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5037
4981 TTCCAAATTTATATTTATCAAG 5040
5038 GCACTGTGTCTTGTGAG 5097
5041 GCACTGTGTCTTGTGAG 5100
5098 GCCAGCCCGACATTCACCAACCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5157
5101 GCCAGCCCGACATTCACCAACCAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5160
5158 GCAGGAG 5217
5161 GCAGGAG 5220
5218 CTCCGCTACACGAAACCTCAGCAAAATCTGATCCGAGAGAGAGAGAGAGAGAGAGAGAG 5277
5221 CTCCGCTACACGAAACCTCAGCAAAATCTGATCCGAGAGAGAGAGAGAGAGAGAGAGAG 5280
5278 CCCTGAG 5337
5281 CCCTGAG 5340
5338 GAAATGAGATGAG 5397
5341 GAAATGAGATGAG 5400
5398 GCACTGT 5457
5401 GCACTGT 5460
5458 AGGAG 5517
5461 AGGAG 5520
5518 TCTTACGAG 5577
5521 TCTTACGAG 5580
5578 GCTTACAG 5637
5581 GCTTACAG 5640
5638 CAGGAG 5697
5641 CAGGAG 5700
5698 TACCTGGGCTGTGCAATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5757
5701 TACCTGGGCTGTGCAATTTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5760
5758 TTAAGAGGTATTTGTGTGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5817
5761 TTAAGAGGTATTTGTGTGCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5820
5818 GGGCCGCTCACCTCCCGAG 5877
5821 GGGCCGCTCACCTCCCGAG 5880
5878 ATCACAAG 5937
5881 ATCACAAG 5940
5938 CCAAGCAACCCACCGCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5997
5941 CCAAGCAACCCACCGCTTACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6000
5998 GGGCCGCTGTGAG 6057
6001 GGGCCGCTGTGAG 6060

QY 6058 TCCCGGCGAGGCTGTTTGAAGACAGACAGAGGCGGCTGCTGCGGAGCGGTGAGG 6117
DB 6061 TCCCGGCGAGGCTGTTTGAAGACAGACAGAGGCGGCTGCTGCGGAGCGGTGAGG 6120
QY 6118 ACCCGGCTGCTCCAGGTGAACAGAGCTGTGGACCACTC 6155
DB 6121 ACCCGGCTGCTCCAGGTGAACAGAGCTGTGGACCACTC 6158
RESULT 8
ABS63436
ID ABS63436 standard; cDNA; 6189 BP.
XX
AC ABS63436;
XX
DT 15-NOV-2002 (first entry)
XX
DE RHO/RAC-interacting citron kinase-like human cDNA, designated NOV3b.
XX
KM Human; gene; ss; NOV; NOVX-associated disorder; cardiomyopathy;
KM atherosclerosis; diabetes; cell signalling; metabolic pathway;
KM cellular receptor; downstream effector; cancer; gene therapy;
KM hypertension; congenital heart defect; aortic stenosis; obesity;
KM infectious disease; anorexia; Alzheimer's disease; Parkinson's disease;
KM neurodegenerative disorder; haemophilia; dyslipidemia; vaccine;
KM haematopoietic disease; scleroderma; fertility; immunogen;
KM idiopathic thrombocytopenic purpura; graft versus host disease;
KM Crohn's disease; multiple sclerosis; cirrhosis; autoimmune disease;
KM systemic lupus erythematosus; asthma; arthritis; psoriasis; allergy;
KM stroke; anxiety; Leech-Nyman syndrome; schizophrenia; cerebellar ataxia;
KM pain; alcoholism; transgenic.
XX
OS Homo sapiens.
XX
PN WO200226826-A2.
XX
PD 04-APR-2002.
XX
PF 27-SEP-2001; 2001WO-US042336.
XX
PR 27-SEP-2000; 2000US-0235631P.
XX
PR 27-SEP-2000; 2000US-0235633P.
XX
PR 27-SEP-2000; 2000US-0235808P.
XX
PR 27-SEP-2000; 2000US-0236064P.
XX
PR 27-SEP-2000; 2000US-0236065P.
XX
PR 27-SEP-2000; 2000US-0236066P.
XX
PR 28-SEP-2000; 2000US-0236135P.
XX
PR 03-OCT-2000; 2000US-0237434P.
XX
PR 05-OCT-2000; 2000US-0238321P.
XX
PR 06-OCT-2000; 2000US-0238396P.
XX
PR 06-OCT-2000; 2000US-0238398P.
XX
PR 16-MAR-2001; 2001US-0276667P.
XX
PR 31-MAY-2001; 2001US-0294823P.
XX
PR 12-JUL-2001; 2001US-0304868P.
XX
PR 26-SEP-2001; 2001US-00235631.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Gerlach VL, MacDougall JR, Smithson G, Millet I, Stone D;
PI Gunther E, Ellerman K, Groese WM, Alsbrook JP, Lepley DM;
PI Burgess CE, Padigar M, Kexuda R, Spytek KA, Leach MD, Shinkets RA;
XX
DR WPI; 2002-489860/53.
XX
DR P-PSDB; ABG78363.
XX
PT Novel isolated NOVX polypeptides and polynucleotides homologous to
PT attractin, plexin, papin-like family of proteins, useful for treating
PT atherosclerosis, diabetes, cancer, Alzheimer's disease, hemophilia and
PT stroke.
XX
PS Claim 8; Page 43-44; 308pp; English.

CC The invention discloses the isolated human polypeptides, and
CC polynucleotides encoding them, that have been designated NOVX. The
CC polynucleotides, polynucleotides and antibodies are useful in treating or
CC preventing a NOVX-associated disorder which is cardiomyopathy,
CC atherosclerosis and diabetes in a human, where the disorder is related to
CC cell signal processing and metabolic pathway modulation. They can also be
CC used in determining the presence of, or predisposition to, a disease
CC associated with altered levels of the polypeptides and polynucleotides of
CC any one of the 13 sequences (NOV1-NOV8), for raising antibodies, for
CC identifying an agent that binds to, or that modulates the expression or
CC activity of the polypeptide, for identifying an agent which is cellular
CC receptor or downstream effector, for treating or preventing a NOVX-
CC associated disorder and as a pharmaceutical composition comprising the
CC polypeptide, polynucleotide or the antibody. The polypeptides and
CC polynucleotides are useful in diagnostic applications (e.g. as a marker
CC for cancerous cells or tissue types) where their amounts are assessed, or
CC for the manufacture of a medicament (e.g. gene therapy) for treating or
CC preventing disorders or syndromes such as hypertension, congenital heart
CC defects, aortic stenosis, obesity, infectious disease, anorexia, cancer,
CC Alzheimer's disease, Parkinson's disorder, neurodegenerative disorders,
CC haemophilia, dyslipidemias, haematopoietic diseases, scleroderma,
CC fertility, idiopathic thrombocytopenic purpura, graft versus host
CC diseases, Crohn's disease, multiple sclerosis, cirrhosis, autoimmune
CC disease, systemic lupus erythematosus, asthma, arthritis, psoriasis,
CC allergy, stroke, anxiety, Leech-Nyman syndrome, schizophrenia, cerebellar
CC ataxia, pain and alcoholism. They may also be used as immunogens to
CC produce antibodies specific for the invention, and as vaccines to
CC transgenic cells containing a NOVX expressing construct are useful to
CC produce non-human transgenic animals for studying the function and/or
CC activity of the NOVX proteins and for identifying and/or evaluating
CC modulators of NOVX protein activity. Transgenic cells containing a NOVX
CC expressing construct are useful to produce non-human transgenic animals
CC for studying and/or evaluating modulators of NOVX proteins and for
CC identifying and/or evaluating modulators of NOVX protein activity. The
CC sequences presented in ABS63431-ABS63444 are the human NOV1-NOV8 cDNAs
XX
SQ Sequence 6189 BP; 1742 A; 1554 C; 1690 G; 1203 T; 0 U; 0 Other;
XX
Query Match 99.3%; Score 6121.8; DB 6; Length 6189;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 6145; Conservative 0; Mismatches 17; Indels 3; Gaps 1;
QY 1 ATGTTGAAGTTCAATATGAGAGCGCGAATCTTTGAGTCTGTGCTGAACCCATT 60
DB 1 ATGTTGAAGTTCAATATGAGAGCGCGAATCTTTGAGTCTGTGCTGAACCCATT 60
QY 61 GCCAGCGCGGCTCTCCAGGCTGAATCTGTTTTCACAGGGAACCACTTTATGACTCAA 120
DB 61 GCCAGCGCGGCTCTCCAGGCTGAATCTGTTTTCACAGGGAACCACTTTATGACTCAA 120
QY 121 CAGCAGATGCTCTCTTCCGAGAGGATTTAGATGCCCTTGTCTTTGAA 180
DB 121 CAGCAGATGCTCTCTTCCGAGAGGATTTAGATGCCCTTGTCTTTGAA 180
QY 181 GAATGAGTCAAGCTGCTGTGATGAAGATTAGACAGTGAACAATTGTCCGAAGTAT 240
DB 181 GAATGAGTCAAGCTGCTGTGATGAAGATTAGACAGTGAACAATTGTCCGAAGTAT 240
QY 241 TCCGACACCTAGCTGATGATGACAGAGCTCCAGCTTCGGCAAGAGCTTGAAGTACA 300
DB 241 TCCGACACCTAGCTGATGATGACAGAGCTCCAGCTTCGGCAAGAGCTTGAAGTACA 300
QY 301 AGCTTGTAGTGTGTGTGCTCACTTGTGAGAGTCAAGTGTGAAGAGAAAGCAACCGGG 360
DB 301 AGCTTGTAGTGTGTGTGCTCACTTGTGAGAGTCAAGTGTGAAGAGAAAGCAACCGGG 360
QY 361 GACATCTATGCTATGAAGATGAAGAGAGCTTTATTTGCCCCAGAGAGGTTTCA 420
DB 361 GACATCTATGCTATGAAGATGAAGAGAGCTTTATTTGCCCCAGAGAGGTTTCA 420
QY 421 TTTTGTGAGGAAGAGGGAACATTTATCTCGAAGCAAGCCCGTGGATCCCCCAATTA 480
DB 421 TTTTGTGAGGAAGAGGGAACATTTATCTCGAAGCAAGCCCGTGGATCCCCCAATTA 480

QY 481 CAGTATGCTTTGAGACAAAATCACCCTTATCTGCTCATGGAATATCAGCTTGAGGG 540
DB 481 CAGTATGCTTTGAGACAAAATCACCCTTATCTGCTCATGGAATATCAGCTTGAGGG 540
QY 541 GACTTGTGCTGACTTTTGAATAGATATGAGGACAGGTAGATGAAAACCTGATCAGTTT 600
DB 541 GACTTGTGCTGACTTTTGAATAGATATGAGGACAGGTAGATGAAAACCTGATCAGTTT 600
QY 601 TACTTACGTGAGCTGATTTTGGCTGTTTCAAGCGTTCACTCTGATGGGATACGTGCATCGA 660
DB 601 TACTTACGTGAGCTGATTTTGGCTGTTTCAAGCGTTCACTCTGATGGGATACGTGCATCGA 660
QY 661 GACATCAAGCCTGAGCAATTTCTGTTGACCGGACAGGACATCAAGCTGTGGAATTTT 720
DB 661 GACATCAAGCCTGAGCAATTTCTGTTGACCGGACAGGACATCAAGCTGTGGAATTTT 720
QY 721 GGAATCTCCGCGAAAATGAATTTCAAAACAGATGTGTAATGCGAACTCCCGATTGGGAGC 780
DB 721 GGAATCTCCGCGAAAATGAATTTCAAAACAGATGTGTAATGCGAACTCCCGATTGGGAGC 777
QY 781 CCAGATTACATGGCTCTCTGTAAGTCTGACTGTGATGTAACGGGAGTGGAAAAGCACCCTAC 840
DB 778 CCAGATTACATGGCTCTCTGTAAGTCTGACTGTGATGTAACGGGAGTGGAAAAGCACCCTAC 837
QY 841 GGGCTGGACTGTGACTGTGTGTGCTGAGTGGCGTGAATTGCTATGATGATGATTTATGGAGA 900
DB 838 GGGCTGGACTGTGACTGTGTGTGCTGAGTGGCGTGAATTGCTATGATGATGATTTATGGAGA 897
QY 901 TCCCCCTCGCAGAGGGACCTCTGCAGAACCTTCAATTAACATTAGAAATTTCCAGCGG 960
DB 898 TCCCCCTCGCAGAGGGACCTCTGCAGAACCTTCAATTAACATTAGAAATTTCCAGCGG 957
QY 961 TTTTGAATTTTCAGATGACCCCAAGTGAAGTGAAGTCTTGTGATCTGATTCAAAGC 1020
DB 958 TTTTGAATTTTCAGATGACCCCAAGTGAAGTGAAGTCTTGTGATCTGATTCAAAGC 1017
QY 1021 TTGTTGTGGGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTGTGCTGCCATCTTTCTTC 1080
DB 1018 TTGTTGTGGGCGCAGAAAGAGAGACTGAAGTTTGAAGTCTTGTGCTGCCATCTTTCTTC 1077
QY 1081 TCTAAATTTGACTGGAACAACTTCGTAACTCTCTCCCGCCCTTCGTTCCCAACCTCAAG 1140
DB 1078 TCTAAATTTGACTGGAACAACTTCGTAACTCTCTCCCGCCCTTCGTTCCCAACCTCAAG 1137
QY 1141 TCTGACGATGACACTTCGAAATTTTGAATGTAACAGAGAAGAAATTCGTGGGTTTCATCTCT 1200
DB 1138 TCTGACGATGACACTTCGAAATTTTGAATGTAACAGAGAAGAAATTCGTGGGTTTCATCTCT 1197
QY 1201 CCGTGCACCTGAGCCCTTCAGGCTTCTGGGTTGAAGAACTGCCGTTTGTGGGGTTTTCG 1260
DB 1198 CCGTGCACCTGAGCCCTTCAGGCTTCTGGGTTGAAGAACTGCCGTTTGTGGGGTTTTCG 1257
QY 1261 TACAGCAAGGCACTGGGGATTTCTTGTAGATCTGAGTCTGTTGTGTGGGCTTGAGCTCC 1320
DB 1258 TACAGCAAGGCACTGGGGATTTCTTGTAGATCTGAGTCTGTTGTGTGGGCTTGAGCTCC 1317
QY 1321 CCTGCCAAGACTAGCTCAATGGAAGAAATTTCTCATCAAAAGCAAGAGCTTACAAGAC 1380
DB 1318 CCTGCCAAGACTAGCTCAATGGAAGAAATTTCTCATCAAAAGCAAGAGCTTACAAGAC 1377
QY 1381 TCTCAGGACAAAGTGTCAAGAATGAGCAAGAAATGACCCGGTTACATCGAGAGTGTCA 1440
DB 1378 TCTCAGGACAAAGTGTCAAGAATGAGCAAGAAATGACCCGGTTACATCGAGAGTGTCA 1437
QY 1441 GAGGTGAGGCGTGTGTTAGTCAAGAGAGGTGAGGCTGAAGCCCTCTGAGACTCAGANA 1500
DB 1438 GAGGTGAGGCGTGTGTTAGTCAAGAGAGGTGAGGCTGAAGCCCTCTGAGACTCAGANA 1497
QY 1501 TCCCTCTCGAGCAGAGACTTGTCTACTTACATCAAGAAATGCAAGTACTTAAAGCGAAGT 1560
DB 1498 TCCCTCTCGAGCAGAGACTTGTCTACTTACATCAAGAAATGCAAGTACTTAAAGCGAAGT 1557

QY 1561 TTGAGCAAGACCGATGAGAGTGTCTCCAGAGAGATGACAAAGCACTGCAGCTTCTCAT 1620
DB 1558 TTGAGCAAGACCGATGAGAGTGTCTCCAGAGAGATGACAAAGCACTGCAGCTTCTCAT 1617
QY 1621 GATATCAGAGAGCAGACCCGGAAGCTCCAGAAATTCAAAGAGCAGAGTACCAAGCTCAA 1680
DB 1618 GATATCAGAGAGCAGACCCGGAAGCTCCAGAAATTCAAAGAGCAGAGTACCAAGCTCAA 1677
QY 1681 GTGAGAAATTAAGTGTGATGATGAATCAATTGGAAGAGATCTTGTCTCAGCAAGAGA 1740
DB 1678 GTGAGAAATTAAGTGTGATGATGAATCAATTGGAAGAGATCTTGTCTCAGCAAGAGA 1737
QY 1741 CGAGTGTATCTTACGAATTTGACTGAGAGAGTCTCGGCTTGTGCTGTAAGAAATTCAG 1800
DB 1738 CGAGTGTATCTTACGAATTTGACTGAGAGAGTCTCGGCTTGTGCTGTAAGAAATTCAG 1797
QY 1801 CGGAAAGCGACAGAAATGTCAGCATTAATCTGTAAGGCTTAAGATTCAGAGGAACTTGAA 1860
DB 1798 CGGAAAGCGACAGAAATGTCAGCATTAATCTGTAAGGCTTAAGATTCAGAGGAACTTGAA 1857
QY 1861 GTGAGAAATTAAGTGTGATGATGAATCAATTGGAAGAGATCTTGTCTCAGCAAGAGA 1920
DB 1858 GTGAGAAATTAAGTGTGATGATGAATCAATTGGAAGAGATCTTGTCTCAGCAAGAGA 1917
QY 1921 CTCGAAGAGAACTGAGAGAGGCTGTAAAGCCAGACCGAGGCCCAACCGAGCTGTGAG 1980
DB 1918 CTCGAAGAGAACTGAGAGAGGCTGTAAAGCCAGACCGAGGCCCAACCGAGCTGTGAG 1977
QY 1981 AATATCCGCGCAGGCAAAAGAGCCGAGAGGAGACTGAGAAAGCTGCGAACCAGAG 2040
DB 1978 AATATCCGCGCAGGCAAAAGAGCCGAGAGGAGACTGAGAAAGCTGCGAACCAGAG 2037
QY 2041 GATTTCTTGAAGGCTATCAGAAAGAAAGAGCTGTGGAAGCTGAGGAAGCCGCCATTTCTTG 2100
DB 2038 GATTTCTTGAAGGCTATCAGAAAGAAAGAGCTGTGGAAGCTGAGGAAGCCGCCATTTCTTG 2097
QY 2101 GAGACAAAGGTAAAGAGACTAGAGACCATGAGAGCTGAGAAACAGACTGAAGATGAC 2160
DB 2098 GAGACAAAGGTAAAGAGACTAGAGACCATGAGAGCTGAGAAACAGACTGAAGATGAC 2157
QY 2161 ATCCAGACAAATCCCAAGATCCAGAGATGAGCTGATTAATTTCTGAGCTCGAAGAG 2220
DB 2158 ATCCAGACAAATCCCAAGATCCAGAGATGAGCTGATTAATTTCTGAGCTCGAAGAG 2217
QY 2221 AAAATCGGAGGCGCCAAAGTCTCAGCCAGCACTTGAAGTGCACCTGAAAAGAAAGAG 2280
DB 2218 AAAATCGGAGGCGCCAAAGTCTCAGCCAGCACTTGAAGTGCACCTGAAAAGAAAGAG 2277
QY 2281 CAGCACTATGAGAAAGATTAAGTGTGGAACAATCAGATTAAGAAAGACCTGACTGAC 2340
DB 2278 CAGCACTATGAGAAAGATTAAGTGTGGAACAATCAGATTAAGAAAGACCTGACTGAC 2337
QY 2341 AAGGAGACCTGAGAAACATGATGAGAGACACAGAGAGAGAGCCCATGAGAAAGGCAAA 2400
DB 2338 AAGGAGACCTGAGAAACATGATGAGAGACACAGAGAGAGAGCCCATGAGAAAGGCAAA 2397
QY 2401 ATTCTCAGCGAAACAGAGGCGATGATCAATGCTATGAGATTTCAAGATCAGATCCCTGAA 2460
DB 2398 ATTCTCAGCGAAACAGAGGCGATGATCAATGCTATGAGATTTCAAGATCAGATCCCTGAA 2457
QY 2461 CAGAGATTTGTGAACTGTCTGAGCCAAATAACTTGACAGCAATATGACGTCTTTTTCAC 2520
DB 2458 CAGAGATTTGTGAACTGTCTGAGCCAAATAACTTGAGCAAAATATGACGTCTTTTTCAC 2517
QY 2521 CAAAGAAACATGAAAGCCCAAGAAAGATGATTTCTGAACTTAGGCAACAGAAATTTTAC 2580
DB 2518 CAAAGAAACATGAAAGCCCAAGAAAGATGATTTCTGAACTTAGGCAACAGAAATTTTAC 2577
QY 2581 CTGAGAGACAGGCTGGGAAAGTTGAGGCGCAGAAACCGAAACCTGAGAGAGAGCTGGAG 2640
DB 2578 CTGAGAGACAGGCTGGGAAAGTTGAGGCGCAGAAACCGAAACCTGAGAGAGAGCTGGAG 2637
QY 2641 AAGATCAGCCACCAAGACCAAGTGAACAAGATCGGCTGTGGAACCTGAGACAAAGATTG 2700

Db 2638 AAGATCGCCACCAAGACCAAGTGAAGATGAGCTGAGAACTGGAGACAAAGATTG 2697
Qy 2701 CGGGAGGTCTAGTCTAGACACAGAGACAGAACTGAGCTCAAGCCAGCTCACAGAG 2760
Db 2698 CGGGAGGTGAGTCTAGAGACAGAGACAGAACTGAGCTCAAGCCAGCTCACAGAG 2757
Qy 2761 CTACAGCTCTCCCTGACAGAGCGGAGTCAAGTTGAACGCTTCAGGCTGCACGGGCG 2820
Db 2758 CTACAGCTCTCCCTGACAGAGCGGAGTCAAGTTGAACGCTTCAGGCTGCACGGGCG 2817
Qy 2821 GCCCTGAGAGCCAGCTTCCGACAGCGCAAGACAGAGCTGAGAGACACACAGAGAGCT 2880
Db 2818 GCCCTGAGAGCCAGCTTCCGACAGCGCAAGACAGAGCTGAGAGACACACAGAGAGCT 2877
Qy 2881 GAAGAGAGATCCAGGACTCAAGGACATAGAGATGAAATCCAGCCAAATTTGATGCT 2940
Db 2878 GAAGAGAGATCCAGGACTCAAGGACATAGAGATGAAATCCAGCCAAATTTGATGCT 2937
Qy 2941 CTTGTAACAGCTGTACTGTATATCAGACCTGAGAGACAGCTAAACAGCTGACCGAG 3000
Db 2938 CTTGTAACAGCTGTACTGTATATCAGACCTGAGAGACAGCTAAACAGCTGACCGAG 2997
Qy 3001 GACAACTCTGAACTCAACAAACAAATCTTCTACTTTGTCAAACAACTTCGATGAGGCTTCT 3060
Db 2998 GACAACTCTGAACTCAACAAACAAATCTTCTACTTTGTCAAACAACTTCGATGAGGCTTCT 3057
Qy 3061 GGGGCGCAAGACGAGATTGTATCAACTGGAAGTGAAGCACTCCGCGGGGAGATC 3120
Db 3058 GGGGCGCAAGACGAGATTGTATCAACTGGAAGTGAAGCACTCCGCGGGGAGATC 3117
Qy 3121 ACCGAAACGAGATGACAGCTTACCCAGCCAGAGACAAACGATGAGGCTTGAGAACCAAG 3180
Db 3118 ACCGAAACGAGATGACAGCTTACCCAGCCAGAGACAAACGATGAGGCTTGAGAACCAAG 3177
Qy 3181 TGCACATGCTGAGAGAAACAGCTCATGATTTGAGGCTTAAACGATGAGCTCTAGAA 3240
Db 3178 TGCACATGCTGAGAGAAACAGCTCATGATTTGAGGCTTAAACGATGAGCTCTAGAA 3237
Qy 3241 AAAGAGCGGAGTGGAGGCGCTGAGAGAGCTCTGGGTGATGAGAAATCCCACTTTGAG 3300
Db 3238 AAAGAGCGGAGTGGAGGCGCTGAGAGAGCTCTGGGTGATGAGAAATCCCACTTTGAG 3297
Qy 3301 TGTGCGGTTGAGAGCTGACAGAGATCTGGAACACGAGAAACAGACAGGCGCAGAGCC 3360
Db 3298 TGTGCGGTTGAGAGCTGACAGAGATCTGGAACACGAGAAACAGACAGGCGCAGAGCC 3357
Qy 3361 GATCAGCGGATCACCGAGTCTCCGACAGTGTGTGAGCTGCGATGAAAGAGACAAAGGCT 3420
Db 3358 GATCAGCGGATCACCGAGTCTCCGACAGTGTGTGAGCTGCGATGAAAGAGACAAAGGCT 3417
Qy 3421 GAGATTTCCCTCTGACAGACAGGCTCTCAAAAGACAGAAAGTGAAGGCCGAGAGCTCTCT 3480
Db 3418 GAGATTTCCCTCTGACAGACAGGCTCTCAAAAGACAGAAAGTGAAGGCCGAGAGCTCTCT 3477
Qy 3481 GACAACTCATGACTGAGAGAAAGACATGCTTGAATGAAATGACCCGAAAGCTTA 3540
Db 3478 GACAACTCATGACTGAGAGAAAGACATGCTTGAATGAAATGACCCGAAAGCTTA 3537
Qy 3541 CAGCAGAACTGAGACTGAACGAGACTCAACAGAGGCTTCTGAGAGACCAAGCCAA 3600
Db 3538 CAGCAGAACTGAGACTGAACGAGACTCAACAGAGGCTTCTGAGAGACCAAGCCAA 3597
Qy 3601 TTACAGACAGATGACCTGACAGAAATATCAATTTCCGTCTGACTCAAGAGCTGCA 3660
Db 3598 TTACAGACAGATGACCTGACAGAAATATCAATTTCCGTCTGACTCAAGAGCTGCA 3657
Qy 3661 GAAGCTCTAGATCGGGCTGATCTACTGAAAGACAGAAAGATGACTTGAAGTATCAGCTG 3720
Db 3658 GAAGCTCTAGATCGGGCTGATCTACTGAAAGACAGAAAGATGACTTGAAGTATCAGCTG 3717
Qy 3721 GAAACATTCAGGTTCTTATTTCTATGAAAGGTGAAATGAAAGGACATATTTCTCAA 3780

Db 3718 GAAACATTCAGGTTCTTATTTCTATGAAAGGTGAAATGAAAGGACATATTTCTCAA 3777
Qy 3781 CAACCAAACTATTGATTTTCTGCAAGCCAAATGACCAACTGCTTAAAAAGAAAAAG 3840
Db 3778 CAACCAAACTATTGATTTTCTGCAAGCCAAATGACCAACTGCTTAAAAAGAAAAAG 3837
Qy 3841 GTTCTCTGACATACATGAGCTGAACTGGCCCTGAGAAAGAGAAAGTCCGCTGAGCA 3900
Db 3838 GTTCTCTGACATACATGAGCTGAACTGGCCCTGAGAAAGAGAAAGTCCGCTGAGCA 3897
Qy 3901 GAGCTAGAGAAAGCCCTTCAAGAAAGACCCGATCGAGCTCCGCTCCGCGGAGAAAGCT 3960
Db 3898 GAGCTAGAGAAAGCCCTTCAAGAAAGACCCGATCGAGCTCCGCTCCGCGGAGAAAGCT 3957
Qy 3961 GCCCAGCGCAAGACGAGACCAACCAACCATTCACAGCCAGCCACCGCGAGCAGAG 4020
Db 3958 GCCCAGCGCAAGACGAGACCAACCAACCATTCACAGCCAGCCACCGCGAGCAGAG 4017
Qy 4021 ATGCGCATGTCGCGCATGTCGCGTCCGACAGAGACCAAGCCATGACATGAGCTGCTG 4080
Db 4018 ATGCGCATGTCGCGCATGTCGCGTCCGACAGAGACCAAGCCATGACATGAGCTGCTG 4077
Qy 4081 GCCCGGCAATCCAGCGGCAAGAGAGTCTTCAACTCCAGAGAAATTTAGTCGGGCTT 4140
Db 4078 GCCCGGCAATCCAGCGGCAAGAGAGTCTTCAACTCCAGAGAAATTTAGTCGGGCTT 4137
Qy 4141 AAGAAACGATGACCACAATATTTCTCACCGATTCACAGTGAAGTGAACATGAGAGCC 4200
Db 4138 AAGAAACGATGACCACAATATTTCTCACCGATTCACAGTGAAGTGAACATGAGAGCC 4197
Qy 4201 ACAAAGTGTGTGTGTCTGAGATCCGTGACCTTGAAGCGCCAGGCAATCCAAATGCTC 4260
Db 4198 ACAAAGTGTGTGTGTCTGAGATCCGTGACCTTGAAGCGCCAGGCAATCCAAATGCTC 4257
Qy 4261 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4320
Db 4258 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4317
Qy 4321 CTTGCTGAATATGACACACACTTACCGAGGCTTCTGCGGTGACAAATGAACTCCCA 4380
Db 4318 CTTGCTGAATATGACACACACTTACCGAGGCTTCTGCGGTGACAAATGAACTCCCA 4377
Qy 4381 GGTCTCCAGACCAAGAGGCCGACAGAGCTTGAACCTGAGAGGATGAGAGTGCCTC 4440
Db 4378 GGTCTCCAGACCAAGAGGCCGACAGAGCTTGAACCTGAGAGGATGAGAGTGCCTC 4437
Qy 4441 AGGAATTAACAAAGAGACAGCAAGGCTGGGACAGAAATGATCATTTCTCTGAGAGATCA 4500
Db 4438 AGGAATTAACAAAGAGACAGCAAGGCTGGGACAGAAATGATCATTTCTCTGAGAGATCA 4497
Qy 4501 AAAGTCTCATTTATGACATGAAAGCAGAGAAAGCTGGAACAGAGCCGCTGGAAGATTT 4560
Db 4498 AAAGTCTCATTTATGACATGAAAGCAGAGAAAGCTGGAACAGAGCCGCTGGAAGATTT 4557
Qy 4561 GAGCTGTGCTTCCCGACGGGGATGATATTAATGATGATGATGATGATGATGATGATG 4620
Db 4558 GAGCTGTGCTTCCCGACGGGGATGATATTAATGATGATGATGATGATGATGATGATG 4617
Qy 4621 GCAAAATACAGCAAGACAGATGTCCTATCATATGAAAGATGAAATCTCACCCGACACC 4680
Db 4618 GCAAAATACAGCAAGACAGATGTCCTATCATATGAAAGATGAAATCTCACCCGACACC 4677
Qy 4681 ACCGCTGAGCCCGGAGAACCTCTACTGTTAGTCCAGCTTCCCTGACAAACAGGCG 4740
Db 4678 ACCGCTGAGCCCGGAGAACCTCTACTGTTAGTCCAGCTTCCCTGACAAACAGGCG 4737
Qy 4741 TGGGTCAACGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4800
Db 4738 TGGGTCAACGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4797
Qy 4801 GCTGATGCTAACTGCTTGAAGATCTCCCTGTGAAACTGGAAGGTGATGACCTGTAGAC 4860
Db 4798 GCTGATGCTAACTGCTTGAAGATCTCCCTGTGAAACTGGAAGGTGATGACCTGTAGAC 4857

QY	4861	ATGAACCTGACCGCTGCTCTTCACTGTAACAGGTGTGTGTGTGTGGCAACCGAAGAGGGCTC	4920
Db	4858	ATGAACCTGACCGCTGCTCTTCACTGTAACAGGTGTGTGTGTGTGGCAACCGAAGAGGGCTC	4917
QY	4921	TACGGCCCTGAAGTCTGTGAAAACTCCCTAACCCATGTGCCAGAAATTGGACACTCTTC	4988
Db	4918	TACGGCCCTGAAGTCTGTGAAAACTCCCTAACCCATGTGCCAGAAATTGGACACTCTTC	4977
QY	4981	CAAAATTATATATCAAGGACCTGGAAGAGCTACATCATGATGTAGAGGAAGAGGGGCA	5048
Db	4978	CAAAATTATATATCAAGGACCTGGAAGAGCTACATCATGATGTAGAGGAAGAGGGGCA	5037
QY	5041	CTGTGTCTTGTGTGACGTGAGAGAAAGTAAACAGTCCCTGGCCAGTCCACCTGTGCTCC	5100
Db	5038	CTGTGTCTTGTGTGACGTGAGAGAAAGTAAACAGTCCCTGGCCAGTCCACCTGTGCTCC	5097
QY	5101	CAGCCCGACATCTCACCCCAACATTTTGAAGCTGTCAAGGGGTGCACCTTGTGTGGGGCA	5160
Db	5098	CAGCCCGACATCTCACCCCAACATTTTGAAGCTGTCAAGGGGTGCACCTTGTGTGGGGCA	5157
QY	5161	GGCAAGATTGAGAAAGGGCTCTGCATCTGTGACGACATGCCAGAAAGTGGTCAATTGTC	5220
Db	5158	GGCAAGATTGAGAAAGGGCTCTGCATCTGTGACGACATGCCAGAAAGTGGTCAATTGTC	5217
QY	5221	CGCTACAAAGAAACCTTGACAAATATCTGCATCCGAAAAGATAGAACCTCAGAGCC	5280
Db	5218	CGCTACAAAGAAACCTTGACAAATATCTGCATCCGAAAAGATAGAACCTCAGAGCC	5277
QY	5281	TGCAGCTGTATCCACTTTCACCAATTACAGTATCTCTCATTTGGAACCAATTAATTCTACGA	5340
Db	5278	TGCAGCTGTATCCACTTTCACCAATTACAGTATCTCTCATTTGGAACCAATTAATTCTACGA	5337
QY	5341	ATCCGATGAAGACAGTACACGCTCGAGGAAATTCCGTGAATGAATGACATTCCTGGCA	5400
Db	5338	ATCCGATGAAGACAGTACACGCTCGAGGAAATTCCGTGAATGAATGACATTCCTGGCA	5397
QY	5401	CTGTGTGTGTTCGCGCTCTTCCAAACAGTCCCTGTCTCAATCTGTGACAGTGAACAGC	5460
Db	5398	CTGTGTGTGTTCGCGCTCTTCCAAACAGTCCCTGTCTCAATCTGTGACAGTGAACAGC	5457
QY	5461	GCAGGGCAGCGAAGAGAGTACTTGTGTGTTCACGAATTTGGAGTGTGTGGATTTCT	5520
Db	5458	GCAGGGCAGCGAAGAGAGTACTTGTGTGTTCACGAATTTGGAGTGTGTGGATTTCT	5517
QY	5521	TACGGAACGTAGCCGACGACAGACGATCTCAAGTGAAGTGGCTTACCTTGGCCTTTGCC	5580
Db	5518	TACGGAACGTAGCCGACGACAGACGATCTCAAGTGAAGTGGCTTACCTTGGCCTTTGCC	5577
QY	5581	TACAGAGAACCTTATCTGTGTGTGACCACTTCAACTCATCTCGAAGTAAATTGAATCCAG	5640
Db	5578	TACAGAGAACCTTATCTGTGTGTGACCACTTCAACTCATCTCGAAGTAAATTGAATCCAG	5637
QY	5641	GCACGCTCTTCAGACAGGACCCCTGTGCCGACGTACTTGAACATCCCGAACCCGCGCTAC	5700
Db	5638	GCACGCTCTTCAGACAGGACCCCTGTGCCGACGTACTTGAACATCCCGAACCCGCGCTAC	5697
QY	5701	CTGGGGCCCTGCATTTTCTCAAGAGCCATTTACTTGGGTCTCTATACAGAGATAAATTGA	5760
Db	5698	CTGGGGCCCTGCATTTTCTCAAGAGCCATTTACTTGGGTCTCTATACAGAGATAAATTGA	5757
QY	5761	AGGCTCATTTTCTCAAGAGGAAACCTCGTGAAGAGTCCGGCACTGAACACACACCGGGGC	5820
Db	5758	AGGCTCATTTTCTCAAGAGGAAACCTCGTGAAGAGTCCGGCACTGAACACACACCGGGGC	5817
QY	5821	CCGTTCACCTTCGCGACAGCCCAACAGAGGAGGCCACCCACGTACAAAGACATATC	5880
Db	5818	CCGTTCACCTTCGCGACAGCCCAACAGAGGAGGCCACCCACGTACAAAGACATATC	5877
QY	5881	ACCAAGGCGTGTGCTTCAAGCCAGCGCCGCCGAAGGCCCAAGCCACCGCGAGAGCCA	5940
Db	5878	ACCAAGGCGTGTGCTTCAAGCCAGCGCCGCCCGAAGGCCCAAGCCACCGCGAGAGCCA	5937

[illegible]

PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malayakar UM;
 PI Ort T, Gorman L, Zehusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
 PI Shinkete RA, Rothenberg ME, Leach MD, Agee ML, Bergins C, Dipippo VA;
 PI Eisen AJ, Gangoli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI; 2003-381626/36.
 XX P-PSDB; ADA05642.
 PT
 PT New NOX polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOX-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 20; Page 98-99; 586pp; English.
 XX
 CC The present invention describes NOX proteins, where X can be 1 to 55
 CC (e.g. NOY1). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid
 CC molecule which encodes a NOX protein of the invention; (4) a vector
 CC comprising the nucleic acid molecule described above; (5) a cell
 CC comprising the above vector; (6) an antibody that immunospecifically
 CC binds to the polypeptide described above; (7) methods for determining the
 CC presence or amount of the above polypeptide or nucleic acid molecule in a
 CC sample; (8) methods for determining the presence of or predisposition to
 CC a disease associated with altered levels of expression of the above
 CC polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 CC method of identifying an agent that binds to the polypeptide described
 CC above; (10) a method for identifying a potential therapeutic agent for
 CC use in treating a pathology that is related to an aberrant expression or
 CC aberrant physiological interactions of the polypeptide; (11) a method of
 CC screening for a modulator of activity or of latency or predisposition to
 CC a pathology associated with the polypeptide; (12) a method for modulating
 CC the activity of the polypeptide described above; (13) methods of treating
 CC or preventing a pathology associated with the above polypeptide in a
 CC mammal; and (14) a method for producing the above polypeptide. NOX
 CC sequences have antidiabetic, anorectic, antibacterial, vincidic,
 CC immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian
 CC and antilipemic activities, and can be used in gene therapy. The
 CC polypeptide is useful in manufacturing a medicament for treating a
 CC syndrome associated with a human disease. The polypeptide or the nucleic
 CC acid molecule may be used to diagnose, treat or prevent metabolic
 CC disorders such as diabetes or obesity, infections, cachexia, cancer,
 CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
 CC disease, immune disorders, haematopoietic disorders and various
 CC dyslipidemias. The nucleic acids can also be used as hybridisation
 CC probes, in chromosome mapping, tissue typing, preventive medicine and
 CC pharmacogenomics. The present sequence encodes a human NOX protein from
 CC the present invention.
 XX
 SQ Sequence 6189 BP; 1742 A; 1554 C; 1690 G; 1203 T; 0 U; 0 Other;
 Query Match 99.3%; Score 6121.8; DB 8; Length 6189;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 6145; Conservative 0; Mismatches 17; Indels 3; Gaps 1;
 QY 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCTTGTGATGCTGTGCTGAACCAATT 60
 DB 1 ATGTGAAGTTCAAAATATGAGCGCGGAATCTTGTGATGCTGTGCTGAACCAATT 60
 QY 61 GCGACGCGGCGCTCCAGGCTGAATCTTCTTCCAGAGGAAACACACCTTATATCACTCA 120
 DB 61 GCGACGCGGCGCTCCAGGCTGAATCTTCTTCCAGAGGAAACACACCTTATATCACTCA 120

QY 121 CAGCAGATGCTCTCTCTTTTCCGAGAGAGATATAGATGCCCTTGTCTTCTTGAA 180
 DB 121 CAGCAGATGCTCTCTCTTTTCCGAGAGAGATATAGATGCCCTTGTCTTCTTGAA 180
 QY 181 GAATGAGTGAAGCTGCTGATGAAGATTAAGACGTGAGCACTTGTCCGGAAGTAT 240
 DB 181 GAATGAGTGAAGCTGCTGATGAAGATTAAGACGTGAGCACTTGTCCGGAAGTAT 240
 QY 241 TCCGACACCATAGCTGATGATGAGAGAGCTCAGGCTTCGCGCAAGACTTGAAGTACA 300
 DB 241 TCCGACACCATAGCTGATGATGAGAGAGCTCAGGCTTCGCGCAAGACTTGAAGTACA 300
 QY 301 AGCTTGTGATGTTGTGTGCTCACTTGTCTGAAGTGAAGTGTGAAGAGCAACCGGG 360
 DB 301 AGCTTGTGATGTTGTGTGCTCACTTGTCTGAAGTGAAGTGTGAAGAGCAACCGGG 360
 QY 361 GACATCATGCTATGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 361 GACATCATGCTATGAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 QY 421 TTTTGTGAG 480
 DB 421 TTTTGTGAG 480
 QY 481 CAGTATGCTTTTCAAGACAAAATACCTTATCTGTGATGAGATACGCTGAGAGG 540
 DB 481 CAGTATGCTTTTCAAGACAAAATACCTTATCTGTGATGAGATACGCTGAGAGG 540
 QY 541 GACTGTGCTCACTTTGATATGATATGAGACCAAGTATATGAAACCTGATACGTT 600
 DB 541 GACTGTGCTCACTTTGATATGATATGAGACCAAGTATATGAAACCTGATACGTT 600
 QY 601 TACCTAGCTAGCTGATTTTGGCTGTTTCAAGAGCTTATGATGAGATACGTCATGCA 660
 DB 601 TACCTAGCTAGCTGATTTTGGCTGTTTCAAGAGCTTATGATGAGATACGTCATGCG 660
 QY 661 GACATCAAGCTGAGAAATTTCTGTTGACCGACAGAGACATCAAGCTGTGATTTT 720
 DB 661 GACATCAAGCTGAGAAATTTCTGTTGACCGACAGAGACATCAAGCTGTGATTTT 720
 QY 721 GATATGCTGCGGAGAAATTTGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 780
 DB 721 GATATGCTGCGGAGAAATTTGAAATGAAATGAAATGAAATGAAATGAAATGAAAT 780
 QY 781 CCGATTTACATGCTGCTGTAAGTCTGATGATGAGACGGAGTGAAGAAAGCACTTAC 840
 DB 781 CCGATTTACATGCTGCTGTAAGTCTGATGATGAGACGGAGTGAAGAAAGCACTTAC 840
 QY 841 GGCCTGACCTGATCTGTGCTGATGAGGCGGTGATGCTATGAGATGATTTATGAGAGA 900
 DB 841 GGCCTGACCTGATCTGTGCTGATGAGGCGGTGATGCTATGAGATGATTTATGAGAGA 900
 QY 901 TCCGCTTCCGAG 960
 DB 901 TCCGCTTCCGAG 960
 QY 961 TTTTGAATTTTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 961 TTTTGAATTTTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 QY 1021 TTTTGTGCGGAG 1080
 DB 1021 TTTTGTGCGGAG 1080
 QY 1081 TCTTAAATTTGATGAG 1140
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Db 1318 CCGGCCAAGCTAGCTCCATCGAATAAGAACTTCTCATCAAAACCAAGAGCTCAAGAC 1377
Qy 1381 TCTCAGAGCAAGTGTCACAAGATGAGCAGGAATGACCCGGTTACATCCGAGAGTCA 1440
Db 1378 TCTCAGAGCAAGTGTCACAAGATGAGCAGGAATGACCCGGTTACATCCGAGAGTCA 1437
Qy 1441 GAGGTGAGGCTGTCTTAACTCAGAGAGAGGTGAGGCTGAAGGCTCTGAGACTCAGAGA 1500
Db 1438 GAGGTGAGGCTGTCTTAACTCAGAGAGAGGTGAGGCTGAAGGCTCTGAGACTCAGAGA 1497
Qy 1501 TCCCTCCTGAGCAGAGACTTTCCTACCTACATCAAGAAATGCAATGCACTTAAGCGAAGT 1560
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DB 5518 TACGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5577
QY 5581 TACGAGAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5640

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Db 5998 CGCCTCCCTGAGAGAGAAAGTCCCGCGAGTACTCAGCAAGCGAGAGAGCGGTCC 6057
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RESULT 10
ADN62806
ID ADN62806 standard; DNA; 6189 BP.
AC ADN62806;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human NOV1a DNA.
XX
XX ds; gene; human; NOVX; metabolic disorder; diabetes; obesity;
XX infectious disease; anorexia; cancer; cancer-associated cachexia;
XX neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
XX immune disorder; haematopoietic disorder; dyslipidaemia;
XX metabolic syndrome X; wasting disorder; SNP;
XX single nucleotide polymorphism.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX variation replace(4319,t)
XX FT /tag= a
XX FT /note= "Single nucleotide polymorphism"
XX
XX US2004038223-A1.
XX
XX 26-FEB-2004.
XX
XX 01-OCT-2002; 2002US-00262511.
XX
XX 02-OCT-2001; 2001US-0326483P.
XX 05-OCT-2001; 2001US-0327435P.
XX 05-OCT-2001; 2001US-0327449P.

PR 09-OCT-2001; 2001US-0327917P.
PR 09-OCT-2001; 2001US-0328029P.
PR 09-OCT-2001; 2001US-0328044P.
PR 09-OCT-2001; 2001US-0328056P.
PR 12-OCT-2001; 2001US-0328849P.
PR 15-OCT-2001; 2001US-0329414P.
PR 17-OCT-2001; 2001US-0330142P.
PR 18-OCT-2001; 2001US-0330309P.
PR 22-OCT-2001; 2001US-0341058P.
PR 24-OCT-2001; 2001US-0339266P.
PR 24-OCT-2001; 2001US-0343629P.
PR 29-OCT-2001; 2001US-0349575P.
PR 01-NOV-2001; 2001US-0346357P.
PR 17-APR-2002; 2002US-0373260P.
PR 19-APR-2002; 2002US-0373815P.
PR 19-APR-2002; 2002US-0373817P.
PR 19-APR-2002; 2002US-0373826P.
PR 19-APR-2002; 2002US-0373884P.
PR 22-APR-2002; 2002US-0374977P.
PR 16-MAY-2002; 2002US-0381037P.
PR 16-MAY-2002; 2002US-0381038P.
PR 16-MAY-2002; 2002US-0381042P.
PR 17-MAY-2002; 2002US-0381642P.
PR 28-MAY-2002; 2002US-0383656P.
PR 29-MAY-2002; 2002US-0383831P.
PR 25-JUN-2002; 2002US-0391335P.
XX
PA (SMIT/) SMITHSON G.
PA (MILL/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEKUDA R.
PA (UJUU/) JU J.
PA (LILL/) LI L.
PA (GUOX/) GUO X.
PA (BAT/) PATTRAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALY/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERTUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILL/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENNA/) PENNA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKERS R A.
PA (ROTH/) ROTHENBERG M B.
PA (LEAC/) LEACH M D.
PA (AGER/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX
PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Pattrajan M, Spytke KA, Edinger SR, Ellerman K, Malyanakar UM;
PI Ort T, Gorman L, Zertusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkers RA, Rothenberg ME, Leach MD, Agee ML, Bergths C, Dipippo VA;
PI Eissen A, Gangolli EA, Rieger DK, Spaderna SK;
XX
XX MPI; 2004-213931/20.
XX P-PsDB; ADN62807.
XX
XX Isolated NOVX polypeptides and nucleic acids, useful for preventing,


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QY 1621 GATTTCAGAGCGAGCCGAGAGCTCCAGAAATCAAAGCGAGAGTACAGGCTCAA 1680
Db 1618 GAAATACGAGAGCGAGACCCGAGAGCTCCAGAAATCAAAGAGCGAGTACAGGCTCAA 1677
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Db 2638 AAGATCAGCCACCAAGACCAAGTGAACAAGAAATCGGCTCTGGAATCTGAGACAAGATTG 2697
QY 2701 CGGAGGTCAGTCTTAGACACAGAGAGAGAAAATGAGAGCTCAAGCCCAAGCTCAAGAG 2760
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QY 2761 CTAAGCTCTCCCTGAGAGAGCCGAGTCAAGTTGACAGCCCTGAGGCTGACCGGCG 2820
Db 2758 CTAAGCTCTCCCTGAGAGAGCCGAGTCAAGTTGACAGCCCTGAGGCTGACCGGCG 2817
QY 2821 GCCCTGAGAGCCAGCTTCGCAAGCGCAAGACAGAGCTGGAAGAGACACAGCAAGAGCT 2880
Db 2818 GCCCTGAGAGCCAGCTTCGCAAGCGCAAGACAGAGCTGGAAGAGACACAGCAAGAGCT 2877
QY 2881 GAAGAGAGATCCAGGCACTCAGCGACATAGAGATTAATCCAGCCCAATTTGATGCT 2940
Db 2878 GAAGAGAGATCCAGGCACTCAGCGACATAGAGATTAATCCAGCCCAATTTGATGCT 2937
QY 2941 CTTCTGTAAAGCTGTACTGTATCAAGACCTGAGAGAGAGCTTAAACAGCTGACCGAG 3000
Db 2938 CTTCTGTAAAGCTGTACTGTATCAAGACCTGAGAGAGAGCTTAAACAGCTGACCGAG 2997
QY 3001 GACAGGCTGAACTCAACCAACCAAACTTCTACTTGTCCAAACACTCGATGAGGCTTCT 3060
Db 2998 GACAGGCTGAACTCAACCAACCAAACTTCTACTTGTCCAAACACTCGATGAGGCTTCT 3057
QY 3061 GCGCGCAACGACGAGATTGTACAATGCGAAGTGAAGTGAACCATCTCGCGGAGATC 3120
Db 3058 GCGCGCAACGACGAGATTGTACAATGCGAAGTGAAGTGAACCATCTCGCGGAGATC 3117
QY 3121 ACGGAACGAGAGATGAGAGCTTACAGCCAGAACCAACATGGAAGCTCTGAAAGACCAAG 3180
Db 3118 ACGGAACGAGAGATGAGAGCTTACAGCCAGAACCAACATGGAAGCTCTGAAAGACCAAG 3177
QY 3181 TGCACCATGCTGAGAGAACAGGTCATGATTTTGAAGGCCCTTAAACGATGAGCTTAGAA 3240
Db 3178 TGCACCATGCTGAGAGAACAGGTCATGATTTTGAAGGCCCTTAAACGATGAGCTTAGAA 3237
QY 3241 AAGAGCGGAGTGGAGAGCTGAGAGAGCTCTGGGTGATGAGAAATCCAGTTTGAAG 3300
Db 3238 AAGAGCGGAGTGGAGAGCTGAGAGAGCTCTGGGTGATGAGAAATCCAGTTTGAAG 3297
QY 3301 TGTGCGGTTTGAAGCTGAGAGAGATGCTGGAACCGGAAGAACAGAGCGGGGAGAGGCC 3360
Db 3298 TGTGCGGTTTGAAGCTGAGAGAGATGCTGGAACCGGAAGAACAGAGCGGGGAGAGGCC 3357
QY 3361 GATCAGCGGATCACCCAGTCTCGCCAGGTGTGAGAGCTGAGTGAAGAGCAAGAGCT 3420
Db 3358 GATCAGCGGATCACCCAGTCTCGCCAGGTGTGAGAGCTGAGTGAAGAGCAAGAGCT 3417
QY 3421 GAGATTTCTGCTGTGACAGAGCTCTCAAAAGACAGAAAGCTGAAGGCCAGAGCTTCT 3480
Db 3418 GAGATTTCTGCTGTGACAGAGCTCTCAAAAGACAGAAAGCTGAAGGCCAGAGCTTCT 3477
QY 3481 GACAAAGCTCAATGACCTGAGAGAAAGCATGCTATGCTTGAATGAATGCCGAGGCTTA 3540
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Qy 3901 GAGCTAGAGAGAGCCCTTCAGAGAGCCCGCATGAGCTCCGCTCGCCGGAGAGAGCT 3960
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Db 3958 GCCCACCAG 4017
Qy 4021 ATGCGCATGTCCGCGCATGTGCGGTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4080
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Qy 4141 AAGGAGCGCATGCAACCAATATTCCTACCGGATTCAGTGAAGTGAAGTGAAGTGAAG 4200
Db 4138 AAGGAGCGCATGCAACCAATATTCCTACCGGATTCAGTGAAGTGAAGTGAAGTGAAG 4197
Qy 4201 ACAAGGTGCTGT 4260
Db 4198 ACAAGGTGCTGT 4257
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Db 4258 GAATGTGAGT 4317
Qy 4321 CTGTGTGATGT 4380
Db 4318 CTGTGTGATGT 4377
Qy 4381 GGTCTCCAGACCAAG 4440
Db 4378 GGTCTCCAGACCAAG 4437
Qy 4441 AGGATTAACAAACGAG 4500
Db 4438 AGGATTAACAAACGAG 4497
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Qy 4561 GAGGTGTGCTTCCCGAG 4620
Db 4558 GAGGTGTGCTTCCCGAG 4617
Qy 4621 GCAAATACAGCAAG 4680
Db 4618 GCAAATACAGCAAG 4677
Qy 4681 ACCTGTGAGCCCGAG 4740
Db 4678 ACCTGTGAGCCCGAG 4737
Qy 4741 TGGGTACCGGCTTAAATCAATGTTGTGCGAGGTGGAGAGAGAGAGAGAGAGAGAGAGAG 4800
Db 4738 TGGGTACCGGCTTAAATCAATGTTGTGCGAGGTGGAGAGAGAGAGAGAGAGAGAGAGAG 4797
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Db 4798 GCTGATGCTAAACGCTTGTGAG 4857
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Db 4978 CAAATTTATTTATTCAG 5037
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Db 5038 CTGTGTCTTGTGAG 5097
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Qy 5161 GCGAAGTTGAG 5220
Db 5158 GCGAAGTTGAG 5217
Qy 5221 CGCTACAG 5280
Db 5218 CGCTACAG 5277
Qy 5281 TGCAAGTGTATTCAGCTTCAACCAATTCAGTATCTCATTTGAGAGAGAGAGAGAGAGAG 5340
Db 5278 TGCAAGTGTATTCAGCTTCAACCAATTCAGTATCTCATTTGAGAGAGAGAGAGAGAGAG 5337
Qy 5341 ATGCAATGAAG 5400
Db 5338 ATGCAATGAAG 5397
Qy 5401 CTGT 5460
Db 5398 CTGT 5457
Qy 5461 GCAG 5520
Db 5458 GCAG 5517
Qy 5521 TACGAG 5580
Db 5518 TACGAG 5577
Qy 5581 TACGAG 5640
Db 5578 TACGAG 5637
Qy 5641 GCAAGCTCTCAG 5700
Db 5638 GCAAGCTCTCAG 5697
Qy 5701 CTGGGCTCTGCAATTTCTCAG 5760
Db 5698 CTGGGCTCTGCAATTTCTCAG 5757
Qy 5761 AGGATCATTTGTGCAAG 5820
Db 5758 AGGATCATTTGTGCAAG 5817
Qy 5821 CCGTCCAG 5880
Db 5818 CCGTCCAG 5877
Qy 5881 ACCAAGCGCTGAGCTTCCAG 5940
Db 5878 ACCAAGCGCTGAGCTTCCAG 5937
Qy 5941 AGCAGACCCCAACGCTTACCGAG 6000
Db 5938 AGCAGACCCCAACGCTTACCGAG 5997

QY 6001 CGCCCCGTGAGCAGAGAGTCCCCCGCGCGGATCTACAGACCGCGAGAGCGGCTCC 6060
 DB 5998 CGCCCCCTGAGCAGAGAGTCCCCCGCGCGGATCTACAGACCGCGAGAGCGGCTCC 6057
 QY 6061 CCGCGAGGCTGTTTGAAGACAGACAGAGGGCGCGCTGCTGGCGGAGCCGTAGAGACC 6120
 DB 6058 CCGCGAGGCTGTTTGAAGACAGACAGAGGGCGCGCTGCTGGCGGAGCCGTAGAGACC 6117
 QY 6121 CCGCTGTCCAGAGTGAACAGAGTGTGGAGCCAGTCTTCAGTATATA 6165
 DB 6118 CCGCTGTCCAGAGTGAACAGAGTGTGGAGCCAGTCTTCAGTATATA 6162

RESULT 11
 ABS63435 ID ABS63435 standard; cDNA; 6201 BP.
 AC ABS63435;
 DT 15-NOV-2002 (first entry)
 DE Human cDNA, homologous to kinases, designated NOV3a.
 XX
 KM Human; gene; ss; NOV; NOVX; NOVX-associated disorder; cardiomyopathy;
 KM atherosclerosis; diabetes; cell signalling; metabolic pathway;
 KM cellular receptor; downstream effector; cancer; gene therapy;
 KM hypertension; congenital heart defect; aortic stenosis; obesity;
 KM infectious disease; anorexia; Alzheimer's disease; Parkinson's disease;
 KM neurodegenerative disorder; haemophilia; dyslipidemia; vaccine;
 KM haematopoietic disease; scleroderma; fertility; immunogen;
 KM idiopathic thrombocytopenic purpura; graft versus host disease;
 KM Crohn's disease; multiple sclerosis; cirrhosis; autoimmune disease;
 KM systemic lupus erythematosus; asthma; arthritis; psoriasis; allergy;
 KM stroke; anxiety; Lesch-Nyhan syndrome; schizophrenia; cerebellar ataxia;
 KM pain; alcoholism; transgenic.
 XX
 OS Homo sapiens.
 PN WO20026826-A2.
 XX
 PD 04-APR-2002.
 PF 27-SEP-2001; 2001WO-US042336.
 XX
 XX 27-SEP-2000; 2000US-0235631P.
 PR 27-SEP-2000; 2000US-0235633P.
 PR 27-SEP-2000; 2000US-0235808P.
 PR 27-SEP-2000; 2000US-0236064P.
 PR 27-SEP-2000; 2000US-0236065P.
 PR 27-SEP-2000; 2000US-0236066P.
 PR 28-SEP-2000; 2000US-0236135P.
 PR 03-OCT-2000; 2000US-0237434P.
 PR 05-OCT-2000; 2000US-0238321P.
 PR 06-OCT-2000; 2000US-0238396P.
 PR 16-MAR-2001; 2001US-027667P.
 PR 31-MAY-2001; 2001US-0294823P.
 PR 12-JUL-2001; 2001US-0304688P.
 PR 26-SEP-2001; 2001US-00235631.
 XX
 PA (CUBA-) CUBAGEN CORP.
 XX
 PI Gerlach VL, MacDougall JR, Smithson G, Millett I, Stone D;
 PI Gunther E, Ellerman K, Grose WM, Alsobrook JP, Lepley DM;
 PI Burgess CE, Padigar M, Kekuda R, Spytek KA, Leach MD, Shimkets RA.
 XX
 XX MPI: 2002-499860/53.
 DR P-PSDB; ABG78362.
 XX
 PT Novel isolated NOVX polypeptides and polynucleotides homologous to
 PT attractin, plexin, plexin-like family of proteins, useful for treating
 PT atherosclerosis, diabetes, cancer, Alzheimer's disease, hemophilia and

PT stroke.
 XX
 PS Claim 8; Page 40-42; 308pp; English.
 XX
 CC The invention discloses the isolated human polypeptides, and
 CC polynucleotides encoding them, that have been designated NOVX. The
 CC polypeptides, polynucleotides and antibodies are useful in treating or
 CC preventing a NOVX-associated disorder which is cardiomyopathy,
 CC atherosclerosis and diabetes in a human, where the disorder is related to
 CC cell signal processing and metabolic pathway modulation. They can also be
 CC used in determining the presence of, or predisposition to, a disease
 CC associated with altered levels of the polypeptides and polynucleotides of
 CC any one of the 13 sequences (NOV1-NOV8), for raising antibodies, for
 CC identifying an agent that binds to, or that modulates the expression or
 CC activity of the polypeptide, for identifying an agent which is cellular
 CC receptor or downstream effector, for treating or preventing a NOVX-
 CC associated disorder and as a pharmaceutical composition comprising the
 CC polypeptide, polynucleotide or the antibody. The polypeptides and
 CC polynucleotides are useful in diagnostic applications (e.g. as a marker
 CC for cancerous cells or tissue types) where their amounts are assessed, or
 CC for the manufacture of a medicament (e.g. gene therapy) for treating or
 CC preventing disorders or syndromes such as hypertension, congenital heart
 CC defects, aortic stenosis, obesity, infectious disease, anorexia, cancer,
 CC Alzheimer's disease, Parkinson's disorders, neurodegenerative disorders,
 CC hemophilia, dyslipidemias, haematopoietic diseases, scleroderma,
 CC fertility, idiopathic thrombocytopenic purpura, graft versus host
 CC diseases, Crohn's disease, multiple sclerosis, cirrhosis, autoimmune
 CC disease, systemic lupus erythematosus, asthma, arthritis, psoriasis,
 CC allergy, stroke, anxiety, Lesch-Nyhan syndrome, schizophrenia, cerebellar
 CC ataxia, pain and alcoholism. They may also be used as immunogens to
 CC produce antibodies specific for the invention, and as vaccines.
 CC Transgenic cells containing a NOVX expressing construct are useful to
 CC produce non-human transgenic animals for studying the function and/or
 CC activity of the NOVX proteins and for identifying and/or evaluating
 CC modulators of NOVX protein activity. Transgenic cells containing a NOVX
 CC expressing construct are useful to produce non-human transgenic animals
 CC for studying the function and/or activity of the NOVX proteins and for
 CC identifying and/or evaluating modulators of NOVX protein activity. The
 CC sequences presented in ABS63431-ABS63444 are the human NOV1-NOV8 cDNAs
 XX
 SQ Sequence 6201 BP; 1736 A; 1552 C; 1707 G; 1206 T; 0 U; 0 Other;

Query Match 99.0%; Score 6105.4; DB 6; Length 6201;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 6131; Conservative 0; Mismatches 21; Indels 3; Gaps 1;

QY 1 ATGTTGAAGTCAAAATAGAGAGCGCGAGTCCCTTGGAGTGTGCTGTGAACCCATT 60
 DB 1 ATGTTGAAGTCAAAATAGAGAGCGCGAGTCCCTTGGAGTGTGCTGTGAACCCATT 60
 QY 61 GCCAGCGGGCTCCAGAGCTGAATCTGTTCTTCAAGGGAAACCACTTTATGACTCAA 120
 DB 61 GCCAGCGGGCTCCAGAGCTGAATCTGTTCTTCAAGGGAAACCACTTTATGACTCAA 120
 QY 121 CAGCAGATGTCCTCTTCCGAGAGGGATATTAGATGCCCTTGTCTTTGAA 180
 DB 121 CAGCAGATGTCCTCTTCCGAGAGGGATATTAGATGCCCTTGTCTTTGAA 180
 QY 181 GAATGAGTCAAGCCGCTCTGATGAAGATTAGCAAGTGAACATTTCCGGAAGTAT 240
 DB 181 GAATGAGTCAAGCCGCTCTGATGAAGATTAGCAAGTGAACATTTCCGGAAGTAT 240
 QY 241 TCCGACACCATAGCTGAGTGAAGAGAGCTTCAGCTTGGCAAGAGACTTCAAGTCA 300
 DB 241 TCCGACACCATAGCTGAGTGAAGAGAGCTTCAGCTTGGCAAGAGACTTCAAGTCA 300
 QY 301 AGCTTTGAGTGTGTGTCACCTTGTCTGAAGTGAAGAGAGAAAGCAACCGGG 360
 DB 301 AGCTTTGAGTGTGTGTCACCTTGTCTGAAGTGAAGAGAGAAAGCAACCGGG 360
 QY 361 GACATCTATGCTATGAAAGATGAAGAAAGAGGCTTTATTTGGCCAGAGAGAGGTTTCA 420
 DB 361 GACATCTATGCTATGAAAGATGAAGAAAGAGGCTTTATTTGGCCAGAGAGAGGTTTCA 420

Db 2578 CTGAGACACAGGCTGGAAAGTTGGAAGCCAGAAACGAAAACTGAGAGACACTGGAG 2637
Qy 2641 AAGATCACCAACCAAGACCAACAGTGAACAGATGGCTGTCTGAACTGAGACAAGATTG 2700
Db 2638 AAGATCAGCAACCAAGACCAACAGTGAACAGATGGCTGTCTGAACTGAGACAAGATTG 2697
Qy 2701 GGGAGGTCAGTCTGAGAGACAGAGACCAAAATCTGAGCTCAAGCCCACTGACAGAG 2760
Db 2698 GGGAGGTCAGTCTGAGAGACAGAGACCAAAATCTGAGCTCAAGCCCACTGACAGAG 2757
Qy 2761 CTACAGCTCTCCCTGACAGAGCGGAGTCAAGTTGACAGCCCTGACAGCTGACAGGCG 2820
Db 2758 CTACAGCTCTCCCTGACAGAGCGGAGTCAAGTTGACAGCCCTGACAGCTGACAGGCG 2817
Qy 2821 GCCCTGAGAGCCAGCTTTCGCCAGGCGAAGACAGAGCTGGAAGAGACACAGCAGAACT 2880
Db 2818 GCCCTGAGAGCCAGCTTTCGCCAGGCGAAGACAGAGCTGGAAGAGACACAGCAGAACT 2877
Qy 2881 GAAGAGAGATCCAGAGACTCAAGGCACTACAGGCAATGAGATGAAATCCAGGCGAAATTTGATGCT 2940
Db 2878 GAAGAGAGATCCAGAGACTCAAGGCACTACAGGCAATGAGATGAAATCCAGGCGAAATTTGATGCT 2937
Qy 2941 CTTCGTAACAGCTGTACTGTATATCAAGACCTGAGAGAGAGCTAAACAGCTGACCGAG 3000
Db 2938 CTTCGTAACAGCTGTACTGTATATCAAGACCTGAGAGAGAGCTAAACAGCTGACCGAG 2997
Qy 3001 GACACGCTGAACCTCAACAAACAACTTCTATCTTGTCCAAACAACTCGATGAGCTTCT 3060
Db 2998 GACACGCTGAACCTCAACAAACAACTTCTATCTTGTCCAAACAACTCGATGAGCTTCT 3057
Qy 3061 GGGGCCACACAGAGATTGTACACTGCGAAGTGAAGTGAACCACTCCCGCGAGATC 3120
Db 3058 GGGGCCACACAGAGATTGTACACTGCGAAGTGAAGTGAACCACTCCCGCGAGATC 3117
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Qy 3301 TGTGCGGTTGAGAGCTGACAGAGATGCTGGAACACGAGAAACAGACGGCGAGAGCC 3360
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Qy 3361 GATCAGCGGATCACCGAGTCTCGCCAGGTGTGAGACTGCACTGAGAGACCAAGGCT 3420
Db 3358 GATCAGCGGATCACCGAGTCTCGCCAGGTGTGAGACTGCACTGAGAGACCAAGGCT 3417
Qy 3421 GAGATTCTGCTGTGAGAGGCTTCAAAAGACAGAGCTGAAGGCCCGAGACTCTCT 3480
Db 3418 GAGATTCTGCTGTGAGAGGCTTCAAAAGACAGAGCTGAAGGCCCGAGACTCTCT 3477
Qy 3481 GACAAGCTAATGACCTGAGAGAGAGAGATGCTATGCTTGAATGAATGCCAGACTTA 3540
Db 3478 GACAAGCTAATGACCTGAGAGAGAGAGATGCTATGCTTGAATGAATGCCAGACTTA 3537
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Db 3538 CAGCAGAAAGCTGAGACTGAACGAGAGCTCAACAGAGCTTCTGAGAGACCAAGCAAA 3597
Qy 3601 TTACAGCAGCAGATGACCTGCAAGAAAATCAATTTTCGTTGACTCAAGACTGCAA 3660
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Db 3658 GAAGCTTAGATCGGCTGACTTACTGAGACAGAAAGAAAGTGAATGAGACTATCAGCTG 3717
Qy 3721 GAAAACATTCAGGTTCTATATTCATGAAAGGTGAAAAATGGAAGCACTATTTCTCAA 3780
Db 3718 GAAAACATTCAGGTTCTATATTCATGAAAGGTGAAAAATGGAAGCACTATTTCTCAA 3777
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Db 3838 GTTCCTGTGAGTACAAATGAGCTGAAGCTGAGCCCTGGAAGAGAAAGCTCGCTGCA 3897
Qy 3901 GAGCTAGAGAAACCTTTCAGAAAGCCCGATGAGCTCCGCTCCCGCGAGAAAGCT 3960
Db 3898 GAGCTAGAGAAACCTTTCAGAAAGCCCGATGAGCTCCGCTCCCGCGAGAAAGCT 3957
Qy 3961 GCCCACCGCAACCAACGACCAACCCATCCATCCACGCCAGCACCCGAGGACAG 4020
Db 3958 GCCCACCGCAACCAACGACCAACCCATCCATCCACGCCAGCACCCGAGGACAG 4017
Qy 4021 ATGCGCATGTCGCGCATTCGTCGAGGTCAGAGACCAAGCCGATGAGCTGCTG 4080
Db 4018 ATGCGCATGTCGCGCATTCGTCGAGGTCAGAGACCAAGCCGATGAGCTGCTG 4077
Qy 4081 GCCCGCGCATTCAGCGCAGAGAAAGAGTCTTCACTCAGAGGAATTTAGTCGCGCTT 4140
Db 4078 GCCCGCGCATTCAGCGCAGAGAAAGAGTCTTCACTCAGAGGAATTTAGTCGCGCTT 4137
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Db 4138 AAGAAACGATGACCAACAAATATTTCTCACCGATTCAAGTGAAGTGAACATGCGAGCC 4197
Qy 4201 ACAAGTGTGTCGTGTGTGTGATACCGTGAACCTTTGAGCGCAGGATCCAAATGTCTC 4260
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 Db 5218 CGCTACACAGAAACTCTGAGAAATCTGCATCCGGAAGAGATAGAGACCTCAGAGCCC 5277
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 Db 5338 ATGACATGAGAGAGTACAGCTCAGAGAAATCTGTGATTAAGATGACATTCCTTGGCA 5397
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 Db 5398 CTGTGCTGTTTGGCGCTCTTCCACAGCTTCCCTGTCTCAATGCTGACAGTGAACAGC 5457
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 Db 5518 TACGAGAGAGTACGCGACAGACGATCTCAAGTGAAGTGCCTTACCTTTGGCCTTTGCC 5577
 QY 5581 TACAGAGAACCTATCTGTTTGTGACCACCTTCACTCACTCGAAGTAATTGAGATCAG 5640
 Db 5578 TACAGAGAACCTATCTGTTTGTGACCACCTTCACTCACTCGAAGTAATTGAGATCAG 5637
 QY 5641 GCAGGCTCTCAG 5700
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 QY 5701 CTGGGCGCTGCACTTCTCTCAGAGAGAGATTAATTTGAGAGTCTCATACAGATTAATTA 5760
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 QY 5821 CCGTTCACCTTCCGAG 5880
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QY 5881 ACCAAGCGCTGCGCTTCCAGCCCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5940
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 QY 6001 CGCCCGCTGAG 6060
 Db 5998 CGCCCGCTGAG 6057
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 Db 6058 CCGCGAGAGCTGTTTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6117
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 AC ADA05653;
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 DT 06-NOV-2003 (first entry)
 DE Human NOVIg encoding cDNA SEQ ID NO:13.
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 KW human; NOVIg; antidiabetic; anorectic; antibacterial; virucide;
 KW immunomodulator; cytoskeletal; neurotrophic; neuroprotective;
 KW antiparkinsonian; antilipemic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia; gene; ss.
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 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..6201
 FT /*tag= a
 FT /product= "NOVIg"
 XX
 PN M02003029424-A2.
 PD 10-APR-2003.
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 PF 02-OCT-2002; 2002MO-US031373.
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 05-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
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 PR 09-OCT-2001; 2001US-0328056P.
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 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
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 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.


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Db 1258 TACAGCAAGGCACTGGGGATTTCTTGGTAGATCTGAGTCTGTGTGTGTGGGGTCTGGAATCC 1317
Qy 1321 CTTGCCAAGACTAGCTCCATGAGAAAAGAACTTCTATCAAAAGCAAAAGACTACAGAC 1380
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Db 1378 TCTCAGAGCAAGTGTCACAAGATGAGAGAAATGACCCGGTTACATCCGAGAGTGTCA 1437
Qy 1441 GAGGTGAGGCTGTGCTTAGTCAAGAGAGAGTGAAGGCTCTGAGACTCAGAGA 1500
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Qy 1501 TCCCTCTGAGAGAGAGCTTTGCTAATCAATCAAGATGCAATGCACTTAAGCGAAGT 1560
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Qy 1861 GTGGAGAGATATGCGAAATGAGAGAGATCAATGCTGAGCAGAGCTCAAAATTCAGAG 1920
Db 1858 GTGGAGAGATATGCGAAATGAGAGAGATCAATGCTGAGCAGAGCTCAAAATTCAGAG 1917
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Qy 2041 GATTTCTTCTGAAGGATCAGAAAGAGCTGTGTGAAGCTGAGAAACGCGCATTTCTCTG 2100
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Qy 2281 CAGCACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Db 2278 CAGCACTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2337
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Db 2338 AAGAGAGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2397
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Db 2818 GCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2877
Qy 2881 GAGAGAGAGATCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940
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[illegible]

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 ID ADN62818 standard; DNA, 6201 BP.
 XX
 AC ADN62818;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human NOV1g DNA.
 XX
 XX de; gene; human; NOVX; metabolic disorder; diabetes; obesity;
 XX infectious disease; anorexia; cancer; cancer-associated cachexia;
 KM neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KM immune disorder; haematopoietic disorder; dyslipidaemia;
 KM metabolic syndrome X; wasting disorder.
 XX
 OS Homo sapiens.
 XX
 PN US2004038223-A1.
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 PD 26-FEB-2004.
 XX
 PF 01-OCT-2002; 2002US-00262511.
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 PR 02-OCT-2001; 2001US-0326483P.
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PR 09-OCT-2001; 2001US-0328044P.
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 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
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 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 XX (SMIT/) SMITHSON G.
 PA (MILT/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUJU/) JU J.
 PA (LIL/) LI L.
 PA (GUOX/) GUO X.
 PA (PAT/) PATTURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELBE/) ELLERMAN K.
 PA (MALY/) MALYANKAR U M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERRHUSEN B D.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATY/) CATTERTON E.
 PA (JIW/) JI W.
 PA (MILT/) MILLER C E.
 PA (RAST/) RASTRELLI L.
 PA (STON/) STONE D J.
 PA (PENNA/) PENNA C E A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.
 PA (AGER/) AGER M L.
 PA (BERG/) BERGHS C.
 PA (DIP/) DIPILPO V A.
 PA (BISE/) EISEN A.
 PA (GANG/) GANGCOLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 XX Smitheon G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X,
 PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, MalYankar UM;
 PI Ort T, Gorman L, Zerrhuse BD, Anderson DW, Zhong M, Catterton E,
 PI Ji W, Miller CE, Rastrelli L, Stone DJ, Penn CE, Sheno Sg,
 PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipilpo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI: 2004-213931/20.
 DR P-PSDB; ADN62819.
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

PS Claim 20; SEQ ID NO 13; 395bp; English.

XX
CC The invention relates to isolated NOVX polypeptides and polynucleotides.
CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
CC treat a medical condition in human related to the aberrant expression and
CC activity of NOVX polypeptides. For example, NOVX polypeptides and
CC polynucleotides may be used to treat disorders associated with decreased
CC expression or activity of NOVX by supplementing the patient with
CC production or to rectify mutations. Conversely, antisense NA molecules
CC may be administered to down regulate expression of NOVX polypeptides by
CC binding with the cells own genes and preventing their expression. NOVX
CC polynucleotides and complementary sequences may also be used as DNA
CC probes in diagnostic assays to detect and quantitate the presence of
CC similar sequences in samples, and so which patients may be in need of
CC restorative therapy. NOVX polypeptides may also be used as antigens in
CC the production of antibodies and in assays to identify modulators
CC (agonists and antagonists) of the expression and activity of NOVX. The
CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
CC used to modulate NOVX polynucleotide expression and activity of NOVX
CC polypeptides. The anti-NOVX polypeptide antibodies may also be used as
CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
CC polypeptides and polynucleotides may be used in this way to prevent,
CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
CC hematopoietic disorders, and the various dyslipidaemias, metabolic
CC disturbances associated with obesity, the metabolic syndrome X and
CC wasting disorders associated with chronic diseases and various cancers.
CC They may also be used as antibacterial agents. The present sequence
CC represents DNA encoding a human NOVX protein.
XX

SO Sequence 6201 BP; 1735 A; 1551 C; 1709 G; 1206 T; 0 U; 0 Other;

Query Match 98.8%; Score 6091; DB 12; Length 6201;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 6122; Conservative 0; Mismatches 30; Indels 3; Gaps 1;

QY 1 ATGTGGAAGTTCAAAATATGAGAGCGCGAATCCTTTGATCTGTGCTGTGAACCCATT 60
DB 1 ATGTGGAAGTTCAAAATATGAGAGCGCGAATCCTTTGATCTGTGCTGTGAACCCATT 60
QY GCCAGCGGGGCTCCAGGCTGAATCTGTTCCAGGGGAAACACCCCTTAATGACTCA 120
DB GCCAGCGGGGCTCCAGGCTGAATCTGTTCCAGGGGAAACACCCCTTAATGACTCA 120
QY 121 CAGCAGATGTCCTCTTTCCGAGAAAGGATATTAGATGCCCTCTTTGTTCTTTGAA 180
DB 121 CAGCAGATGTCCTCTTTCCGAGAAAGGATATTAGATGCCCTCTTTGTTCTTTGAA 180
QY 181 GAATGACATGAGCTCTCTGATGAAGATTAAACAGTGAGCAACTTTGTCGGAAGTGT 240
DB 181 GAATGACATGAGCTCTCTGATGAAGATTAAACAGTGAGCAACTTTGTCGGAAGTGT 240
QY 241 TCCGACACCAATGCTAGTTACAGGAGCTCCAGCTTCGGCAAAAGACCTTGAAGTCA 300
DB 241 TCCGACACCAATGCTAGTTACAGGAGCTCCAGCTTCGGCAAAAGACCTTGAAGTCA 300
QY 301 AGTCTTGATGATGTCATCTTGTCTGAAGTCAAGTGGTAAAGAGAAACCGGG 360
DB 301 AGTCTTGATGATGTCATCTTGTCTGAAGTCAAGTGGTAAAGAGAAACCGGG 360
QY 361 GACATCTATGCTATGAAAGTATGAAGAAAGGCTTTATTGGCCAGAGACGAGTTTCA 420
DB 361 GACATCTATGCTATGAAAGTATGAAGAAAGGCTTTATTGGCCAGAGACGAGTTTCA 420
QY 421 TTTTGTGAGAGAGGCGAACAATATATCTCCAGACACAAGCCCGTGAATCCCCCAATTA 480
DB 421 TTTTGTGAGAGAGGCGAACAATATATCTCCAGACACAAGCCCGTGAATCCCCCAATTA 480
QY 481 CAGTATGCTTTTCAAGACAAAATCACTTTATCTGTGATGGAATATACGCTGAGGG 540
DB 481 CAGTATGCTTTTCAAGACAAAATCACTTTATCTGTGATGGAATATACGCTGAGGG 540

QY 541 GACTGTGCTGACTTTTGAATATGATATGAGACCAAGTTAATGAAAACCTGATACAGTTT 600
DB 541 GACTGTGCTGACTTTTGAATATGATATGAGACCAAGTTAATGAAAACCTGATACAGTTT 600
QY 601 TACCTACATGAGCTGATTTGGCTGTTTCAAGGCTTATCGATGGATACGTGACATCA 660
DB 601 TACCTACATGAGCTGATTTGGCTGTTTCAAGGCTTATCGATGGATACGTGACATCA 660
QY 661 GACATCAAGCCTGAGAACATCTCTGTGACCGGACAGACACATCAAGCTGTGGATTTT 720
DB 661 GACATCAAGCCTGAGAACATCTCTGTGACCGGACAGACACATCAAGCTGTGGATTTT 720
QY 721 GATCTGCGCGGAAATGAATTTAAACAGATGATGATCCAACTCCGATTTGGAGC 780
DB 721 GATCTGCGCGGAAATGAATTTAAACAGATGATGATCCAACTCCGATTTGGAGC 780
QY 781 CCGATTTACATGCTCTCTGAAGTGTGACCTGATATGAACGGGATGGAAGGACACTAC 840
DB 781 CCGATTTACATGCTCTCTGAAGTGTGACCTGATATGAACGGGATGGAAGGACACTAC 840
QY 841 GGCCTGACTGTGACTGTGTCAGTGGGCGTGAATGCTATGAGATGATTTATGGAGA 900
DB 841 GGCCTGACTGTGACTGTGTCAGTGGGCGTGAATGCTATGAGATGATTTATGGAGA 900
QY 897 GGCCTGACTGTGACTGTGTCAGTGGGCGTGAATGCTATGAGATGATTTATGGAGA 957
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DB 961 TTTTGAATTTTCCAAATGACCCCAAGAGAGAGATCTTCTGATGATTCGATTCAGAG 1020
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DB 1021 TTGTTGTGCGGCGAGAAAGAGAGACTGAAGTTGAAGTCTTTGCTGCCATCTTTCTTC 1080
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DB 1141 TCTGACATGACACCTCCCAATTTTGAATGAACCAAGAAATTCGTTGCTTCACTCTCT 1200
QY 1197 TCTGACATGACACCTCCCAATTTTGAATGAACCAAGAAATTCGTTGCTTCACTCTCT 1197
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DB 1201 CCGTGCACGCTGAGCCCTCAAGCTTCTCGGGTGAAGAACTGCGCTTTGAGGGTTTTCG 1260
QY 1257 CCGTGCACGCTGAGCCCTCAAGCTTCTCGGGTGAAGAACTGCGCTTTGAGGGTTTTCG 1257
DB 1257 CCGTGCACGCTGAGCCCTCAAGCTTCTCGGGTGAAGAACTGCGCTTTGAGGGTTTTCG 1257
QY 1261 TACAGCAAGGCACTGGGGATTTCTTGGTATGATCTGAATCTGTTGTGTGGTCTGACTCC 1320
DB 1261 TACAGCAAGGCACTGGGGATTTCTTGGTATGATCTGAATCTGTTGTGTGGTCTGACTCC 1320
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DB 1258 TACAGCAAGGCACTGGGGATTTCTTGGTATGATCTGAATCTGTTGTGTGGTCTGACTCC 1317
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DB 1321 CCGTGCACGCTGAGCCCTCAAGCTTCTCGGGTGAAGAACTGCGCTTTGAGGGTTTTCG 1380
QY 1318 CCGTGCACGCTGAGCCCTCAAGCTTCTCGGGTGAAGAACTGCGCTTTGAGGGTTTTCG 1377
DB 1318 CCGTGCACGCTGAGCCCTCAAGCTTCTCGGGTGAAGAACTGCGCTTTGAGGGTTTTCG 1377
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DB 1378 TCTCAGAGCAATGTCACAAATGAGAGAGAAATGACCCGGTTACATGAGAGTGTCA 1437
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QY 1438 GAGGTGAGGCTGTGCTTATGTCAGAAAGAGTGAAGCTGGAAGCTTCTGAGACTAGAGA 1497
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QY 1561 TTGAGAGCAAGCAGATGAGGATGTCAGAGAGATGACAAAGCACTGCAAGCTTCTCCAT 1620
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Qy 1861 GTGGAGAAATATGCGAAATCGAGAAAGATCAATGCTGAGCAGCTCAAAATTCAGAG 1920
Db 1858 GTGGAGAAATATGCGAAATCGAGAAAGATCAATGCTGAGCAGCTCAAAATTCAGAG 1917
Qy 1921 CTCGAAGAGAACTGAGAGAGGCTGTAAAGCCAGCAGCAGAGGCAACCGAGCTTGCAG 1980
Db 1918 CTCGAAGAGAACTGAGAGAGGCTGTAAAGCCAGCAGCAGAGGCAACCGAGCTTGCAG 1977
Qy 1981 AATATCCGCGCAGGCAAGAGAGCCGAGAGGAGCTGAGAGAGCTGCAAAACCGAG 2040
Db 1978 AATATCCGCGCAGGCAAGAGAGCCGAGAGGAGCTGAGAGAGCTGCAAAACCGAG 2037
Qy 2041 GATTCTTCTGAAGCATCAGAAAGAGCTGTGGAAGCTGAGAGAGCCGCAATTCCTG 2100
Db 2038 GATTCTTCTGAAGCATCAGAAAGAGCTGTGGAAGCTGAGAGAGCCGCAATTCCTG 2097
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Qy 2401 ATTCTCAGGAAACAGAGGCGATGATCAATGCTATGATTCGAAGATCAATCCCTGGAA 2460
Db 2398 ATTCTCAGGAAACAGAGGCGATGATCAATGCTATGATTCGAAGATCAATCCCTGGAA 2457
Qy 2461 CAGAGATTTGTGAACTGTCTGAAGCCAAATTAATTCAGCAAAATAGCAGCTTTTACC 2520
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Qy 3001 GACACGCTGAACTCAACAAACCAAACTTCTACTTGTCCAAACATCTCGATGAGCTTCT 3060
Db 2998 GACACGCTGAACTCAACAAACCAAACTTCTACTTGTCCAAACATCTCGATGAGCTTCT 3057
Qy 3061 GCGGCCAAGAGAGATTTGACACTGCGAAGTGAAGTGAACCATCTCCGCGGGAGATC 3120
Db 3058 GCGGCCAAGAGAGATTTGACACTGCGAAGTGAAGTGAACCATCTCCGCGGGAGATC 3117
Qy 3121 ACGGAACGAGAGATGAGCTTACACAGCAGAACCAACGATGAGGCTTGAAGACCAAG 3180
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Qy 3421 GAGATTTCTGCTCTGACAGAGGCTCTCAAGAGCAAGAGCTGAAGGCGGAGAGCTTCT 3480
Db 3418 GAGATTTCTGCTCTGACAGAGGCTCTCAAGAGCAAGAGCTGAAGGCGGAGAGCTTCT 3477
Qy 3481 GACAGCTCAATGACCTGGAGAGAAAGCATGTATGCTTGAATGATGCCGAAAGCTTA 3540
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Db 3538 CAGCAGAGCTGAGACTGAACGAGAGAGCTCAACAGAGGCTTCTGAAAGACAGCCAA 3597
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QY 3841 GTTCCTTGAGTAACAATGAGCTGAAGCTGGCCCTTGAGAAAGAAAGCTCGCTGCGCA 3900
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QY 3901 GAGCTAGAGAAAGCCCTTTCAGAAAGCCGCACTCGAGCTCCGGTCCGGCCGGAGAAAGCT 3960
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QY 4021 ATGCGCAATGCTCCGCAATGCTGGGCTGGCGAGAGACCAAGCCCAAGCTGACATGAGCTCTG 4080
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QY 4141 AAGGAACGATGACCAACAATATTTCTCACGATTCACGTAAGACTGAACATGCGAGCC 4200
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QY 4441 AAGGAATACAAAGAGAGACAGAAAGGTGGAGACAGAAAGTACATTTGCTCGAGGGATCA 4500
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QY 4501 AAAGTCTCATTTATGACAAATGAAGCAGAGAACTGACAGAGGCGGTGAGAAATTT 4560
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Db 6118 CCGCTGTCCAGGTGAACAAAGGTGAGCAGCATTC 6152
RESULT 14
AB07871
ID AB07871 standard; cDNA; 5877 BP.
XX
AC AB07871;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human kinase cDNA #2.
XX
KM Human; kinase; enzyme; serine-threonine kinase; nontropic; cytosolic;
KM Citron rho-interacting kinase; gene therapy; mental disorder; cancer;
KM gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..5877
FT /*tag= a
FT /product= "Kinase"
PN W0200259325-A2.
XX
PD 01-AUG-2002.
XX
XX 20-DEC-2001; 2001WO-US050497.
XX
XX 27-DEC-2000; 2000US-0258335P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Yu X, Miranda M, Fiddle CJ;
XX
XX WPI: 2002-599796/64.
XX
XX P-PSDB; ABB81928.
XX
XX Novel polynucleotide encoding human proteins that are structurally
XX similar to animal kinases, useful for drug screening, diagnosis, in gene
XX therapy of disorders and diseases e.g. cancer and pharmacogenomic
XX applications.
XX
XX Disclosure; Page 44-45; 50pp; English.
XX
XX The invention relates to a novel human protein that shares structural
XX similarity with animal kinases, including serine-threonine kinases,
XX particularly Citron rho-interacting kinases. The proteins of the
XX invention have nontropic and cytosolic activity. The polynucleotides may
XX have a use in gene therapy. The encoded novel polypeptides are useful for
XX generating antibodies, as reagents in diagnostic assays, for identifying
XX other cellular gene products related to NHP and as reagents in assays for
XX screening for compounds that are useful in the treatment of mental,
XX biological or medical disorders and diseases including cancer. The
XX sequence encodes a novel human kinase of the invention
XX
XX Sequence 5877 BP; 1680 A; 1433 C; 1583 G; 1181 T; 0 U; 0 Other;
SQ
Query Match 94.7%; Score 5837; DB 6; Length 5877;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5837; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTGAAGTTCAAAATATGAGCGCGAATCCTTTGATGCTGCTGCTGAACCCATT 60

Db 1 ATGTGAAGTTCAAAATATGAGCGCGAATCCTTTGATGCTGCTGCTGAACCCATT 60
Qy 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATAGTCA 120
Db 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTCCAGGGGAAACCAACCTTTATAGTCA 120
Qy 121 CAGCAGATGCTCTCTTTTCCCGAAGAGATATTAATGCTCTTTGTTCTTTGAA 180
Db 121 CAGCAGATGCTCTCTTTTCCCGAAGAGATATTAATGCTCTTTGTTCTTTGAA 180
Qy 181 GAATGAGTACGCTGCTGATGAATTAAGACCTGAGCACTTTGTCGGGAAT 240
Db 181 GAATGAGTACGCTGCTGATGAATTAAGACCTGAGCACTTTGTCGGGAAT 240
Qy 241 TCCGACACATAGCTGATTAACAGAGCTCAGCTTCGGCAAGAGACTTCGAAGTGA 300
Db 241 TCCGACACATAGCTGATTAACAGAGCTCAGCTTCGGCAAGAGACTTCGAAGTGA 300
Qy 301 AGTCTGTAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTGAAGAAACCAACCGG 360
Db 301 AGTCTGTAGTGTGTGCTCACTTTGCTGAAGTGCAGGTGTGAAGAAACCAACCGG 360
Qy 361 GACATCTATGCTATGAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 GACATCTATGCTATGAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Qy 421 TTTTGTGAGAGAGCGGAAATATTAATCTGAAGCAAGACCGGTGATCCCAATTA 480
Db 421 TTTTGTGAGAGAGCGGAAATATTAATCTGAAGCAAGACCGGTGATCCCAATTA 480
Qy 481 CAGTATGCTTTGAGAGCAAAATATCACTTTATCTGTGCTATGAAATATCAAGCTGAG 540
Db 481 CAGTATGCTTTGAGAGCAAAATATCACTTTATCTGTGCTATGAAATATCAAGCTGAG 540
Qy 541 GACTTGCTGCTGCTTTGAAATATGATGAGAGCAAGTAAATGAAAACCTGATCACTTT 600
Db 541 GACTTGCTGCTGCTTTGAAATATGATGAGAGCAAGTAAATGAAAACCTGATCACTTT 600
Qy 601 TACCTAGCTGAGGATTTTGGCTGTCACAGCGGTATCATGATGAGGATAGTGCATG 660
Db 601 TACCTAGCTGAGGATTTTGGCTGTCACAGCGGTATCATGATGAGGATAGTGCATG 660
Qy 661 GACATCAAGCCTGAGAACTTCTGTTGACCGACAGACACATCAAGCTGTGATTTT 720
Db 661 GACATCAAGCCTGAGAACTTCTGTTGACCGACAGACACATCAAGCTGTGATTTT 720
Qy 721 GATCTGCGCGAAATGAATTCAAACAGATGATGCAATCCGATTTGGAGC 780
Db 721 GATCTGCGCGAAATGAATTCAAACAGATGATGCAATCCGATTTGGAGC 780
Qy 781 CCAATTAACATGCTGCTGAGAGCTGACCTGTATGAACGAGGATGAAAAGCACCTAC 840
Db 781 CCAATTAACATGCTGCTGAGAGCTGACCTGTATGAACGAGGATGAAAAGCACCTAC 840
Qy 841 GGCCTGACCTGATGATGCTGATGAGTGGGCTGATTTCTATGATGATTTATGGAGA 900
Db 841 GGCCTGACCTGATGATGCTGATGAGTGGGCTGATTTCTATGATGATTTATGGAGA 900
Qy 901 TCCCTCTGCGAAGGAGACCTTCCGAACTTCAATTAATTAATTAATTTCCAGCG 960
Db 901 TCCCTCTGCGAAGGAGACCTTCCGAACTTCAATTAATTAATTAATTTCCAGCG 960
Qy 961 TTTTGAATTTTCAAGTGAACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
Db 961 TTTTGAATTTTCAAGTGAACCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1020
Qy 1021 TTGTTGTGCGCGAAG 1080
Db 1021 TTGTTGTGCGCGAAG 1080
Qy 1081 TCTAAATTAATGAGAAATATTCGTAATCTTCTCTCCCTGTTCCACCTCTGAG 1140

Dh 1081 TCTAAATTGACTGGAAACAAGATTGTAACCTCTCTCCCTCCCTTCGTTCCACCTCAG 1140
Qy 1141 TCTGACGATGACCTCCAAATTTTGTATGAAACCAAGAAATTCGTGGTTTCATCTCT 1200
Db 1141 TCTACCAATGACACTCCAAATTTTGTATGAAACCAAGAAATTCGTGGTTTCATCTCT 1200
Qy 1201 CCGTGCAGCTGAGCCCCCTCAGGCTTCCTCGGTGAAAGACCGCGTTTGTGGGGTTTTCG 1260
Db 1201 CCGTGCAGCTGAGCCCCCTCAGGCTTCCTCGGTGAAAGACCGCGTTTGTGGGGTTTTCG 1260
Qy 1261 TACAGCAAGGCACTGGGGATTCTTGTAGATCTGAGTCTGTTGTGTGGGTCTGAACTCC 1320
Db 1261 TACAGCAAGGCACTGGGGATTCTTGTAGATCTGAGTCTGTTGTGTGGGTCTGAACTCC 1320
Qy 1321 CTTGCCAAGACTACTCCATGAGAAAGAACTTTCATCAAAAGCAAAAGACTCAAGAC 1380
Db 1321 CTTGCCAAGACTACTCCATGAGAAAGAACTTTCATCAAAAGCAAAAGACTCAAGAC 1380
Qy 1381 TCTCAGGACAAGTGTCAACAAGTGGAGCAAGAAATGACCCGGTTACATCGAGAGTGTCA 1440
Db 1381 TCTCAGGACAAGTGTCAACAAGTGGAGCAAGAAATGACCCGGTTACATCGAGAGTGTCA 1440
Qy 1441 GAGGTGAGGCTGTCTTAAGTCAGAAAGAGTGGAGCTGAAAGCCTCTGAGACTCAGAGA 1500
Db 1441 GAGGTGAGGCTGTCTTAAGTCAGAAAGAGTGGAGCTGAAAGCCTCTGAGACTCAGAGA 1500
Qy 1501 TCCCTCTGAGCAAGCACTTGTCTCACTCAACAATGCAATGCAATGCAATGCAATGCAATG 1560
Db 1501 TCCCTCTGAGCAAGCACTTGTCTCACTCAACAATGCAATGCAATGCAATGCAATGCAATG 1560
Qy 1561 TTGGAGCAAGCAAGTGTGAGAGTGTCCAGAGAGTGAACAAGACCTGCAAGCTTCTCAT 1620
Db 1561 TTGGAGCAAGCAAGTGTGAGAGTGTCCAGAGAGTGAACAAGACCTGCAAGCTTCTCAT 1620
Qy 1621 GATATCAGAGCAAGCAAGCTCCGAAAGCTCAAGAAATCAAGAGCAAGAGTACAGGCTCAA 1680
Db 1621 GATATCAGAGCAAGCAAGCTCCGAAAGCTCAAGAAATCAAGAGCAAGAGTACAGGCTCAA 1680
Qy 1681 GTGGAAGAAATGAGTGTGATGATGATCACTTGGAGAGAGATCTTGTCTCAGCAAGAGA 1740
Db 1681 GTGGAAGAAATGAGTGTGATGATGATCACTTGGAGAGAGATCTTGTCTCAGCAAGAGA 1740
Qy 1741 CGGAGTATCTTACGAATCTGAGCTGAGAGAGTCTCGGCTTCTGTGTAAGAAATTCAG 1800
Db 1741 CGGAGTATCTTACGAATCTGAGCTGAGAGAGTCTCGGCTTCTGTGTAAGAAATTCAG 1800
Qy 1801 CGGAAAGCAGCAAGATGTGAGCATTAACCTTGAAGGCTAAGATCAAAGGAGCCTGAA 1860
Db 1801 CGGAAAGCAGCAAGATGTGAGCATTAACCTTGAAGGCTAAGATCAAAGGAGCCTGAA 1860
Qy 1861 GTGGGAGATATCGAAATCGAGAAAGATCAATGCTGAGCAGAGCTCAAAAATTCAGAG 1920
Db 1861 GTGGGAGATATCGAAATCGAGAAAGATCAATGCTGAGCAGAGCTCAAAAATTCAGAG 1920
Qy 1921 CTCAGAAGAAATCGAGAAAGGCTGTAAAAAGCCAGACCGAGGCTGAGAGAGCTGAG 1980
Db 1921 CTCAGAAGAAATCGAGAAAGGCTGTAAAAAGCCAGACCGAGGCTGAGAGAGCTGAG 1980
Qy 1981 AATATCCGCGCAAGCAAGAGCGAGCGAGAGGAGCTGAGAGAGCTGAGAGAGCGAGAG 2040
Db 1981 AATATCCGCGCAAGCAAGAGCGAGCGAGAGGAGCTGAGAGAGCTGAGAGAGCGAGAG 2040
Qy 2041 GATTTCTTGTGAAGCATCAAGAAAGAGCTGTGAAAGCTGAGAGAGCGCGCATTCCTG 2100
Db 2041 GATTTCTTGTGAAGCATCAAGAAAGAGCTGTGAAAGCTGAGAGAGCGCGCATTCCTG 2100
Qy 2101 GAGAACAAAGTAAAGACTGAGAGCAATGAGAGCTGAGAGAAACGACTGAAAGAGTAC 2160
Db 2101 GAGAACAAAGTAAAGACTGAGAGCAATGAGAGCTGAGAGAAACGACTGAAAGAGTAC 2160
Qy 2161 ATCCAGACAAGATCCCAAGAGATCCAGAGATGCTGATAAATTTCTGAGCTCGAAGAG 2220
Db 2161 ATCCAGACAAGATCCCAAGAGATCCAGAGATGCTGATAAATTTCTGAGCTCGAAGAG 2220

Qy 2221 AACATGCGGAGGCCCAAGTCTAGGCCAGACCTAAGTGCACCTGAAAACAGAAAGAG 2280
Db 2221 AACATGCGGAGGCCCAAGTCTAGGCCAGACCTAAGTGCACCTGAAAACAGAAAGAG 2280
Qy 2281 CAGCACTATGAGAAAGATTTAAAGTGTGAGCAATGATTAAGAAAGAGCTGGCTGAC 2340
Db 2281 CAGCACTATGAGAAAGATTTAAAGTGTGAGCAATGATTAAGAAAGAGCTGGCTGAC 2340
Qy 2341 AAGGAGACACTGAGAAACATGATGACAGACACGAGAGAGAGGCCCATGAGAAAGGCAAA 2400
Db 2341 AAGGAGACACTGAGAAACATGATGACAGACACGAGAGAGAGGCCCATGAGAAAGGCAAA 2400
Qy 2401 ATTCTAGCGAACAAGAGCGATGATCAATGATTCAGATTCAGATTCAGATTCCTGAA 2460
Db 2401 ATTCTAGCGAACAAGAGCGATGATCAATGATTCAGATTCAGATTCAGATTCCTGAA 2460
Qy 2461 CAGAGATTTGTGAACTGTCTGAAAGCCAAATTAACCTGACAGAAATGACATCTTTTACC 2520
Db 2461 CAGAGATTTGTGAACTGTCTGAAAGCCAAATTAACCTGACAGAAATGACATCTTTTACC 2520
Qy 2521 CAAAGGAACATGAAGGCCCAAGAGATGATTTCTGAACTCAGGCAACGAAATTTTAC 2580
Db 2521 CAAAGGAACATGAAGGCCCAAGAGATGATTTCTGAACTCAGGCAACGAAATTTTAC 2580
Qy 2581 CTGAGACACAGGCTGGGAAATTGAGAGCCAGAACCGAAACTGAGAGCAGCTGAG 2640
Db 2581 CTGAGACACAGGCTGGGAAATTGAGAGCCAGAACCGAAACTGAGAGCAGCTGAG 2640
Qy 2641 AAGATCACCAACCAACCAACCACTGACAAAGATTCGCTGTGAACTGAGACAAAGTTG 2700
Db 2641 AAGATCACCAACCAACCAACCACTGACAAAGATTCGCTGTGAACTGAGACAAAGTTG 2700
Qy 2701 CGGAGAGTCACTTAAGCAACGAGAGCAAGAACTGAGCTCAAGGCCAGCTCAGAG 2760
Db 2701 CGGAGAGTCACTTAAGCAACGAGAGCAAGAACTGAGCTCAAGGCCAGCTCAGAG 2760
Qy 2761 CTACAGCTCTCCCTGAGAGCGCGAGTCAAGTGAACAGCCCTGACAGGCTGACGGGCG 2820
Db 2761 CTACAGCTCTCCCTGAGAGCGCGAGTCAAGTGAACAGCCCTGACAGGCTGACGGGCG 2820
Qy 2821 GCCCTGAGAGCCAGCTTGGCCAGGCGGAAACAGACTGGAAGACCAACAGAAAGCT 2880
Db 2821 GCCCTGAGAGCCAGCTTGGCCAGGCGGAAACAGACTGGAAGACCAACAGAAAGCT 2880
Qy 2881 GAAAGAGATCCAGGCACTCAGGCACTAAGAGATGAATCCAGGCAAAATTTGATGCT 2940
Db 2881 GAAAGAGATCCAGGCACTCAGGCACTAAGAGATGAATCCAGGCAAAATTTGATGCT 2940
Qy 2941 CTTCTGAACAGCTGTACTGTAAATCAAGACTTGGAGAGCAGCTAAACAGCTGACCGAG 3000
Db 2941 CTTCTGAACAGCTGTACTGTAAATCAAGACTTGGAGAGCAGCTAAACAGCTGACCGAG 3000
Qy 3001 GACAAAGCTGAACCTCAACCAACCAAACTTCTGCTCAAAACACTGATGAGGCTTCT 3060
Db 3001 GACAAAGCTGAACCTCAACCAACCAAACTTCTGCTCAAAACACTGATGAGGCTTCT 3060
Qy 3061 GGGCGCAACGAGAGTTGTAACACTGCGAAGTGAAGTGAACATTCGCGCGGAGATC 3120
Db 3061 GGGCGCAACGAGAGTTGTAACACTGCGAAGTGAAGTGAACATTCGCGCGGAGATC 3120
Qy 3121 ACGGAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
Db 3121 ACGGAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3180
Qy 3181 TGCACCAATGCTGAGAGCAAGTCAATGATTTGGAGGCTTAAAGATGAGTCTGAGAA 3240
Db 3181 TGCACCAATGCTGAGAGCAAGTCAATGATTTGGAGGCTTAAAGATGAGTCTGAGAA 3240
Qy 3241 AAAAGAGCGCAGTGGAGGCTGAGAGAGCGCTCGGGGATGAGAAATCCAGATTGAG 3300
Db 3241 AAAAGAGCGCAGTGGAGGCTGAGAGAGCGCTCGGGGATGAGAAATCCAGATTGAG 3300

QY 3301 TGTGCGTTTCAGAGCTGCAGAGATGCTGGAACCCGAGAAACAGAGAGGCGAGAGCC 3360
DB 3301 TGTGCGTTTCAGAGCTGCAGAGATGCTGGAACCCGAGAAACAGAGAGGCGAGAGCC 3360
QY 3361 GATCAGCGGATCACCGAGTCTCGCAGAGTGTGAGCTGCGAGTGAAGAGACACAGGCT 3420
DB 3361 GATCAGCGGATCACCGAGTCTCGCAGAGTGTGAGCTGCGAGTGAAGAGACACAGGCT 3420
QY 3421 GAGATTCTCGCTTCGACAGAGGCTCTCAAGAGCAGAAAGCTGAAGGCGGAGAGCTCTCT 3480
DB 3421 GAGATTCTCGCTTCGACAGAGGCTCTCAAGAGCAGAAAGCTGAAGGCGGAGAGCTCTCT 3480
QY 3481 GACAACTCAATGACTCTGAGAGAAAGAGATCTTCTGTAATGAAATGCCGAAGCTTA 3540
DB 3481 GACAACTCAATGACTCTGAGAGAAAGAGATCTTCTGTAATGAAATGCCGAAGCTTA 3540
QY 3541 CAGCAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGGCTTCTGAAAGCAGAGCCAA 3600
DB 3541 CAGCAGAGCTGAGAGCTGAACGAGAGCTCAACAGAGGCTTCTGAAAGCAGAGCCAA 3600
QY 3601 TTACAGCAGCAGATGAGACTGTCAGAAAAATCAATTTTCCGTCTGACTCAAGAGCTGCA 3660
DB 3601 TTACAGCAGCAGATGAGACTGTCAGAAAAATCAATTTTCCGTCTGACTCAAGAGCTGCA 3660
QY 3661 GAAGCTTAGATCGGCGCTGATCTACTGAGAGCAGAAAGAGTGAAGTCTGAGATCACTG 3720
DB 3661 GAAGCTTAGATCGGCGCTGATCTACTGAGAGCAGAAAGAGTGAAGTCTGAGATCACTG 3720
QY 3721 GAAACACTGAGTCTCTATTTCTATGTAAGAAAGTGAAGAAATGAAAGGACATTTCTCA 3780
DB 3721 GAAACACTGAGTCTCTATTTCTATGTAAGAAAGTGAAGAAATGAAAGGACATTTCTCA 3780
QY 3781 CAACCAAACTCAATGATTTTCTGCAAGCCCAAAATGAGCAACCTGCTAAAAAGAAAAAG 3840
DB 3781 CAACCAAACTCAATGATTTTCTGCAAGCCCAAAATGAGCAACCTGCTAAAAAGAAAAAG 3840
QY 3841 GTTCTCTGCAAGTACATGAGCTGAGAGTGGCCCTGAGAAAGAGAAAGCTCGCTGTCGA 3900
DB 3841 GTTCTCTGCAAGTACATGAGCTGAGAGTGGCCCTGAGAAAGAGAAAGCTCGCTGTCGA 3900
QY 3901 GAGCTAAGAGAGCCCTTCAGAAACCCGCAATCGAGCTCCGCTCCGCGGAGAGAAAGCT 3960
DB 3901 GAGCTAAGAGAGCCCTTCAGAAACCCGCAATCGAGCTCCGCTCCGCGGAGAGAAAGCT 3960
QY 3961 GCCCAGCGCAAGAGAGAGAGACCCCAACCCATTCAGCGAGCCACCGAGGAGAGAG 4020
DB 3961 GCCCAGCGCAAGAGAGAGAGACCCCAACCCATTCAGCGAGCCACCGAGGAGAGAG 4020
QY 4021 ATGCGCATGTCGCGCATCTGTCGAGTGCAGAGACCAAGCCAGTGCATGAGGCTGCTG 4080
DB 4021 ATGCGCATGTCGCGCATCTGTCGAGTGCAGAGACCAAGCCAGTGCATGAGGCTGCTG 4080
QY 4081 GCCCGGCAATTCAGCGGAGAGAGAGAGTCTTCACTCAGAGAGAAATTAATGTCGCGCTT 4140
DB 4081 GCCCGGCAATTCAGCGGAGAGAGAGAGTCTTCACTCAGAGAGAAATTAATGTCGCGCTT 4140
QY 4141 AAGGAAGCATGAGCAACATATTCCTCAACGATTCAGAGTGAAGCTGAAGCATGAGAGCC 4200
DB 4141 AAGGAAGCATGAGCAACATATTCCTCAACGATTCAGAGTGAAGCTGAAGCATGAGAGCC 4200
QY 4201 ACAAGT 4260
DB 4201 ACAAGT 4260
QY 4261 GAATGTGAGT 4320
DB 4261 GAATGTGAGT 4320
QY 4321 CCTGCTGAATATGCAACATTTCAACGAGGCTTTCTGCGCTGACAAATATGATCTCCCA 4380
DB 4321 CCTGCTGAATATGCAACATTTCAACGAGGCTTTCTGCGCTGACAAATATGATCTCCCA 4380
QY 4381 GGTCTCAGACCAAGAGGCCAGAGAGCTTGTGACCTGAAAGGAGTGTGTGTGTGTGTGT 4440

DB 4381 GGTCTCAGACCAAGAGGCCAGAGAGCTTGTGACCTGAAAGGAGTGTGTGTGTGTGTGTGT 4440
QY 4441 AGGAATTAACAAAGAGAGACAGAAAGCTGAGACAGAAAGTACATTTGCTCTGAGAGATCA 4500
DB 4441 AGGAATTAACAAAGAGAGACAGAAAGCTGAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGT 4500
QY 4501 AAAGCTCTATTTATGCAATTAAGCAGAGAAAGCTGAGACAGAGGCGGTGGAAGATTT 4560
DB 4501 AAAGCTCTATTTATGCAATTAAGCAGAGAAAGCTGAGACAGAGGCGGTGGAAGATTT 4560
QY 4561 GAGCTGTGCTTCCCGAGGAGAGTGTATCTATTCATGAGTGTGTGTGTGTGTGTGTGTGTGT 4620
DB 4561 GAGCTGTGCTTCCCGAGGAGAGTGTATCTATTCATGAGTGTGTGTGTGTGTGTGTGTGTGT 4620
QY 4621 GCAAAATACAGCAAGAGAGATGTCCTATACATGTAAGTGAAGTGAATCTCACCCGACACC 4680
DB 4621 GCAAAATACAGCAAGAGAGATGTCCTATACATGTAAGTGAAGTGAATCTCACCCGACACC 4680
QY 4681 ACCTGTGAGCCGAGAGAACCTCTACTGTGCTAGCTCCAGCTTCCCTGACAAACAGCCG 4740
DB 4681 ACCTGTGAGCCGAGAGAACCTCTACTGTGCTAGCTCCAGCTTCCCTGACAAACAGCCG 4740
QY 4741 TGGGTCAACGCTTGAATATGATGTGTGAGAGTGGGAGTGTGTGTGTGTGTGTGTGTGTGT 4800
DB 4741 TGGGTCAACGCTTGAATATGATGTGTGAGAGTGGGAGTGTGTGTGTGTGTGTGTGTGTGT 4800
QY 4801 GGTGATGCTAAACGCTTGGAAACTCCCTGCTGAACTGGAAGGTGATGACCTGTAGAC 4860
DB 4801 GGTGATGCTAAACGCTTGGAAACTCCCTGCTGAACTGGAAGGTGATGACCTGTAGAC 4860
QY 4861 ATGAATGACAGCTGCTGCTTCACTGAGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920
DB 4861 ATGAATGACAGCTGCTGCTTCACTGAGACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 4920
QY 4921 TAGGCTTGAATGT 4980
DB 4921 TAGGCTTGAATGT 4980
QY 4981 CAATTTATATTTATCAAGAGACTGAGAGCTACTCATGATGAGAGAGAGAGAGGAGCA 5040
DB 4981 CAATTTATATTTATCAAGAGACTGAGAGCTACTCATGATGAGAGAGAGAGAGGAGCA 5040
QY 5041 CTGTGTCTGTGAGCTGGAAGAAAGTGAACAGTCCCTGAGCCAGTCCACTGCTGCC 5100
DB 5041 CTGTGTCTGTGAGCTGGAAGAAAGTGAACAGTCCCTGAGCCAGTCCACTGCTGCC 5100
QY 5101 CAGCCGACATCTCAACCAATTTTGAAGCTGTCAAGGAGCTGCACTTGTGTGTGTGTGTGT 5160
DB 5101 CAGCCGACATCTCAACCAATTTTGAAGCTGTCAAGGAGCTGCACTTGTGTGTGTGTGTGT 5160
QY 5161 GGCAGATTGAGAAAGGAGCTCTGATCTGTGAGCCATGAGCCAGCAAGTGTGTGTGTGTGT 5220
DB 5161 GGCAGATTGAGAAAGGAGCTCTGATCTGTGAGCCATGAGCCAGCAAGTGTGTGTGTGTGT 5220
QY 5221 CGCTACAGCAAAACCTCAGCAATATCTGATCCGAAAGAGATAGAGACTCTCAGAGCC 5280
DB 5221 CGCTACAGCAAAACCTCAGCAATATCTGATCCGAAAGAGATAGAGACTCTCAGAGCC 5280
QY 5281 TGCAGCTGTATCCACTTCAACCAATTAAGATCTCTATTTGAAACCAATTAATTTACGAA 5340
DB 5281 TGCAGCTGTATCCACTTCAACCAATTAAGATCTCTATTTGAAACCAATTAATTTACGAA 5340
QY 5341 ATGCAATGAGAGAGTACAGGCTGAGAGAAATCTGTGATTAAGATGACATTCCTGTGCA 5400
DB 5341 ATGCAATGAGAGAGTACAGGCTGAGAGAAATCTGTGATTAAGATGACATTCCTGTGCA 5400
QY 5401 CCTGCTGT 5460
DB 5401 CCTGCTGT 5460
QY 5461 GCAGGAGAGAGAGATCTTGT 5520

Db 5461 GCAGGCGACGAGAGAGTACTTGTGTTTCCACGAAATTGGAGTGTGATTTCT 5520
 QY 5521 TACGGAAGAGCTAGCCGACAGACGATCTCAAGTGAAGTCTTACCTTTGGCTTTGCC 5580
 Db 5521 TACGGAAGAGCTAGCCGACAGACGATCTCAAGTGAAGTGTGCTTACCTTTGGCTTTGCC 5580
 QY 5581 TACGGAAGAGCTAGCCGACAGACGATCTCAAGTGAAGTGTGCTTACCTTTGGCTTTGCC 5580
 Db 5581 TACGGAAGAGCTAGCCGACAGACGATCTCAAGTGAAGTGTGCTTACCTTTGGCTTTGCC 5580
 QY 5641 GCAAGCTCTCAGAGAGAGACCCCTGCGAGAGCTAGTACGATCCGAGCCGCGCTAC 5700
 Db 5641 GCAAGCTCTCAGAGAGAGACCCCTGCGAGAGCTAGTACGATCCGAGCCGCGCTAC 5700
 QY 5701 CTGGGCGCTTGCATTTCTCTCAGAGAGAGATTTACTTGGCGTCTCATACAGATTAATTA 5760
 Db 5701 CTGGGCGCTTGCATTTCTCTCAGAGAGAGATTTACTTGGCGTCTCATACAGATTAATTA 5760
 QY 5761 AGGCTCATTTGCTGCAAGAGAGAACTGTGAGAGATCCGCACTGAACACACCGGGGC 5820
 Db 5761 AGGCTCATTTGCTGCAAGAGAGAACTGTGAGAGATCCGCACTGAACACACCGGGGC 5820
 QY 5821 CCGTCCACTCCGCGAG 5837
 Db 5821 CCGTCCACTCCGCGAG 5837

RESULT 15.

ADFe0993

ADFe0993 standard; cDNA; 6162 BP.

AC ADF60993;

DT 12-FEB-2004 (first entry)

DE ORF of pain associated human gene, 2207.

KW Pain modulation; pain disorder; painful disorder; potassium channel;
 KW kinase expression; inflammatory pain; chronic pain; neuropathic pain;
 KW analgesia; fibromyalgia; cancer pain; migraine; headache; tissue pain;
 KW analgesic; antiinflammatory; gene; ss.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT CDS 1..6162
 FT /*tag= a
 FT /product= "2207 polypeptide"
 PN US003153525-A1.

PD 14-AUG-2003.

PF 19-DEC-2002; 2002US-00325430.

PR 19-DEC-2001; 2001US-0341953P.

PA (MILL-) MILLENNIUM PHARM INC.

PI Silos-Santiago I, Rosenfeld JB;

DR WPI, 2003-897732/82.

XX P-PSDB; ADFe0994.

PT Identifying a compound capable of treating a pain disorder comprises
 PT assaying the ability of the compound to modulate specific, e.g., kinases
 PT or potassium channel, nucleic acid expression or polypeptide activities.
 XX Disclosure; SEQ ID NO 11, 80bp; English.

CC The present invention relates to a method for identifying a compound
 CC capable of modulating pain or painful disorders. The method comprises
 CC assaying the ability of the compound to modulate specific nucleic acid

CC expression or polypeptide activity e.g. potassium channel, or kinase
 CC expression/activity. The method and compounds are useful for treating
 CC pain or painful disorders e.g. inflammatory pain, chronic pain,
 CC neuropathic pain, causalgia, fibromyalgia, cancer pain, migraine/headache
 CC pain and tissue pain. The present sequence encodes a human protein
 CC associated with pain.

SQ Sequence 6162 BP; 1746 A; 1528 C; 1680 G; 1208 T; 0 U; 0 Other;

Query Match 91.8%; Score 5661.4; DB 10; Length 6162;

Best Local Similarity 95.8%; Pred. No. 0;

Matches 5944; Conservative 0; Mismatches 16; Indels 243; Gaps 3;

QY 1 ATGTTGAAGTTCAAAATATGAGAGCGCGAATCTTTGAGTCTGTGCTGAACCCATT 60
 Db 1 ATGTTGAAGTTCAAAATATGAGAGCGCGAATCTTTGAGTCTGTGCTGAACCCATT 60
 QY 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCAA 120
 Db 61 GCCAGCGGGGCTCCAGGCTGAATCTGTTCTTCCAGGGGAAACCACTTTATGACTCAA 120
 QY 121 CAGCAGATGCTCTCTTCCGAGAGAGGATTTAGATGCCCTTGTCTCTTTGAA 180
 Db 121 CAGCAGATGCTCTCTTCCGAGAGAGGATTTAGATGCCCTTGTCTCTTTGAA 180
 QY 181 GAATGAGTCAAGCTGCTGATGAAGATTAACAGTGAACATTTGTCCGGAAGTAT 240
 Db 181 GAATGAGTCAAGCTGCTGATGAAGATTAACAGTGAACATTTGTCCGGAAGTAT 240
 QY 241 TCCGACACCATAGCTGATTAACAGAGCTCCAGCTTCCGCAAGACATTCGAATCAGA 300
 Db 241 TCCGACACCATAGCTGATTAACAGAGCTCCAGCTTCCGCAAGACATTCGAATCAGA 300
 QY 301 AGTCTTGAGTGTGTGTGCTGACCTTGTGAGAGTCAAGTGTGAGAGAGAACCCGGG 360
 Db 301 AGTCTTGAGTGTGTGTGCTGACCTTGTGAGAGTCAAGTGTGAGAGAGAACCCGGG 360
 QY 361 GACATCTATGCTATGAAGATGATGAAGAGAGGCTTTATTTGGCCGAGAGAGTTTCA 420
 Db 361 GACATCTATGCTATGAAGATGATGAAGAGAGGCTTTATTTGGCCGAGAGAGTTTCA 420
 QY 421 TTTTGTGAGAGAGAGGCGAATATTTATCTCCAGACACAAAGCCGTGATCCCCAAATTA 480
 Db 421 TTTTGTGAGAGAGAGGCGAATATTTATCTCCAGACACAAAGCCGTGATCCCCAAATTA 480
 QY 481 CAGTATGCTTTCAGAGACAAATATCACTTTATCTGATGAGAGATATCAAGCTGAGAGG 540
 Db 481 CAGTATGCTTTCAGAGACAAATATCACTTTATCTGATGAGAGATATCAAGCTGAGAGG 540
 QY 541 GACTTGCTGCTCACTTTGATATGATATGAGACCACTTATGATGAGAGAGAGTTTCA 600
 Db 541 GACTTGCTGCTCACTTTGATATGATATGAGACCACTTATGATGAGAGAGAGTTTCA 600
 QY 601 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCTTCATCTGATGAGAGATATCAAGCTGAGAGG 660
 Db 601 TACCTAGCTGAGCTGATTTTGGCTGTTCACAGCTTCATCTGATGAGAGATATCAAGCTGAGAGG 660
 QY 661 GACATCAAGCTGAGAGACATTTCTGTTGACCGGACAGACATCAAGCTGAGAGTTT 720
 Db 661 GACATCAAGCTGAGAGACATTTCTGTTGACCGGACAGACATCAAGCTGAGAGTTT 720
 QY 721 GGATCTGCGCGAATAATGAAATCAAAAGATGTAATCCAACTCCGATTTGGAGCC 780
 Db 721 GGATCTGCGCGAATAATGAAATCAAAAGATGTAATCCAACTCCGATTTGGAGCC 780
 QY 781 CCAATTAATAGCTCTCTGAAAGTCTGACTGATGAGAACGCGAGATGAAAGGACATTC 840
 Db 781 CCAATTAATAGCTCTCTGAAAGTCTGACTGATGAGAACGCGAGATGAAAGGACATTC 840
 QY 841 GGCCTGAGCTGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGAGAG 900
 Db 841 GGCCTGAGCTGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGATGAGTGTGAGAG 900

QY 901 TCCCCCTTCGAGAGGGAACCTTCGCAAGAACCTTCAATAACATTATGAATTTCCAGCG 960
Db 901 TCCCCCTTCGAGAGGGAACCTTCGCAAGAACCTTCAATAACATTATGAATTTCCAGCG 960
QY 961 TTTTGAATTTTCAGATGACCCCAAGTAGAGCATCTTCTTGATCTGATTCAGAGC 1020
Db 961 TTTTGAATTTTCAGATGACCCCAAGTAGAGCATCTTCTTGATCTGATTCAGAGC 1020
QY 1021 TTGTTGCGCGCCGAGAAAGAGAGACTGAAGTTTGAAGGTCCTTTCCTCCATCCTTTCTC 1080
Db 1021 TTGTTGCGCGCCGAGAAAGAGAGACTGAAGTTTGAAGGTCCTTTCCTCCATCCTTTCTC 1080
QY 1081 TCTTAAATTTGATGAGAACATCTGTAATCTCTCTCCCTCTGTTTCCACCTCAAG 1140
Db 1081 TCTTAAATTTGATGAGAACATCTGTAATCTCTCTCCCTCTGTTTCCACCTCAAG 1140
QY 1141 TCTGACATGACACCTCCATTTTGTATGAAACAGAGAAATTTGTTGGGTTTCACTCT 1200
Db 1141 TCTGACATGACACCTCCATTTTGTATGAAACAGAGAAATTTGTTGGGTTTCACTCT 1200
QY 1201 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGTTGAGAACTGCCGTTTGTGGGTTTTCG 1260
Db 1201 CCGTGCCAGCTGAGCCCTCAGGCTTCTCGGTTGAGAACTGCCGTTTGTGGGTTTTCG 1260
QY 1261 TACAGCAAGGCACTGGGGAATCTTGTATGATCTGATGCTGTTGTGCGGCTTGACTCC 1320
Db 1261 TACAGCAAGGCACTGGGGAATCTTGTATGATCTGATGCTGTTGTGCGGCTTGACTCC 1320
QY 1321 CCGGCCAAGCTAGCTCCATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTTCAAGAC 1380
Db 1321 CCGGCCAAGCTAGCTCCATGAGAAAGAACTTCTCATCAAAAGCAAGAGCTTCAAGAC 1380
QY 1381 TCTCAGAGCAAGTGTCAACAAGATGAGCAGAGAAATGACCCGGTTTCACTCGGAGTGTCA 1440
Db 1381 TCTCAGAGCAAGTGTCAACAAGATGAGCAGAGAAATGACCCGGTTTCACTCGGAGTGTCA 1440
QY 1441 GAGGTGAGGCTGTGCTTAACTCAGAGAGAGGTGAGGCTGAAGGCTCTGAGACTCAGAGA 1500
Db 1441 GAGGTGAGGCTGTGCTTAACTCAGAGAGAGGTGAGGCTGAAGGCTCTGAGACTCAGAGA 1500
QY 1501 TCCCTCCTGAGAGAGAGCTTGTCTAATCAATCAAGATTCAGTACTTAAAGCAAGT 1560
Db 1501 TCCCTCCTGAGAGAGAGCTTGTCTAATCAATCAAGATTCAGTACTTAAAGCAAGT 1560
QY 1561 TTGGAGCAAGCAGAGTAGAGGTGTCCAGAGAGATGACAAAGCACTGACGCTCTCAT 1620
Db 1561 TTGGAGCAAGCAGAGTAGAGGTGTCCAGAGAGATGACAAAGCACTGACGCTCTCAT 1620
QY 1621 GATATCAGAGAGCAGAGCCGAGAGCTTCAAGAAATCAAGAGCAGAGTACAGGCTCAA 1680
Db 1621 GATATCAGAGAGCAGAGCCGAGAGCTTCAAGAAATCAAGAGCAGAGTACAGGCTCAA 1680
QY 1681 GTGGAAGAAATGAGGTGATGATGATCAAGTTGGAAGAGATCTTGTCTCAGCAAGAGA 1740
Db 1681 GTGGAAGAAATGAGGTGATGATGATCAAGTTGGAAGAGATCTTGTCTCAGCAAGAGA 1740
QY 1741 CGAGGTATCTCTAAGATCTGAGCTGAGAGGCTGCGGCTTGCTGTAAGAAATTCAG 1800
Db 1741 CGAGGTATCTCTAAGATCTGAGCTGAGAGGCTGCGGCTTGCTGTAAGAAATTCAG 1800
QY 1801 CGGAAGAGCAGAGATGTCAGCATTAACCTGTTGAAGCTTAAGATCAAGGGAAGCTGAA 1860
Db 1801 CGGAAGAGCAGAGATGTCAGCATTAACCTGTTGAAGCTTAAGATCAAGGGAAGCTGAA 1860
QY 1861 GTGGAGAAATATGCGAAATGAGAGAGATCAATGCTGAGCAGAGCTCAAAATTCAGAG 1920
Db 1861 GTGGAGAAATATGCGAAATGAGAGAGATCAATGCTGAGCAGAGCTCAAAATTCAGAG 1920
QY 1921 CTCGAAGAGAACTGGAAGAGGCTGTAAAGCCAGCAGCAGAGGCAACGAGCTGCTCAG 1980
Db 1921 CTCGAAGAGAACTGGAAGAGGCT- 1944
QY 1981 AATATCCGCAAGGCAAGAGAGCAGCCGAGAGGAGGAGCTGAGAACTGCAAGAACGAGAG 2040

Db 1945 -----GCAAGAGAGCCGAGAGGAGCTGAGAAAGCTGCAAGAACGAGAG 1992
QY 2041 GATTCCTCTGAAGGCAATCAGAAAGAGCTGTGAGACTGAGAGACCCGCTATCTCTG 2100
Db 1993 GATTCCTCTGAAGGCAATCAGAAAGAGCTGTGAGACTGAGAGACCCGCTATCTCTG 2052
QY 2101 GAGAACAGGTAAAGAGACTGAGAGCCTAGAGCGTGAAGAGAAACAGACTGAAGATGAC 2160
Db 2053 GAGAACAGGTAAAGAGACTGAGAGCCTAGAGCGTGAAGAGAAACAGACTGAAGATGAC 2112
QY 2161 ATCCAGCAAAATCCCAAGATCCAGATGAGATGAGTGAATTAATCTGAGCTGAGAGAG 2220
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QY 2221 AAACATGAGGAGGCCCAAGCTCAGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2280
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QY 2281 CAGCACTATGAGAGAAAGATTAAGTGTGGAACAATGATTAAGAAAGACTGCTGAC 2340
Db 2233 CAGCACTATGAGAGAAAGATTAAGTGTGGAACAATGATTAAGAAAGACTGCTGAC 2292
QY 2341 AAGGAGCACTGAGAGAACTGATGAGAGACAGAGAGAGAGGCTTGAAGAGGCAAA 2400
Db 2293 AAGGAGCACTGAGAGAACTGATGAGAGACAGAGAGAGAGGCTTGAAGAGGCAAA 2352
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QY 2461 CAGAGATTTGTGAATCTGTCTGAAGCCAAATTAACCTGCAAGAAATGACAGTCTTTTACC 2520
Db 2413 CAGAGATTTGTGAATCTGTCTGAAGCCAAATTAACCTGCAAGAAATGACAGTCTTTTACC 2472
QY 2521 CAAAGGAACATGAAGGCCCAAGAGAGATGATTTCTGAATCAGGCAACAGAAATTTTAC 2580
Db 2473 CAAAGGAACATGAAGGCCCAAGAGAGATGATTTCTGAATCAGGCAACAGAAATTTTAC 2532
QY 2581 CTGAGAGCAAGGCTGGGAGGTTGAGAGGCCAGAACCGAAACTGAGAGAGCAGCTGAG 2640
Db 2533 CTGAGAGCAAGGCTGGGAGGTTGAGAGGCCAGAACCGAAACTGAGAGAGCAGCTGAG 2592
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QY 2701 CGGAGGTCACTTGAAGCAGAGAGCAGAGAACTGAGGCTCAAGGCCAGCTCAGAG 2760
Db 2653 CGGAGGTCACTTGAAGCAGAGAGCAGAGAACTGAGGCTCAAGGCCAGCTCAGAG 2712
QY 2761 CTACAGCTCCCTCGAGAGAGCCGAGTCAAGTTGACAGCCCTGCAAGGCTGACAGGCGG 2820
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QY 2821 GCCCTGAGAGCAGCTTCCGCAAGGCAAGAGCAGAGCTGGAAGAGACCAAGAGAGCT 2880
Db 2773 GCCCTGAGAGCAGCTTCCGCAAGGCAAGAGCAGAGCTGGAAGAGACCAAGAGAGCT 2832
QY 2881 GAAAGAGATTCAGAGCACTCAGGCAATGAGATGAATTCAGCGCAATTTGATGCT 2940
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Db 2953 GACCAAGCTGACCTCAACCAAGCAAACTTCACTTGTCCAACCAATCTGATGAGGCTTCT 3012
QY 3061 GGGCCCAAGCAGAGATTGTACACTGCAAGTGAAGTGAACCATCTCGCCGGAGATC 3120

Dh 3013 GGCGCCAACGACGATTGTACAACTGCGAAGTGAAGTGCATCTCCCGCGGAGATC 3072
Qy 3121 ACCGAACGAGAGATGACGCTTACACGCCAGAAACAAAGATGAGGCTTGAAGACACG 3180
Db 3073 ACCGAACGAGAGATGACGCTTACACGCCAGAAACAAAGATGAGGCTTGAAGACACG 3132
Qy 3181 TGCACATGCTGGAGAAACAGGTGATGATTTGGAGGCCCTTAACGATGAGCTGCTGAA 3240
Db 3133 TGCACATGCTGGAGAAACAGGTGATGATTTGGAGGCCCTTAACGATGAGCTGCTGAA 3192
Qy 3241 AAAGAGCGGAGTGGAGAGGCTGGAGAGGCGTCTGGGTGATGAGAAATCCCACTTGAG 3300
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Qy 3301 TGTGGGTTTGAGAGCTGCGAGAGATGCTTGACAACCGAAGAACAGACAGGCGAGAGCC 3360
Db 3253 TGTGGGTTTGAGAGCTGCGAGAGATGCTTGACAACCGAAGAACAGACAGGCGAGAGCC 3312
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Db 3313 GATCAGCGGATCACCGGATCTCGCGAGTGTGAGCTGGCAGTGAAGAGACACAAAGCT 3372
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Db 3373 GAGATTCTCGCTCTGACGACGCTCTCAAGAGCAGAGCTGAAGGCGGAGAGCTCTCT 3432
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Qy 3541 CACGAGAGCTGAGACTGAAACGAGGCTGAACAGAGGCTTGGAGAGGCAAGCCAAA 3600
Db 3493 CACGAGAGCTGAGACTGAAACGAGGCTGAACAGAGGCTTGGAGAGGCAAGCCAAA 3552
Qy 3601 TTACAGCAGCAGATGAGACTGCGAAGAAATACATTTCCGTCGACTCAAGACCTGCA 3660
Db 3553 TTACAGCAGCAGATGAGACTGCGAAGAAATACATTTCCGTCGACTCAAGACCTGCA 3612
Qy 3661 GAAGCTTAGATGCGGCTGATCTTAGAGACAGAAAGAAAGTGAAGTGAAGTACAGCTG 3720
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Qy 3721 GAAAAATTCAGGTTCTTATTTCTCATGAAAAGTGAAGTGAAGGCACTATTTCTCA 3780
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Qy 3781 CAAACCAAACTCATGATTTTCTGCAAGCCAAATGGAACCACTGTGTAAGAAAAAGAAA 3838
Db 3733 CAAACCAAACTCATGATTTTCTGCAAGCCAAATGGAACCACTGTGTAAGAAAAAG 3792
Qy 3839 -----AGGTTCTCTGCAATAC 3855
Db 3793 GGTTTATTTAGTCGACGAAAGAGACCTGCTTTACCCACACAGGTTCTCTGCAATAC 3852
Qy 3856 AATGACCTGAAGTGGCCCTTGAAGAGAGAAAGTCTGCTGTCAAGAGCTTAGAGAAAGCC 3915
Db 3853 AATGACCTGAAGTGGCCCTTGAAGAGAGAAAGTCTGCTGTCAAGAGCTTAGAGAAAGCC 3912
Qy 3916 CTTTCAGAAAGCCCGCATGCGACTCGGTCGCGCCGGGAGGAAAGCTGCCACCGCAAGCA 3975
Db 3913 CTTTCAGAAAGCCCGCATGCGACTCGGTCGCGCCGGGAGGAAAGCTGCCACCGCAAGCA 3972
Qy 3976 ACGGACCAACCAACCCATTCAGCGCCAGCCACCGGAGGAGCAGATGCGCATGTCCGCC 4035
Db 3973 ACGGACCAACCAACCCATTCAGCGCCAGCCACCGGAGGAGCAGATGCGCATGTCCGCC 4032
Qy 4036 ATTCGTGGGTTCGCGAGAGCAGAGCCAGGCTGCTGAGCTGTGGCCCGCGCATTCAGC 4095
Db 4033 ATTCGTGGGTTCGCGAGAGCAGAGCCAGGCTGCTGAGCTGTGGCCCGCGCATTCAGC 4092
Qy 4096 CCGAGAAAGAGTCTTCAACTCCAGAGGAATTTAGTCGGGCTTTAAGAAAGCATGAC 4155
Db 4093 CCGAGAAAGAGTCTTCAACTCCAGAGGAATTTAGTCGGGCTTTAAGAAAGCATGAC 4152

Qy 4156 CACAATTTCTCTACCGATTCAACGTAGACTGAACATGCGAGCCACAAAGTGTGCTGTG 4215
Db 4153 CACAATTTCTCTACCGATTCAACGTAGACTGAACATGCGAGCCACAAAGTGTGCTGTG 4212
Qy 4216 TGTCTGATACCGGTGACCTTTGAGACGCGACGATCCAAAGTGTCCGAATGTGAGGTATG 4275
Db 4213 TGTCTGATACCGGTGACCTTTGAGACGCGACGATCCAAAGTGTCTCGAATGTGAGGTATG 4272
Qy 4276 TGTACCCCAAGTGTCTCCACGTCCTTGCACGACCTCGGCTTGCCTGTGATATGCC 4335
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Qy 4336 ACACACTTCAACGAGGCTTTCGCGGTGACAAATGAACTTCCAGGTCTTCAGACCAAG 4395
Db 4333 ACACACTTCAACGAGGCTTTCGCGGTGACAAATGAACTTCCAGGTCTTCAGACCAAG 4392
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Db 4393 GAGCCCAAGCAGAGCTTTCGACCTTGAAGGTTGATGAAGTGTCCAGGAATTAACAAAG 4452
Qy 4456 GGAACAGCAAGGCTGGAGACAGAGATCAATGTCCTGAGAGGATCAAAAGTCTCATTTAT 4515
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Qy 4516 GACATGAAACGAGAGAGCTGGAACAGAGGCGGTGGAAGATTTGAGCTGTGCTTCCC 4575
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Qy 4576 GACGGGAGTATCTTATTTCAATGTTGCGGTTGTCGTTCCGAATCCCAATACAGCCAA 4635
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Qy 4636 GCAGATGTCCCAATCACTAGTAAGATGAAATCAACCCGCAACCACTTGCCCGCGG 4695
Db 4633 GCA----- 4635
Qy 4696 AGAACCTTACTTGTAGCTCCAGCTTCCCTGACAAACAGCGTGGGTACCGCCTTA 4755
Db 4636 ----- 4635
Qy 4756 GAATCAGTTGTGCGAGGTGGAGAGTTTCTAGGAGAAAAAGCAACTGATGCTAAACTG 4815
Db 4636 -----GAAAAAGCAAGACTGATGCTAAACTG 4662
Qy 4816 CTTGGAACCTCCCTGTAACCTGAGAGGTGATGACCGTCTAGACATGAACTGACGCTG 4875
Db 4663 CTTGGAACCTCCCTGTAACCTGAGAGGTGATGACCGTCTAGACATGAACTGACGCTG 4722
Qy 4876 CCGTTCAGTGACCAAGTGTGTTGTGGCACCGAGAAAGGCTCTAGCGCCCTGAATGTC 4935
Db 4723 CCGTTCAGTGACCAAGTGTGTTGTGGCACCGAGAAAGGCTCTAGCGCCCTGAATGTC 4782
Qy 4936 TTGAAAAAATCCCTTAACCATGTCCAGGAATTTGAGAGCTTCCAAATTTATATATATC 4995
Db 4783 TTGAAAAAATCCCTTAACCATGTCCAGGAATTTGAGAGCTTCCAAATTTATATATATC 4842
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Db 4843 AAGGACCTGAGAGAGTACTCATGATAGCAGAGAAAGACGGGACCTGTGCTTGAGAC 4902
Qy 5056 GTGAAGAAAGTGAACAGTCCCTGGCCAGTCCCACTTGCCAGCCGACATCTGA 5115
Db 4903 GTGAAGAAAGTGAACAGTCCCTGGCCAGTCCCACTTGCCAGCCGACATCTGA 4962
Qy 5116 CCCAACATTTTGAAGGCTGTCAAGGGCTGCCACTTGTTTGGGCGACGCAAGTTGAGAC 5175
Db 4963 CCCAACATTTTGAAGGCTGTCAAGGGCTGCCACTTGTTTGGGCGACGCAAGTTGAGAC 5022
Qy 5176 GGGCTCTGACTGTGAGAGCAATGCGCAGCAAAAGTGTGATTTCTCGGCTTCAACAGAAAC 5235
Db 5023 GGGCTCTGACTGTGAGAGCAATGCGCAGCAAAAGTGTGATTTCTCGGCTTCAACAGAAAC 5082

QY 5236 CTGACGAATACTGCAATCCGAAAAGAGATGAGACTCAGAGCCCTGACGCTGTATCCAC 5295
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Db 5083 CTCAGCAAAATACGATCCGAAAAGATGAGACTCAGAGCCCTGACGCTGTATCCAC 5142
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Db 5143 TTCAACCAATTAACGATCTCATTTGGAACCAATAATTCTACGAAATGACATGAGCAG 5202
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Db 5263 GCCTCTTCCAAACAGCTTCCCTGTCTCAATCGTGCAAGTGAACAGCGCAGCGCAGAG 5322
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QY 5476 GAGTACTTGTGTGTGTTTCCAGGAATTTGGAGTGTTCGTGATTTCTTACGGAAGACTAGC 5535
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Db 5323 GAGTACTTGTGTGTGTTTCCAGGAATTTGGAGTGTTCGTGATTTCTTACGGAAGACTAGC 5382
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QY 5536 CGCACAGACGATCTCAAGTGAGTGCCTTACCTTTGGCCTTGGCTACAGAAACCTAT 5595
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Db 5383 CGCACAGACGATCTCAAGTGAGTGCCTTACCTTTGGCCTTGGCTACAGAAACCTAT 5442
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Db 5503 GGGACCCCTGCGCGAGGTACTGGAATCCCGAAACCCGCGCTACCTGGGCTTGCCTAT 5562
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Db 5563 TCCTCAGAGAGGATTTACTTGGCGTCTCATPACAGAGATAAATTAAAGGTCATTGCTGC 5622
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QY 5956 TACCGCGAGGGCGGACCGAGCTGCGAGGACAAGTCTCTTGGCCGCCCCCTGAGCGA 6015
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Db 5803 TACCGCGAGGGCGGACCGAGCTGCGAGGACAAGTCTCTTGGCCGCCCCCTGAGCGA 5862
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QY 6016 GAGAAATCCCCCGGCGGATACTCAGCAACGCGAGAGAGCGGTCCCCCGAGGCTGTTT 6075
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Db 5863 GAGAAATCCCCCGGCGGATACTCAGCAACGCGAGAGAGCGGTCCCCCGAGGCTGTTT 5922
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QY 6076 GAAAGACGACGAGGGCGGCTGCTGCGGAGACCGTGAAGACCCGCTGCCAGGTG 6135
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Db 5923 GAAAGACGACGAGGGCGGCTGCTGCGGAGACCGTGAAGACCCGCTGCCAGGTG 5982
| | | | |
QY 6136 AACAAAGTCTGGGACCAAGTCTT 6158
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Db 5983 AACAAAGGAGAGGGGCAAGTGC 6005
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Search completed: May 16, 2005, 10:21:59
Job time : 1981 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 16:31:18 ; Search time 256 Seconds

(without alignment)
4108.635 Million cell updates/sec

Title: US-10-791-666-2

Sequence: 1 MKFKYGRAPLDNAGAAEPT.....AGAVRPLSGVKNKWDQSSV 2054

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10230.5	97.5	2027	086U09	Q86U09 homo sapien
2	10109.5	96.3	2055	088938	088938 mus musculu
3	8161	77.8	1641	088528	088528 mus musculu
4	7935	75.6	1597	CTRO_MOUSE	P49025 mus musculu
5	7851.5	74.8	1618	090X19	Q9GX19 rattus norv
6	6575	62.7	1286	CTRO_HUMAN	Q14578 homo sapien
7	5057.5	48.2	1032	08C101	Q8C101 mus musculu
8	2492	23.7	482	06XU08	Q6XU08 homo sapien
9	2175.5	20.7	494	088937	088937 mus musculu
10	2160.5	20.6	448	088527	088527 rattus norv
11	1822	17.4	1854	09VU78	Q9VU78 dirosophila
12	1524.5	14.5	1732	054874	Q54874 rattus norv
13	1489	14.2	1719	096X03	Q96X03 homo sapien
14	1440	13.7	1760	09UL05	Q9UL05 homo sapien
15	1438	13.7	1711	09Y552	Q9Y552 homo sapien
16	1420.5	13.5	1713	07TT49	Q7TT49 rattus norv
17	1419.5	13.5	1702	054875	Q54875 rattus norv
18	1418.5	13.5	1713	07TT50	Q7TT50 mus musculu
19	1413.5	13.5	1638	096X02	Q96X02 homo sapien
20	1409.5	13.4	1638	08IM07	Q8IM07 homo sapien
21	1401	13.4	1573	07PW87	Q7PW87 anopheles g
22	1340.5	12.8	1551	06DT37	Q6DT37 homo sapien
23	1316.5	12.5	1592	001583	Q01583 caenorhabdi
24	1279	12.2	1369	ROCI_RAT	Q63644 rattus norv
25	1275.5	12.2	1354	ROCI_MOUSE	P70335 mus musculu
26	1270.5	12.1	1637	09W1B0	Q9W1B0 dirosophila
27	1266.5	12.1	1613	044368	Q44368 dirosophila
28	1263.5	12.0	1388	ROCI_BOVIN	Q28021 bos taurus
29	1260	12.0	1388	ROCI_HUMAN	Q13464 homo sapien
30	1257	12.0	1388	ROCI_HUMAN	Q75116 homo sapien
31	1255.5	12.0	1375	Q90Y37	Q90Y37 brachydanio

32	1250.5	11.9	1388	1	ROCI_MOUSE	P70336 mus musculu
33	1249	11.9	1354	1	ROCI_RABIT	O77819 o rtho-asoc
34	1248.5	11.9	1370	2	O73732	O73732 xenopus lae
35	1232.5	11.7	1379	1	ROCI_RAT	O62868 rattus norv
36	1168	11.1	1390	2	O9U779	O9U779 dirosophila
37	1167	11.1	1390	2	O9VX03	O9VX03 dirosophila
38	1167	11.1	1390	2	O961D4	O961D4 dirosophila
39	1143	10.9	933	2	O86TJ1	O86TJ1 homo sapien
40	1126.5	10.7	1173	2	P92199	P92199 caenorhabdi
41	1075	10.2	865	2	O98SN6	O98SN6 gallus gall
42	1072	10.2	1386	2	O7PRV2	O7PRV2 anopheles g
43	1060.5	10.1	717	2	O8AVM0	O8AVM0 xenopus lae
44	1003.5	9.6	1231	2	O7Q1K8	O7Q1K8 anopheles g
45	925	8.8	492	2	O86X28	O86X28 homo sapien

ALIGNMENTS

RESULT 1	086U09	PRELIMINARY;	PRT; 2027 AA.
ID	086U09		
AC	086U09;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Rho/rac-interacting citron kinase.		
GN	Name=CIT;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
NCBI	TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Huang C.Q., Wu S.L., Shan Y.X., Liu S., Xiao P.J.;		
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.		
CC	-1- SIMILARITY: Contains 1 PH domain.		
DR	EMBL; AY257469; APL3528.1; -		
DR	HSSP; P31751; IMRV.		
DR	GO; GO:0005622; C:intracellular; IEA.		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.		
DR	GO; GO:0005083; F:small GTPase regulatory/interacting protein. . .; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:0007242; P:intracellular signaling cascade; IEA.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPR001180; Citron.		
DR	InterPro; IPR005479; Cphp_synch_L_D2.		
DR	InterPro; IPR002219; DAG_P8-bind.		
DR	InterPro; IPR011009; Kinase_like.		
DR	InterPro; IPR001849; PH.		
DR	InterPro; IPR000961; Pkinase_C.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR000861; REM_repeat.		
DR	InterPro; IPR002290; Ser_thr_kinase.		
DR	InterPro; IPR008271; Ser_thr_kin_AS.		
DR	Pfam; PF00130; Cl_1; 1.		
DR	Pfam; PF00780; CNH; 1.		
DR	Pfam; PF00169; PH; 1.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	Pfam; PF00433; Pkinase_C; 1.		
DR	Prodom; PD000001; Prot_kinase; 1.		
DR	SMART; SM00109; Cl_1; 1.		
DR	SMART; SM00036; CNH; 1.		
DR	SMART; SM00233; PH; 1.		
DR	SMART; SM00220; S_TKc; 1.		
DR	SMART; SM00133; S_TK_X; 1.		
DR	PROSITE; PS00867; CPKase_2; UNKNOWN_1.		
DR	PROSITE; PS00479; DAG_P8_BIND_DOM_1; 1.		
DR	PROSITE; PS00881; DAG_P8_BIND_DOM_2; 1.		
DR	PROSITE; PS00003; PH_DOMAIN; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		

DR PROSITE; PSS0011; PROTEIN KINASE, DOM; 1.
DR PROSITE; PSS0108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 2027 AA; 231429 MW; 6B1D8C3F661F357B CRC64;

Query Match 97.5%; Score 10230.5; DB 2; Length 2027;
Best Local Similarity 97.1%; Pred. No. 2e-285;
Matches 2010; Conservative 1; Mismatches 1; Indels 57; Gaps 2;

QY 1 MLKFKYGARPLDGAAPLPIASRASRLNLFQCKPPTMOQMSPLSREGILDALFVLFE 60
DB 1 MLKFKYGARPLDGAAPLPIASRASRLNLFQCKPPTMOQMSPLSREGILDALFVLFE 60
QY 61 ECGQPALMTIKHVSFPRKTSDDTIAELOEPSAKDFVNSLYCCGPAVQVREKATG 120
DB 61 ECGQPALMTIKHVSFPRKTSDDTIAELOEPSAKDFVNSLYCCGPAVQVREKATG 120
QY 121 DIYAMKMKKKALLAQOVSPFEERNILSRSTSPMIPOLQYAFQDKNHLYLWVEYQPG 180
DB 121 DIYAMKMKKKALLAQOVSPFEERNILSRSTSPMIPOLQYAFQDKNHLYLWVEYQPG 180
QY 181 DLSLNRYEDQDENLQFYLAELILAVSHVLMGVHRDIKENILVDRTGHIKLVD 240
DB 181 DLSLNRYEDQDENLQFYLAELILAVSHVLMGVHRDIKENILVDRTGHIKLVD 240
QY 181 DLSLNRYEDQDENLQFYLAELILAVSHVLMGVHRDIKENILVDRTGHIKLVD 240
DB 181 DLSLNRYEDQDENLQFYLAELILAVSHVLMGVHRDIKENILVDRTGHIKLVD 240
QY 241 GSAAKNSNKNVNAKLPITGPDYAPVLTVMNGDGKTYGLDCDWKSVGVIAVEMTYGR 300
DB 241 GSAAKNSNKNVNAKLPITGPDYAPVLTVMNGDGKTYGLDCDWKSVGVIAVEMTYGR 300
QY 241 GSAAKNSNKNVNAKLPITGPDYAPVLTVMNGDGKTYGLDCDWKSVGVIAVEMTYGR 300
DB 241 GSAAKNSNKNVNAKLPITGPDYAPVLTVMNGDGKTYGLDCDWKSVGVIAVEMTYGR 300
QY 301 SPPEEGSARTFNNIMFQRFKPRDDPKYSDFLDLQSLGCGKRLKFBGICCHPFF 360
DB 301 SPPEEGSARTFNNIMFQRFKPRDDPKYSDFLDLQSLGCGKRLKFBGICCHPFF 360
QY 301 SPPEEGSARTFNNIMFQRFKPRDDPKYSDFLDLQSLGCGKRLKFBGICCHPFF 360
DB 301 SPPEEGSARTFNNIMFQRFKPRDDPKYSDFLDLQSLGCGKRLKFBGICCHPFF 360
QY 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWVSSPCQSPSGFSGEELPFVFGS 420
DB 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWVSSPCQSPSGFSGEELPFVFGS 420
QY 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWVSSPCQSPSGFSGEELPFVFGS 420
DB 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWVSSPCQSPSGFSGEELPFVFGS 420
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHMEQEMRLHRRVS 480
DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHMEQEMRLHRRVS 480
QY 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHMEQEMRLHRRVS 480
DB 421 YSKALGILGRSESVSGLDSPAKTSSMEKKLLIKSKELQDSQDKCHMEQEMRLHRRVS 480
QY 481 EYVAVLISQKVELKASTQSLLEODLATYITTESSIKRSLQARMVSEDDKALQLH 540
DB 481 EYVAVLISQKVELKASTQSLLEODLATYITTESSIKRSLQARMVSEDDKALQLH 540
QY 481 EYVAVLISQKVELKASTQSLLEODLATYITTESSIKRSLQARMVSEDDKALQLH 540
DB 481 EYVAVLISQKVELKASTQSLLEODLATYITTESSIKRSLQARMVSEDDKALQLH 540
QY 541 DIREQSRLQEIKEQEQVQVQVEMRLMMQLEEDLVASARRSDLYSELSRLAAEFK 600
DB 541 DIREQSRLQEIKEQEQVQVQVEMRLMMQLEEDLVASARRSDLYSELSRLAAEFK 600
QY 541 DIREQSRLQEIKEQEQVQVQVEMRLMMQLEEDLVASARRSDLYSELSRLAAEFK 600
DB 541 DIREQSRLQEIKEQEQVQVQVEMRLMMQLEEDLVASARRSDLYSELSRLAAEFK 600
QY 601 RKATECQHKLLKAKDQCKPEVGEYAKLEKINAEOQLKIOELQEKLEKAVASTEATLQ 660
DB 601 RKATECQHKLLKAKDQCKPEVGEYAKLEKINAEOQLKIOELQEKLEKAVASTEATLQ 660
QY 601 RKATECQHKLLKAKDQCKPEVGEYAKLEKINAEOQLKIOELQEKLEKAVASTEATLQ 660
DB 601 RKATECQHKLLKAKDQCKPEVGEYAKLEKINAEOQLKIOELQEKLEKAVASTEATLQ 660
QY 661 NITQAKRRARRELQKONREDSSEGTIKKLVAEERHSHLENKYKRLTETMERENRLKD 720
DB 661 NITQAKRRARRELQKONREDSSEGTIKKLVAEERHSHLENKYKRLTETMERENRLKD 720
QY 661 NITQAKRRARRELQKONREDSSEGTIKKLVAEERHSHLENKYKRLTETMERENRLKD 720
DB 661 NITQAKRRARRELQKONREDSSEGTIKKLVAEERHSHLENKYKRLTETMERENRLKD 720
QY 721 IQTFSQOIQQMADKILELEEKHREAVQSAOHLLEVHLKQKQHYEKKIVLDNOIKQDLAD 780
DB 721 IQTFSQOIQQMADKILELEEKHREAVQSAOHLLEVHLKQKQHYEKKIVLDNOIKQDLAD 780
QY 721 IQTFSQOIQQMADKILELEEKHREAVQSAOHLLEVHLKQKQHYEKKIVLDNOIKQDLAD 780
DB 721 IQTFSQOIQQMADKILELEEKHREAVQSAOHLLEVHLKQKQHYEKKIVLDNOIKQDLAD 780
QY 781 KETLENNMQHBEBAHEKGIKLSQKAMINAMDSKIRSLFORIVELSEANKLAANSLFT 840
DB 781 KETLENNMQHBEBAHEKGIKLSQKAMINAMDSKIRSLFORIVELSEANKLAANSLFT 840
QY 739 KETLENNMQHBEBAHEKGIKLSQKAMINAMDSKIRSLFORIVELSEANKLAANSLFT 798
DB 739 KETLENNMQHBEBAHEKGIKLSQKAMINAMDSKIRSLFORIVELSEANKLAANSLFT 798
QY 841 QRMNKAQEMNISELRQCKFYLETOAGLEAONRQLEQLEKISIQHSDSDKNRLLELETRL 900
DB 841 QRMNKAQEMNISELRQCKFYLETOAGLEAONRQLEQLEKISIQHSDSDKNRLLELETRL 900
QY 799 QRMNKAQEMNISELRQCKFYLETOAGLEAONRQLEQLEKISIQHSDSDKNRLLELETRL 858
DB 799 QRMNKAQEMNISELRQCKFYLETOAGLEAONRQLEQLEKISIQHSDSDKNRLLELETRL 858
QY 901 REVSLHEBQKLEKROLTELOLSQERESQLTALQARAALBSQLEQATLELETTAA 960
DB 901 REVSLHEBQKLEKROLTELOLSQERESQLTALQARAALBSQLEQATLELETTAA 960
QY 859 REVSLHEBQKLEKROLTELOLSQERESQLTALQARAALBSQLEQATLELETTAA 918
DB 859 REVSLHEBQKLEKROLTELOLSQERESQLTALQARAALBSQLEQATLELETTAA 918

QY 961 EERTQALTARDEIQKPKPALNSCTVITDLERQNLQLEDAENLNONPFLYSKOLDEAS 1020
DB 919 EERTQALTARDEIQKPKPALNSCTVITDLERQNLQLEDAENLNONPFLYSKOLDEAS 978
QY 1021 GANDEIVQLREVDHARREITEREMQTSQKQMEALKTCTTALBEOVMDLEALNDELLE 1080
DB 979 GANDEIVQLREVDHARREITEREMQTSQKQMEALKTCTTALBEOVMDLEALNDELLE 1038
QY 1081 KERQWEMNSVLGDEKSGPECRVREIQRMILTEKQSRAPADORTTSROYVELAVENKKA 1140
DB 1039 KERQWEMNSVLGDEKSGPECRVREIQRMILTEKQSRAPADORTTSROYVELAVENKKA 1098
QY 1141 EITLALQALKEQKLKKEESLSDKLNDELKKNAMENMARSLQQLLETERELKORLLEQAK 1200
DB 1099 EITLALQALKEQKLKKEESLSDKLNDELKKNAMENMARSLQQLLETERELKORLLEQAK 1158
QY 1201 LQQQMDLQKNHIFRLTQGLQELRADLILKTERSDLEYQLENTQVLYSHEKVMGEGTISQ 1260
DB 1159 LQQQMDLQKNHIFRLTQGLQELRADLILKTERSDLEYQLENTQVLYSHEKVMGEGTISQ 1218
QY 1261 QTKLIDFLQAKMDQPAKKKK-----VPLQYNELKALEKKAQALBEA 1305
DB 1219 QTKLIDFLQAKMDQPAKKKK-----VPLQYNELKALEKKAQALBEA 1278
QY 1306 LQKTRTEASAREAHARATDHPHSTPATARQOIFMSAIVSRPEHPSAMSILAPSS 1365
DB 1279 LQKTRTEASAREAHARATDHPHSTPATARQOIFMSAIVSRPEHPSAMSILAPSS 1338
QY 1366 RRKESSTPEEFSRLKERMHNNIPHRFNVGLNMRATKCAVCLDTVHFGHQAASKLEQVW 1425
DB 1339 RRKESSTPEEFSRLKERMHNNIPHRFNVGLNMRATKCAVCLDTVHFGHQAASKLEQVW 1398
QY 1426 CHPKCSTCLPATGRLPAEYATHTFAFCDDKNSPGLQTEPSSSLHSGMKVPPNNK 1485
DB 1399 CHPKCSTCLPATGRLPAEYATHTFAFCDDKNSPGLQTEPSSSLHSGMKVPPNNK 1458
QY 1486 GQGWDRKTYLVLEGSVLLYDNEAREAGORPVEEFLCPDGGVSIHGAVGASELNTAK 1545
DB 1459 GQGWDRKTYLVLEGSVLLYDNEAREAGORPVEEFLCPDGGVSIHGAVGASELNTAK 1518
QY 1546 ADVPYTLKMHSHPTTQWPGRTLYLLAPSPFDQKQWNTALLESVVAAGRVSREKADAKL 1605
DB 1519 ADVPYTLKMHSHPTTQWPGRTLYLLAPSPFDQKQWNTALLESVVAAGRVSREKADAKL 1578
QY 1606 LQNSLLKLBGDDRLDNNCTLPSSDQVVLVGTBEGLYALNVLKNSLTHVPGIGAVFOIYII 1665
DB 1579 LQNSLLKLBGDDRLDNNCTLPSSDQVVLVGTBEGLYALNVLKNSLTHVPGIGAVFOIYII 1638
QY 1666 KOLEKILMTAGEBRALCLVDYKVKQSLAOSHLPADPDISPNIFEAVKGCHLFGAKIEN 1725
DB 1639 KOLEKILMTAGEBRALCLVDYKVKQSLAOSHLPADPDISPNIFEAVKGCHLFGAKIEN 1698
QY 1726 GLICTCAMPKSVYILKYENLSKYCIKKEIETSEPCSHFTNYSILIGTNKRYEIDMQ 1785
DB 1699 GLICTCAMPKSVYILKYENLSKYCIKKEIETSEPCSHFTNYSILIGTNKRYEIDMQ 1758
QY 1786 YTLLEFLDKNDHSLADAVPAASSNFPVSIYQVNSAGQREBYLLCFHEFGVFDYSYGRS 1845
DB 1759 YTLLEFLDKNDHSLADAVPAASSNFPVSIYQVNSAGQREBYLLCFHEFGVFDYSYGRS 1818
QY 1846 RTDDLEKMSRLPLAFAREBYLPTVHNSLLEVEIQARSSAGTPARAYLDIPNRYLGPPI 1905
DB 1819 RTDDLEKMSRLPLAFAREBYLPTVHNSLLEVEIQARSSAGTPARAYLDIPNRYLGPPI 1878
QY 1906 SSGAIVLASSYQDKLKVICCKGNLVESGTEHHRGSTSRSSPNKAGPTVMEHITKRYA 1965
DB 1879 SSGAIVLASSYQDKLKVICCKGNLVESGTEHHRGSTSRSSPNKAGPTVMEHITKRYA 1938
QY 1966 SSPAPPEGSHRPESTPHRYREGRTLRDRDSGGRPLERKS PGRILSTRERSPARLF 2025
DB 1939 SSPAPPEGSHRPESTPHRYREGRTLRDRDSGGRPLERKS PGRILSTRERSPARLF 1998
QY 2026 BBSRGRPLAAGAVRTPLSQNVKWDQSSV 2054

Db 1999 EDSRGRPLPACAVTPTLSQVKNKWDQSSV 2027

RESULT 2

088938 PRELIMINARY; PRT: 2055 AA.
AC 088938; 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Rho/rac-interacting citron kinase.
GN Name=Cit; Synonym=Citk;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=9909084; PubMed=9792683; DOI=10.1074/jbc.273.45.29706;
RA Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,
RA Decto G.P.;
RT "Citron rho-interacting kinase, a novel tissue-specific ser/thr kinase
RT encompassing the Rho-Rac-binding protein Citron.";
RL J. Biol. Chem. 273:29706-29711(1998).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL: AF086824; AAC72823.1; -.
DR HSP: P31751; 1MRV.
DR MGD; MGI:105313; Cit.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR001180; Citron.
DR InterPro: IPR005479; Cphp synth_L_D2.
DR InterPro: IPR002219; DAG_Pe-bind.
DR InterPro: IPR011009; kinase_like.
DR InterPro: IPR011849; PH.
DR InterPro: IPR000961; kinase_C.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR000861; REM_repeat.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR008271; Ser_thr_kin_AS.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam; PF00130; C1.1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00433; Kinase; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
DR PRODOM; PD000001; Prot kinase; 1.
DR SMART; SM00109; C1.1; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR PROSITE; PS00467; DAG_Pe_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_Pe_BIND_DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 2055 AA; 235480 MW; 2120CB5B454DA940 CRC64;

Query Match 96.3%; Score 10109.5; DB 2; Length 2055;
Best Local Similarity 96.0%; Pred. No. 5.9e-282;

Matches 1974; Conservative 40; Mismatches 39; Indels 3; Gaps 2;

Qy 1 MLKFKYGARNPLDAGAAEPIASRASRLNLFQGGKPPMTQOQMSPLSREGILDALFVLF 60
Db 1 MLKFKYGVNPPPEASASEPIASRASRLNLFQGGKPPMTQOQMSALSREGILDALFALFE 60
Qy 61 ECSQPALMKIKHNSFPRKYSDDTIAELQELQPSAKDEPVNSLVCCGFAEYQVYREKATG 120
Db 61 ECSQPALMKIKHNSFQVKYSDTIAELRELQPSARDEPVNSLVCCGFAEYQVYREKATG 120
Qy 121 DIYMKVKKKALLAOQVSFFFEERNILSSTSPWIPOLQYAPQDNKHLVMEYQGG 180
Db 121 DIYMKVKKKALLAOQVSFFFEERNILSSTSPWIPOLQYAPQDNKHLVMEYQGG 180
Qy 181 DLSLNRYEDQDENIQFYLAELILAVHSVHMGVYHNDIKPENLIVDRTGHIKLVDF 240
Db 181 DLSLNRYEDQDENIQFYLAELILAVHSVHMGVYHNDIKPENLIVDRTGHIKLVDF 240
Qy 241 GSAAKNNSNMVNAKLPIGTPDYAPPEVLTVANGDGKTYGLDCDMSVGYIAYEMTYGR 300
Db 241 GSAAKNNSNK-VPAKLPIGTPDYAPPEVLTVNMEDRGTGGLCDMMSVGVAYEMVYGG 299
Qy 301 SPFAEGTSARTFNNINMFQFLKPPDDPKYSDELDIQSILGQKXRLPFGCCHPFF 360
Db 300 TPFTGTSARTFNNINMFQFLKPPDDPKYSDELDIQSILGQKXRLPFGCCHPFF 359
Qy 361 SKIDMNNIRNSPPFVFTLKSDDDTSNFDEPEKNSWSSPFCQSPSGSGEELPFQGS 420
Db 360 ARDTMNNIRNSPPFVFTLKSDDDTSNFDEPEKNSWMAFLLCPAEPPLAFSGEELPFQGS 419
Qy 421 YSKALGILGSESVSGLSDPATSSMEKKLISKELQDSQDKHMEQEMTLHRVS 480
Db 420 YSKALGILGSESVSGLSDPATSSMEKKLISKELQDSQDKHMEQEMTLHRVS 479
Qy 481 EVAVYSQKVEVLKASTQSLBODLATYITTESSIKRELQARMVSDQEDPAQLQHL 540
Db 480 EVAVYSQKVEVLKASTQSLBODLATYITTESSIKRELQARMVSDQEDPAQLQHL 539
Qy 541 DIREQSRKLOEIKQEOVQAEVEMRLMNOLEEDLVARSRSPLYSELRESRLAAEEFK 600
Db 540 DIREQSRKLOEIKQEOVQAEVEMRLMNOLEEDLVARSRSPLYSELRESRLAAEEFK 599
Qy 601 RKATECQHLKLLAKDQKPEVGEYAKLEKINAEQQLIQELQEXLEKAVASTATELLQ 660
Db 600 RKANECQHLKLLAKDQKPEVGEYAKLEKINAEQQLIQELQEXLEKAVASTATELLQ 659
Qy 661 NITQAKRARELEKLNREDSSEGRKKLVABERHSHLENKYKLETERRENRLLKDD 720
Db 660 NITQAKRARELEKLNREDSSEGRKKLVABERHSHLENKYKLETERRENRLLKDD 719
Qy 721 IOTKSQOIQOMADKILEBEKHEBAQVSAOHLFVHLKQKQYBEKIKVLDNOIKKDLAD 780
Db 720 IOTKSQOIQOMADKILEBEKHEBAQVSAOHLFVHLKQKQYBEKIKVLDNOIKKDLAD 779
Qy 781 KETLENNMQHBEBAHEKGIILSEQAMINAMDSKIRSLRQRYVELSEANKLAANSLLFT 840
Db 780 KETLENNMQHBEBAHEKGIILSEQAMINAMDSKIRSLRQRYVELSEANKLAANSLLFT 839
Qy 841 QRNMKAQEMISLROOKFLFTQAGLEAQRKLEBQLEKISHQHSDQRRLLELTR 900
Db 840 QRNMKAQEMISLROOKFLFTQAGLEAQRKLEBQLEKISHQHSDQRRLLELTR 899
Qy 901 REVSLEHEBQKLEKQLTSLQSLQRESQALALQAAARALSSQLRQAKTELEETTA 960
Db 900 REVSLEHEBQKLEKQLTSLQSLQRESQALALQAAARALSSQLRQAKTELEETTA 959
Qy 961 EEEIQLTAHARDEIQKFDALRNSCTVITDLBEQLNQLTEDNAELNNQNFYLSKQLEAS 1020
Db 960 EEEIQLTAHARDEIQKFDALRNSCTVITDLBEQLNQLTEDNAELNNQNFYLSKQLEAS 1019
Qy 1021 GANDEIVQARSEVDHLRREITEREMQITSQKQMEALKTTCTMLBEQVMDLEALNDELLE 1080
Db 1020 GANDEIVQARSEVDHLRREITEREMQITSQKQMEALKTTCTMLBEQVMDLEALNDELLE 1079

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QY 1081 KEROMEAMRSVLGDEKSGQFECRVAEILQRMIDTEKOSPARADQRTTESROYVELAVKXENKA 1140
DB 1080 KEROMEAMRSVLGDEKSGQFECRVAEILQRMIDTEKOSPARADQRTTESROYVELAVKXENKA 1139
QY 1141 EIALAOLALKEQKLAESLSDKLNLEKXIAMLEMNARSIOQKLETERELKORLLEEQAK 1200
DB 1140 EIALAOLALKEQKLAESLSDKLNLEKXIAMLEMNARSIOQKLETERELKORLLEEQAK 1199
QY 1201 LQOQMDLQKHIFELTQGLQBALDRADLKTERTSLEYQLENTIOVLXSHKXVKMEGTISQ 1260
DB 1200 LQOQMDLQKHIFELTQGLQBALDRADLKTERTSLEYQLENTIOVLXSHKXVKMEGTISQ 1259
QY 1261 QTKLIDFLQAKMDQPAKKKKVPLQYNELKALEKXKACALBEALQKTRIELRSAAEEA 1320
DB 1260 QTKLIDFLQAKMDQPAKKKKVPLQYNELKALEKXKACALBEALQKTRIELRSAAEEA 1319
QY 1321 AHRKATHPHSPATATROQIAMSATVRSPEHQSNAMSLAPPSRKESTPEEFERRL 1380
DB 1320 AHRKATHPHSPATATROQIAMSATVRSPEHQSNAMSLAPPSRKESTPEEFERRL 1379
QY 1381 KERMEHNIHPRFNVGLMNRATKCAVCDTVHFGQAQKCEQVCHPKCSTCLPATCGL 1440
DB 1380 KERMEHNIHPRFNVGLMNRATKCAVCDTVHFGQAQKCEQVCHPKCSTCLPATCGL 1439
QY 1441 PAEYATHTEAFCDKXNNSPGLQTEBSSSLHLEGMMKVPNNKRGQOGMDRKIYILEGS 1500
DB 1440 PAEYATHTEAFCDKXNNSPGLQTEBSSSLHLEGMMKVPNNKRGQOGMDRKIYILEGS 1499
QY 1501 KULIYNDEARAGRPVEFEELCLPDDVDSTHGVAGSELANTRKAVPPTLKMEHPHT 1560
DB 1500 KULIYNDEARAGRPVEFEELCLPDDVDSTHGVAGSELANTRKAVPPTLKMEHPHT 1559
QY 1561 TCWPGRTLYLAPSPFKQWMTLLESVAVAGRRSRKAEADAKLNGSLIKLEGGDRLD 1620
DB 1560 TCWPGRTLYLAPSPFKQWMTLLESVAVAGRRSRKAEADAKLNGSLIKLEGGDRLD 1619
QY 1621 MNCTLPESDQVVLVGTSEGLYALNVLNKSILTHVIGAVFOIYIIXOLEKILMAGEERA 1680
DB 1620 MNCTLPESDQVVLVGTSEGLYALNVLNKSILTHVIGAVFOIYIIXOLEKILMAGEERA 1679
QY 1681 LCLVDYKVKVQSLAQSHTLPAQPDISNIPFAVKGCHLFGAKITENGSLICAMPSKVIL 1740
DB 1680 LCLVDYKVKVQSLAQSHTLPAQPDISNIPFAVKGCHLFGAKITENGSLICAMPSKVIL 1739
QY 1741 RYMNENLSKYCIKRIETSEPCSCHPFTNYSILIGTNKFYEIDMKQYTLDEFLDKNDHSLA 1800
DB 1740 RYMNENLSKYCIKRIETSEPCSCHPFTNYSILIGTNKFYEIDMKQYTLDEFLDKNDHSLA 1799
QY 1801 PAVFAASNSPVSIVQNSAGOREEYILCFHEPGFVDSYGRRSRTDDLKWSRLPLAFA 1860
DB 1800 PAVFAASNSPVSIVQNSAGOREEYILCFHEPGFVDSYGRRSRTDDLKWSRLPLAFA 1859
QY 1861 YREBYLFTVHPNSLEVIETIQARSSAGTPAPAYLIDIPNRYLGAIPASSGAIYIASSYDYL 1920
DB 1860 YREBYLFTVHPNSLEVIETIQARSSAGTPAPAYLIDIPNRYLGAIPASSGAIYIASSYDYL 1919
QY 1921 RVLICCKGNLVKESSTEHHRGSGTSRSPNKRGPPTYMEHTTKRVAASPAPPEGSHREP 1980
DB 1920 RVLICCKGNLVKESSTEHHRGSGTSRSPNKRGPPTYMEHTTKRVAASPAPPEGSHREP 1979
QY 1981 STPHRY--REGRTELRRDKSPGRPLERKSGPRLSTRRERSPARLPEDSSRGLTPAGAV 2038
DB 1980 STPHRY--REGRTELRRDKSPGRPLERKSGPRLSTRRERSPARLPEDSSRGLTPAGAV 2039
QY 2039 RTPPLSQVNAKWDQSSV 2054
DB 2040 RTPPLSQVNAKWDQSSV 2055

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RESULT 3
088528
ID 088528

PRELIMINARY; PRT; 1641 AA.

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AC 088528;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
DE CItion-X kinase (Fragment).
GN Name=Cit;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96128238; Pubmed=8543060; DOI=10.1016/0014-5793(95)01351-2;
RA Madanle P., Furiyashiki T., Reid T., Ishizaki T., Watanabe G.,
RA Morit N., Narumiya S.;
RT "A novel partner for the GTP-bound forms of rho and rac.";
RL FBS Lett. 377:243-248(1995).
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; AF070066; AAC27933.1; -.
DR MGD; MGI:105313; Cit.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016501; F:kinase activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001180; CItion.
DR InterPro; IPR005479; Gnpd_synth_L_D2.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000861; REM_repeat.
DR Pfam; PF00130; CL_1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Kinase.
FT NON_TER
SQ SEQUENCE 1641 AA; 187658 MW; 6723B20ECA3F22AB CRC64;

Query Match 77.8%; Score 8161; DB 2; Length 1641;
Best Local Similarity 95.7%; Pred. No. 3e-226;
Matches 1610; Conservative 15; Mismatches 14; Indels 44; Gaps 2;

QY 374 PVPYTLKSDDDTSNFDPEKNSWSSSPCOLSPSGFSGBELPVGFSYKALGILGRSES 433
DB 1 PVPYTLKSDDDTSNFDPEKNSWSSSPCOLSPSGFSGBELPVGFSYKALGILGRSES 60

QY 434 VVSGLDSPAKTSSMEKKLLIKSKYELDSQDKCKHMEQENTRLRRVSEVAUISQKEVEL 493
DB 61 VVSSLDSPAKVSSMEKKLLIKSKYELDSQDKCKHMEQENTRLRRVSEVAUISQKEVEL 120

QY 494 KASETORSLLEODLATYITECSSLKRSLEQARMEVSOEDDKALQHLHDIRQSRKLOEIK 553
DB 121 KASETORSLLEODLATYITECSSLKRSLEQARMEVSOEDDKALQHLHDIRQSRKLOEIK 180

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Qy 554 EOEYQAOVEEMRLMMNQLEEDLVGARRSDLYESELSRESRLAAEFKKATECOHKLKA 613
Db 181 EOEYQAOVEEMRLMMNQLEEDLVGARRSDLYESELSRESRLAAEFKKATECOHKLKA 240
Qy 614 KDOCKPEVGEVAKLEKINAEOQLKIOEQLKAVKASTATELLONIRAKRAREL 673
Db 241 KDOCKPEVGEVAKLEKINAEOQLKIOEQLKAVKASTATELLONIRAKRAREL 300
Qy 674 EKLONREDSRGIRKCLVEAEERHSLKVKRYLETMERENRRLKDIQTQSQOIQWAD 733
Db 301 EKLHNRDSSSGIKKKLVEAE----- 321
Qy 734 KILEBEKREAOVSAOHLVHLKQEQHYEKKIVLDNQIKDLADKETTENNMOHRE 793
Db 322 ---ELBEHREAOVSAOHLVHLKQEQHYEKKIVLDNQIKDLADKETTENNMOHRE 378
Qy 794 EAHKKGKILSBOKMINAMDSKISLBORIVELSEANLANSSIFQRMKAKOEMISE 853
Db 379 EAHKKGKILSBOKMINAMDSKISLBORIVELSEANLANSSIFQRMKAKOEMISE 438
Qy 854 LRQCKFYLETQAGKLEAQNRLKEQLKISHQSDSKRLLEETRLREVSLEHEQKLE 913
Db 439 LRQCKFYLETQAGKLEAQNRLKEQLKISHQSDSKRLLEETRLREVSLEHEQKLE 498
Qy 914 LKRQLTQLSLOERESQTLQAARALSESQLEQAQTELEETTAABEEIQAALTARHDE 973
Db 499 LKRQLTQLSLOERESQTLQAARALSESQLEQAQTELEETTAABEEIQAALTARHDE 558
Qy 974 IORFEDALRNSCTYTIDLEBQNLQTEBNALNQNFLTSLQDLBAGANDEIYQLESSEV 1033
Db 559 IORFEDALRNSCTYTIDLEBQNLQTEBNALNQNFLTSLQDLBAGANDEIYQLESSEV 618
Qy 1034 DILREITEREMQLTSGKOTMEALKTCTMLEBOVMDLEALNDELLEKEREOMEARSVLG 1093
Db 619 DILREITEREMQLTSGKOTMEALKTCTMLEBOVMDLEALNDELLEKEREOMEARSVLG 678
Qy 1094 DEKSQFECRAVELQRMLEDTEKQSPARADQRTTESQVVELAVKHKKEIILAQALKEOK 1153
Db 679 DEKSQFECRAVELQRMLEDTEKQSPARADQRTTESQVVELAVKHKKEIILAQALKEOK 738
Qy 1154 LKAEESLKDNDLEKKAEMENARSLQCKLETERELKORLEEOAKLOOQMDQKXHIIF 1213
Db 739 LKAEESLKDNDLEKKAEMENARSLQCKLETERELKORLEEOAKLOOQMDQKXHIIF 798
Qy 1214 RLTCGLQDALDRADLKTERTSDLEYOLENIOVLSHEKVKMEGTISQOTKXIDFLQAKMD 1273
Db 799 RLTCGLQDALDRADLKTERTSDLEYOLENIOVLSHEKVKMEGTISQOTKXIDFLQAKMD 858
Qy 1274 QPAKKKKVPLQYNELKLALEKAKCALEBALQKTRIELRSAREEAHRAKTDHPHST 1333
Db 859 QPAKKKKVPLQYNELKLALEKAKCALEBALQKTRIELRSAREEAHRAKTDHPHST 918
Qy 1334 PATRROQIAMSATYRSEPHQPSANSLAPSSRKESSTPEERSRLKERMHNIPIRFN 1393
Db 919 PATRROQIAMSATYRSEPHQPSANSLAPSSRKESSTPEERSRLKERMHNIPIRFN 978
Qy 1394 VGLNMRATKAVCLDYHFGQASKLECOVMCHPKSTCIPATCGLPAYATHTFAFC 1453
Db 979 VGLNMRATKAVCLDYHFGQASKLECOVMCHPKSTCIPATCGLPAYATHTFAFC 1038
Qy 1454 RDKKNSPGLQTKEPSSILHGMKMPRNKRGOQMDRKITVLEGSKVLTYDNEAREAG 1513
Db 1039 RDKKNSPGLQTKEPSSILHGMKMPRNKRGOQMDRKITVLEGSKVLTYDNEAREAG 1098
Qy 1514 QRPVEEBELCPDGDVSIHGAVGASELANTAKADVPYITLKESHPHPTTCWGRITLYILAP 1573
Db 1099 QRPVEEBELCPDGDVSIHGAVGASELANTAKADVPYITLKESHPHPTTCWGRITLYILAP 1158
Qy 1574 SFPDKQWMTALJESVVGARSRKARADALGNSILKJEGDRLLMNCTLPSPDOVYL 1633
Db 1159 SFPDKQWMTALJESVVGARSRKARADALGNSILKJEGDRLLMNCTLPSPDOVYL 1218

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Qy 1634 VGTREGLYALNVLKNLSLTHVGTGAVFOIYITKLEKLMTAGERALCYDYKKVKQSL 1693
Db 1219 VGTREGLYALNVLKNLSLTHVGTGAVFOIYITKLEKLMTAGERALCYDYKKVKQSL 1278
Qy 1694 AQSHLPAPDPISPIFPAVKGCHLEAGKLENGLCIQAAPSKVILRYNENLSKCYCRK 1753
Db 1279 AQSHLPAPDPISPIFPAVKGCHLEAGKLENGLCIQAAPSKVILRYNENLSKCYCRK 1338
Qy 1754 ELETSEPCSIHFTNYSILIGTNKFEYIDMKQYTLLEBLDNKDSLAFAVEAASSNSFPV 1813
Db 1339 ELETSEPCSIHFTNYSILIGTNKFEYIDMKQYTLLEBLDNKDSLAFAVEAASSNSFPV 1398
Qy 1814 SIYVNSAGQREBYLCTFHEFGVVDISYGRSRPTDLKWSLPLAFAYREBYLYTHNS 1873
Db 1399 SIYVNSAGQREBYLCTFHEFGVVDISYGRSRPTDLKWSLPLAFAYREBYLYTHNS 1458
Qy 1874 LEVIEIQARSAGPAPAYADIPAPRYLGPALISSGALYLLASSYODKRLVTCCKNLVES 1933
Db 1459 LEVIEIQARSAGPAPAYADIPAPRYLGPALISSGALYLLASSYODKRLVTCCKNLVES 1518
Qy 1934 GTEHHRGPTSRSSPNKRGPTTYNEHTTKRVASSPAPPEGSHREBSPHRY--REGRT 1991
Db 1519 GTEHHRGPTSRSSPNKRGPTTYNEHTTKRVASSPAPPEGSHREBSPHRY--REGRT 1578
Qy 1992 ELRRDKSPGRPLEREKSPGRILSTRERSPARLFEDSSRGRLPAGAVRTPLSQNVKWQD 2051
Db 1579 ELRRDKSPGRPLEREKSPGRILSTRERSPARLFEDSSRGRLPAGAVRTPLSQNVKWQD 1638
Qy 2052 SSV 2054
Db 1639 SSV 1641

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RESULT 4

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CTRO_MOUSE
ID CTRO_MOUSE STANDARD; PRT: 1597 AA.
AC P49025;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Citron protein (Rho-interacting, serine/threonine kinase 21).
GN Name=Cit;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96128238; PubMed=8543060; DOI=10.1016/0014-5793(95)01351-2;
RA Madanue P., Furuyashiki T., Reid T., Ishizaki T., Watanabe G.,
RA Morita N., Natsumiya S.;
RT "A novel partner for the GTP-bound forms of rho and rac.";
RL FEBS Lett. 377:243-248(1995).
CC -1- FUNCTION: Putative RHO/RAC effector that binds to the GTP-bound
CC forms of RHO and RAC1. It probably binds p21 with a tighter
CC specificity in vivo.
CC -1- SUBUNIT: Homodimer (Probable).
CC -1- TISSUE SPECIFICITY: A major signal was observed in testis and
CC brain, but it was also detected in thymus, spleen, kidney, heart
CC and lung.
CC -1- SIMILARITY: Contains 1 CNH domain.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -1- SIMILARITY: Contains 1 zinc-dependent phospho-ester and DAG
CC binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

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CC EMBL; U39904; AAC52341.1; -
DR PIR; S68420; S68420.
DR MGD; MGI:105313; Cit.
DR InterPro; IPR001180; C1tron.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH-related.
DR InterPro; IPR000861; RRM_repeat.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Coiled coil; Phorbol-ester binding; SH3-binding.
FT DOMAIN 1 845 Coiled coil (potential).
FT DOMAIN 674 870 Interaction with Rho/Rac.
FT DOMAIN 818 821 Poly-Lys.
FT DOMAIN 931 979 Phorbol-ester and DAG binding.
FT DOMAIN 1011 1131 PH.
FT DOMAIN 1160 1457 CNH.
FT SITE 1521 1526 SH3-binding (potential).
SQ SEQUENCE 1597 AA; 183448 MW; 787286C2305676DA CRC64;

Query Match 75.6%; Score 7935; DB 1; Length 1597;

Best Local Similarity 98.2%; Pred. No. 8.7e-220;
Matches 1561; Conservative 16; Mismatches 10; Indels 2; Gaps 1;

QY 468 MEQEMTRHRRVSEVAVLISQKEVELKASRSTORSLLEQDLATYITTECSIKRSLEQARME 527
DB 9 MEQEMTRHRRVSEVAVLISQKEVELKASRSTORSLLEQDLATYITTECSIKRSLEQARME 68
QY 528 VSGEDDKALQLLHDIREQSRKLOEIKOEYQAOYEEMRLMNNQLEEDLVASARRSDLYES 587
DB 69 VSGEDDKALQLLHDIREQSRKLOEIKOEYQAOYEEMRLMNNQLEEDLVASARRSDLYES 128
QY 588 ELRESRLAAEFPRKARECOHKLKAKDOGRPEVGEYAKLEKTNABOOLKIQELQELK 647
DB 129 ELRESRLAAEFPRKARECOHKLKAKDOGRPEVGEYAKLEKTNABOOLKIQELQELK 188
QY 648 AVKASTATELLONIRAKERAERELEKLNREDSSEGRKCLVEAEERHSLSENKVKRL 707
DB 189 AVKASTATELLONIRAKERAERELEKLNREDSSEGRKCLVEAEERHSLSENKVKRL 248
QY 708 ETMERRENRLLKDDIQTYSQOIQQWADKILLEEKHREAOVSAOHLBVHLKQEQHYEKT 767
DB 249 ETMERRENRLLKDDIQTYSQOIQQWADKILLEEKHREAOVSAOHLBVHLKQEQHYEKT 308
QY 768 KVLDDNOIKKOLADKETLENMQRHEERAEHNGKILLSQOKAMINAMDSKISLEIRIYELS 827
DB 309 KVLDDNOIKKOLADKETLENMQRHEERAEHNGKILLSQOKAMINAMDSKISLEIRIYELS 368
QY 828 EANKLANSSILFTQRNKAQOEMISELRQOKFYLETQAGKLEAQNRLKEOLEKISHQDH 887
DB 369 EANKLANSSILFTQRNKAQOEMISELRQOKFYLETQAGKLEAQNRLKEOLEKISHQDH 428
QY 888 SDKNRLLELETRLEVSLEHEEQKLELRQITELQSLQERESQTLAQARAALLESQLR 947
DB 429 SDKNRLLELETRLEVSLEHEEQKLELRQITELQSLQERESQTLAQARAALLESQLR 488
QY 948 QAKTELEETTAEEAEELQALTARHDEIQKFKDALRNSCTVITDLEEQNLQTEENALIN 1007
DB 489 QAKTELEETTAEEAEELQALTARHDEIQKFKDALRNSCTVITDLEEQNLQTEENALIN 548
QY 1008 QNFYLSKQLEBASGANDIIVOLRSEVDHLRREITEREMQULTSQKQTEALKTTCMTLEEQ 1067
DB 549 QNFYLSKQLEBASGANDIIVOLRSEVDHLRREITEREMQULTSQKQTEALKTTCMTLEEQ 608
QY 1068 VMDLEALNDELLEKERQWEAMRSVLDGKSGQFECRVRELQRMLDTERKQSRARADQRTTES 1127

DB 609 VLDLEALNDELLEKERQWEAMRSVLDGKSGQFECRVRELQRMLDTERKQSRARADQRTTES 668
QY 1128 ROYVELAVKHEKAEIITLALQALKEQKLEKESLSDKNDLEKKAMLEMMARSLQOKLETE 1187
DB 669 ROYVELAVKHEKAEIITLALQALKEQKLEKESLSDKNDLEKKAMLEMMARSLQOKLETE 728
QY 1188 RELKORLLEEQALQOQMDLQKXHIFRLTQGLQEALDRADLKTERSDLEYOLENTQVLY 1247
DB 729 RELKORLLEEQALQOQMDLQKXHIFRLTQGLQEALDRADLKTERSDLEYOLENTQVLY 788
QY 1248 SHEKVMMEGTISQOTKLIDFLQAKMDQPAKKKVPLOYNELKALKEKARCALEBALQ 1307
DB 789 SHEKVMMEGTISQOTKLIDFLQAKMDQPAKKKVPLOYNELKALKEKARCALEBALQ 848
QY 1308 KTRIELRSAREEAHKAATDHPSTPATARQOIMASAIYRSEPHQPSAMSLAPSSRR 1367
DB 849 KTRIELRSAREEAHKAATDHPSTPATARQOIMASAIYRSEPHQPSAMSLAPSSRR 908
QY 1368 KESSTPEEFSRRLKERMHNI PHRFVGLMRYATKCAVCLDLYHFGROASKLECYVMCH 1427
DB 909 KESSTPEEFSRRLKERMHNI PHRFVGLMRYATKCAVCLDLYHFGROASKLECYVMCH 968
QY 1428 PKCSTCLPATCGLPARYATHTFAFCRDKNSPGCLQTKPESSSLHLEGMMKVRNNRGQ 1487
DB 969 PKCSTCLPATCGLPARYATHTFAFCRDKNSPGCLQTKPESSSLHLEGMMKVRNNRGQ 1028
QY 1488 QGMDRKTYLVEGSKVLIYDNEAREAGORPVEEFELCLPDGVSIGHAVGASBLANTAKAD 1547
DB 1029 QGMDRKTYLVEGSKVLIYDNEAREAGORPVEEFELCLPDGVSIGHAVGASBLANTAKAD 1088
QY 1548 VPYILKMESSHPTTCWPGRTLYLLAPSFPDKQSVTALLESVAGVSRREKADAKLIG 1607
DB 1089 VPYILKMESSHPTTCWPGRTLYLLAPSFPDKQSVTALLESVAGVSRREKADAKLIG 1148
QY 1608 NSLLKLEGGDRLLMNCITLPPSDQVLYVGTBEGYALNVLKNSLTHYPGIAGVQIYIKD 1667
DB 1149 NSLLKLEGGDRLLMNCITLPPSDQVLYVGTBEGYALNVLKNSLTHYPGIAGVQIYIKD 1208
QY 1668 LEKILMAGEERALCLVDYVKVQSLAQSHLPAQPDISPNIPEAVKCHLFGAKLENG 1727
DB 1209 LEKILMAGEERALCLVDYVKVQSLAQSHLPAQPDISPNIPEAVKCHLFGAKLENG 1268
QY 1728 CICAAMPKSVVILRYNEMISKICIRKEIETSEPCSCIHFTNYSILIGTNKFEYIDMKQYT 1787
DB 1269 CICAAMPKSVVILRYNEMISKICIRKEIETSEPCSCIHFTNYSILIGTNKFEYIDMKQYT 1328
QY 1788 LEEFLDKNDHSLAPAVPASNSFPVSIYOVNAGQREBYLLCFHFGVGVDSYGRSRT 1847
DB 1329 LEEFLDKNDHSLAPAVPASNSFPVSIYOVNAGQREBYLLCFHFGVGVDSYGRSRT 1388
QY 1848 DDLMKSRLLPLAFAYREPYLFVTHFNSLVEIIEQARSAGTAPARAYLDIPNRYLGPALIS 1907
DB 1389 DDLMKSRLLPLAFAYREPYLFVTHFNSLVEIIEQARSAGTAPARAYLDIPNRYLGPALIS 1448
QY 1908 GAIYLLASVODKLRVICCKGNLVKESGTEHHRGPSTSRSSPNRRGPPTYNEHTTKRVASS 1967
DB 1449 GAIYLLASVODKLRVICCKGNLVKESGTEHHRGPSTSRSSPNRRGPPTYNEHTTKRVASS 1508
QY 1968 PAPPEGSHRREESTHRY--REGRTLRDKSFGRLPEKSPGRLISRRERSPARLF 2025
DB 1509 PAPPEGSHRREESTHRY--REGRTLRDKSFGRLPEKSPGRLISRRERSPARLF 1568
QY 2026 EDSRGRLLPAGAVRTPLSQVNAKWDOSSV 2054
DB 1569 EDSRGRLLPAGAVRTPLSQVNAKWDOSSV 1597

RESULT 5
ID 090X19 PRELIMINARY; PRT; 1618 AA.
AC 090X19;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, last annotation update)
 DE Postsynaptic density protein.
 GN Name=Citron;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 NX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhang W., Apperson M.L., Vasquez L.B., Kennedy M.B.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 PH domain.
 DR EMBL; AF039218; AAC25483.1; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR InterPro; IPR001180; Citron.
 DR InterPro; IPR005479; Cphp_synth_L_D2.
 DR InterPro; IPR002219; DAG_Pe-bind.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000861; REM_repeat.
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF001130; Cl_1; 1.
 DR Pfam; PF00780; CNH; 1.
 DR Pfam; PF00169; PH; 1.
 DR PRINTS; PR00194; TROPOMYOSIN.
 DR SMART; SMO0109; Cl_1.
 DR SMART; SMO0036; CNH; 1.
 DR SMART; SMO0233; PH; 1.
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 DR PROSITE; PS00479; DAG_Pe_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_Pe_BIND_DOM_2; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 SQ SEQUENCE 1618 AA; 185924 MW; EAE08079788AA4E9 CRC64;

Query Match 74.8%; Score 7851.5; DB 2; Length 1618;
 Best Local Similarity 96.0%; Pred. No. 2,2e-217;
 Matches 1554; Conservative 18; Mismatches 14; Indels 33; Gaps 4;

DQ 468 MEQSMTLHRRVSEVAVLSQKEVELKASEFORSLSLQDLATYTTESLSLRLEQARME 527
 DB 1 MEQSMALHRRVSEVAVLSQKEVELKASEFORSLSLQDLATYTTESLSLRLEQARME 60

DQ 528 VSQEDDVALQLHDIRESQRLQEIKEQEQVQAYEENKLMNQLEEDLVARRSDIYES 587
 DB 61 VSQEDDVALQLHDIRESQRLQEIKEQEQVQAYEENKLMNQLEEDLVARRSDIYES 120

DQ 588 ELRESRLAAEFKKKATECQHKLLKANDQKPEVGEYAKLEKINAEOQLKIQELQEKLEK 647
 DB 121 ELRESRLAAEFKKKATECQHKLLKANDQKPEVGEYAKLEKINAEOQLKIQELQEKLEK 180

DQ 648 AVKASTATTELQNIROAKERAERLEKLNREDSSEGIKCLVAEARRSLLENKTKYRL 707
 DB 181 AVKASTATTELQNIROAKERAERLEKLNREDSSEGIKCLVAEARRSLLENKTKYRL 240

DQ 708 ETMERERENRLKDDIQTSQOIQOQADKILLEBKGRBAQVSAOHLVYHLKQEQHYEKKI 767
 DB 241 ETMERERENRLKDDIQTSQOIQOQADKILLEBKGRBAQVSAOHLVYHLKQEQHYEKKI 300

DQ 768 KVLNDQIKKDLADKELLENMQRHEEBAHEKGIILSEQKAMINAMDSKIRSLRQRIYELS 827
 DB 301 KVLNDQIKKDLADKELLENMQRHEEBAHEKGIILSEQKAMINAMDSKIRSLRQRIYELS 360

DQ 828 EANTLANSSLPTRNNKAQOEMISELRQCKFYLETQAGKLEAQRKLEBQLEKISQDH 887
 DB 361 EANTLANSSLPTRNNKAQOEMISELRQCKFYLETQAGKLEAQRKLEBQLEKISQDH 420

DQ 888 SDRKRLLETRLEVSLEHEQKLELRQLTELQLSQREESQUTLQAARALLESQLR 947
 DB 421 SDRKRLLETRLEVSLEHEQKLELRQLTELQLSQREESQUTLQAARALLESQLR 480

DQ 948 QAKTELETTAAABEEIQALTAHDEIQRKFDALRNSCTVITDLEQLNQTEDNABLIN 1007

DB 481 QAKTELETTAAABEEIQALTAHDEIQRKFDALRNSCTVITDLEQLNQTEDNABLIN 540

DQ 1008 QNFYLSQDLDEASGANDEIVQLRSEVDHLREITEREMQTLISQKOTMEALKTCTMLEEQ 1067
 DB 541 QNFYLSQDLDEASGANDEIVQLRSEVDHLREITEREMQTLISQKOTMEALKTCTMLEEQ 600

DQ 1068 VMDLEALNDELLEKERQEWAMRSVLDGKSGQFECRVBELQMDLTERKQSRARADQRTIES 1127
 DB 601 VMDLEALNDELLEKERQEWAMRSVLDGKSGQFECRVBELQMDLTERKQSRARADQRTIES 660

DQ 1128 ROVVELAVKHKAEIILQALKEQKIKASLSQKNDLEKXMLENNASISLQOKLETE 1187
 DB 661 ROVVELAVKHKAEIILQALKEQKIKASLSQKNDLEKXMLENNASISLQOKLETE 720

DQ 1188 RELKQRLLEBQAKLQOQMDLQKNIHFRUTQGLQBALRADLKTERSDLEQLENTQVLY 1247
 DB 721 RELKQRLLEBQAKLQOQMDLQKNIHFRUTQGLQBALRADLKTERSDLEQLENTQVLY 780

DQ 1248 SHEKVKMEGTISQGTKLIDFLQAKMDQPAKKKK-----VPLQVNEKLAL 1292
 DB 781 SHEKVKMEGTISQGTKLIDFLQAKMDQPAKKKK-----VPLQVNEKLAL 840

DQ 1293 EKEKARCABELEALQKTRIELRSAREAAHKAIDHHPSTPATARQOIMSAIVRSEH 1352
 DB 841 EKEKARCABELEALQKTRIELRSAREAAHKAIDHHPSTPATARQOIMSAIVRSEH 900

DQ 1353 QPSAMSLIAPSSRRKESSTPEEFSRLKERMHNIHFRFVGLNMBATKCAVCLDTVHF 1412
 DB 901 QPSAMSLIAPSSRRKESSTPEEFSRLKERMHNIHFRFVGLNMBATKCAVCLDTVHF 960

DQ 1413 GRQASKLEBQVCMCHPCSTCLPATCGLPAEYATHTEAFCRDQKNSPGLQTEKPSSLH 1472
 DB 961 GRQASKLEBQVCMCHPCSTCLPATCGLPAEYATHTEAFCRDQKNSPGLQTEKPSSLH 1020

DQ 1473 LEGMMKTPRNKKGQOQMDKRYLYLESSKYLIDYNEAREAGQRVSEBELCPGDDVSIH 1532
 DB 1021 LEGMMKTPRNKKGQOQMDKRYLYLESSKYLIDYNEAREAGQRVSEBELCPGDDVSIH 1080

DQ 1533 GAVGASELANTAKADVYIILKMSHPHTTCMPGRITVLLAPSPFDKQRMVTLSSVAVAG 1592
 DB 1081 GAVGASELANTAKADVYIILKMSHPHTTCMPGRITVLLAPSPFDKQRMVTLSSVAVAG 1140

DQ 1593 RVSRKAEADA-----KLGNSLKLKEGDDRLDMNCTLPSQDQVVLVGE 1637
 DB 1141 RVSRKAEADAAMDCSCEBLPVVVEKLGNSLKLKEGDDRLDMNCTLPSQDQVVLVGE 1200

DQ 1638 EGLYALNVLKNSLTHVPDQIGAVFOIYIILKLEKLMJAGEBRALCLVDYKVKOSLAQSH 1697
 DB 1201 EGLYALNVLKNSLTHVPDQIGAVFOIYIILKLEKLMJAGEBRALCLVDYKVKOSLAQSH 1260

DQ 1698 LPAPQDIPNIPFAVKGCHLPGAGKLENGLCIQAAMSKVYILRYNNLSKYCIKKKEET 1757
 DB 1261 LPAPQDVSPNIPFAVKGCHLPGAGKLENGLCIQAAMSKVYILRYNNLSKYCIKKKEET 1320

DQ 1758 SEPCSCIFHFNYSILITGNKRYEIDMKQYTLLEBFLDKNDLSLAPAVEAASNSPFAVIQ 1817
 DB 1321 SEPCSCIFHFNYSILITGNKRYEIDMKQYTLLEBFLDKNDLSLAPAVEAASNSPFAVIQ 1380

DQ 1818 VNSAGQREBYLCPHEFGVFDVSGRRSRTDCLKMSRLPLAFAYREBYLFTVTHNSLEVI 1877
 DB 1381 ANSTGQREBYLCPHEFGVFDVSGRRSRTDCLKMSRLPLAFAYREBYLFTVTHNSLEVI 1440

DQ 1878 EIQARSSAGTPARAVLIDIPNRYLGPATSSGATYLLASSYDDKLRVITCKKGLVYESGTEH 1937
 DB 1441 EIQARSSAGTPARAVLIDIPNRYLGPATSSGATYLLASSYDDKLRVITCKKGLVYESGTEH 1500

DQ 1938 HRGPSTSRSSPNKRGPTVNEHTTKRVASSPAPPEGSHREBPSTPHRY--REGRTELRR 1995
 DB 1501 HRGPSTSRSSPNKRGPTVNEHTTKRVASSPAPPEGSHREBPSTPHRYDRBERTELRR 1559

DQ 1996 DKSPGRLEREKSPGRILSTRREBSPARLFESSRGFLPAGAVTPLSQVNRKWDQSSV 2054

Db 1560 DKSPGRLEHKSXGRMLSTRERSPRLPFDSSRGRLPAGAVRTPLSQVNVKWDQSSV 1618

```

RESULT 6
CTRO HUMAN
ID CTRO HUMAN STANDARD; PRT, 1286 AA.
AC 014578; O9UP27;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cytion protein (Rho-interacting, serine/threonine kinase 21)
DE (Fragment).
GN Name=CIT: Synonyms=KIAA0949, STRK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Comell M., Goela D., Harper M.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 347-1286 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99246063; Pubmed=10231032;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
CC -1- FUNCTION: Putative RHO/RAC effector that binds to the GTP-bound
CC forms of RHO and RAC1. It probably binds p21 with a tighter
CC specificity in vivo (By similarity).
CC -1- SIMILARITY: Contains 1 CNH domain.
CC -1- SIMILARITY: Contains 1 PH domain.
CC -1- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
CC binding domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
EMBL: AC002563; AAB71327.1; -.
EMBL: AB023166; BAA76793.1; -.
Genew; HGNC:1985; CIT.
DR MIM; 605629; -.
DR InterPro; IPR001180; Cytion.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001849; PH_repeat.
DR InterPro; IPR01036; PH_related.
DR InterPro; IPR000861; KEM_repeat.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00233; PH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
KW Coiled coil; Phorbol-ester binding; SH3-binding.
FT NON_TER 1
FT DOMAIN <1 558 Coiled coil (Potential).
FT DOMAIN 365 561 Rho/Rac binding.
FT DOMAIN 509 512 Poly-Lys.
FT DOMAIN 622 670 Phorbol-ester and DAG binding.
FT DOMAIN 702 822 PH.
FT DOMAIN 851 1148 CNH.

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FT SITE 1212 1217 SH3-binding (Potential).
SQ SEQUENCE 1286 AA; 146506 MM; 498101F79EAA75E85 CAC64;
Query Match 62.7%; Score 6575; DB 1; Length 1286;
Best Local Similarity 99.8%; Pred. No. 6,3e-181;
Matches 1284; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 769 VLNNQIKQIADKETLENNMORHEEFAHEKGLISBOKAMINMDSKIRSLBORIVLSE 828
DB 1 VLNNQIKQIADKETLENNMORHEEFAHEKGLISBOKAMINMDSKIRSLBORIVLSE 60
QY 829 ANKLAANSLEFQNNKAQSEMISELROQKFVLETOAGKLEAONRKLEBDEKISHODS 888
DB 61 ANKLAANSLEFQNNKAQSEMISELROQKFVLETOAGKLEAONRKLEBDEKISHODS 120
QY 889 DKNRLLELETRLEVSLEHEBQKLEIKRQITELQSLQERESQITAIQAARALLESQLRQ 948
DB 121 DKNRLLELETRLEVSLEHEBQKLEIKRQITELQSLQERESQITAIQAARALLESQLRQ 180
QY 949 AKTELEETTAEEAEELQALTARDEIQKFDALRNSCTVITDLEEQNLQTEBNALNNQ 1008
DB 181 AKTELEETTAEEAEELQALTARDEIQKFDALRNSCTVITDLEEQNLQTEBNALNNQ 240
QY 1009 NFLYSQQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQTEALKTCTMLEEQV 1068
DB 241 NFLYSQQLDEASGANDEIVQLRSEVDHLRREITEREMQLTSQKQTEALKTCTMLEEQV 360
QY 1069 MDLEALNDELLEKERQEWANRSVLGDEKSGFECRVRELQMDLTEKQSRADQRTTESR 1128
DB 301 MDLEALNDELLEKERQEWANRSVLGDEKSGFECRVRELQMDLTEKQSRADQRTTESR 360
QY 1129 QVVELAVKEKKAETLALQALKEQKIKASLSKINDLEKHAMLEMNARSLOOKLETER 1188
DB 361 QVVELAVKEKKAETLALQALKEQKIKASLSKINDLEKHAMLEMNARSLOOKLETER 420
QY 1189 ELQRLLEBOAKIQQMDLQKNIIFRLTQGLQALBRADILKTERSDLEFYOLENIQVLYS 1248
DB 421 ELQRLLEBOAKIQQMDLQKNIIFRLTQGLQALBRADILKTERSDLEFYOLENIQVLYS 480
QY 1249 HEKVKMEGTISQQTKLIDFLQAMDQPAKKKKVPLQYNEIKLALKEKARCAELEALQK 1308
DB 481 HEKVKMEGTISQQTKLIDFLQAMDQPAKKKKVPLQYNEIKLALKEKARCAELEALQK 540
QY 1309 TRIEFASAREAAHRAKATDHPHSTATATARQOIAMAVYSPEHOSAMSLAPSSRRK 1368
DB 541 TRIEFASAREAAHRAKATDHPHSTATATARQOIAMAVYSPEHOSAMSLAPSSRRK 600
QY 1369 ESSTPEEFSSRLKERMHNNIPHRFNVGLNMRATKCAVCLDTYAFHGRQASKLEQVWCHP 1428
DB 601 ESSTPEEFSSRLKERMHNNIPHRFNVGLNMRATKCAVCLDTYAFHGRQASKLEQVWCHP 660
QY 1429 KCSTCLPATGCLPAEYATHTFAFCRDKNNSPGLQTKPESSLAHFGMKVPRNNRGGQ 1488
DB 661 KCSTCLPATGCLPAEYATHTFAFCRDKNNSPGLQTKPESSLAHFGMKVPRNNRGGQ 720
QY 1489 GMDRKTIIVLEGSKVLIYDNEARAGAPVEBEFLCPDGDVYHGAVGASLANTAKADV 1548
DB 721 GMDRKTIIVLEGSKVLIYDNEARAGAPVEBEFLCPDGDVYHGAVGASLANTAKADV 780
QY 1549 PYLLKNESSHPTCWPGRGTYLLAPSPDKQKRVATLLESVAVAGARYSREAAEDAKLLGN 1608
DB 781 PYLLKNESSHPTCWPGRGTYLLAPSPDKQKRVATLLESVAVAGARYSREAAEDAKLLGN 840
QY 1609 SLILKGBDRLDMNCTLPFSQDVVLVGTBEGLYALNVLKNSLTHVIGAVFOYIYIKDL 1668
DB 841 SLILKGBDRLDMNCTLPFSQDVVLVGTBEGLYALNVLKNSLTHVIGAVFOYIYIKDL 900
QY 1669 EKLLMAGEERRALCLVDVKKVKOSLAQSHLPAOPDISPINIFBAVKGCHLFGAKITNGLC 1728
DB 901 EKLLMAGEERRALCLVDVKKVKOSLAQSHLPAOPDISPINIFBAVKGCHLFGAKITNGLC 960
QY 1729 ICAAMPSKVILLYNNNLKCYCIKKEITENSEPSCCHFNYSYSLIGNKPKYEITDMQYTL 1788
DB 961 ICAAMPSKVILLYNNNLKCYCIKKEITENSEPSCCHFNYSYSLIGNKPKYEITDMQYTL 1020

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Db 961 ICAMPKVVILRYNENLSKYCIKKEIETSEPCSIHFTNYSILIGTNKFEYIDMKOYTL 1020
 Qy 1789 EEPIDKNDHSLAPVFAASNSPFSVIVQVNSAGOREEYLLCFHEFGVFDVSYGRSRSTD 1848
 Db 1021 EEPIDKNDHSLAPVFAASNSPFSVIVQVNSAGOREEYLLCFHEFGVFDVSYGRSRSTD 1080
 Qy 1849 DLKKSRLPLAFAYREPLYFVTHFNSLEYETEOARSSNACTPARAYLIDINPRYLGPALSSG 1908
 Db 1081 DLKKSRLPLAFAYREPLYFVTHFNSLEYETEOARSSNACTPARAYLIDINPRYLGPALSSG 1140
 Qy 1909 AIYLAASVQDRLARYICCKGNLVKESGTEHHRGPTSRSSPNKRGPPTYNEHITKRVASSP 1968
 Db 1141 AIYLAASVQDRLARYICCKGNLVKESGTEHHRGPTSRSSPNKRGPPTYNEHITKRVASSP 1200
 Qy 1969 APPEGSPHREPSTPHRYREGRTETLRDSDPGRPLEREKSPGRIILSTRERSPARLPEDS 2028
 Db 1201 APPEGSPHREPSTPHRYREGRTETLRDSDPGRPLEREKSPGRIILSTRERSPARLPEDS 1260
 Qy 2029 SRGRLPAGAVTPTLSQVKNKWDQSSV 2054
 Db 1261 SRGRLPAGAVTPTLSQVKNKWDQSSV 1286
 RESULT 7
 ID Q8C1J1 PRELIMINARY; PRT: 1032 AA.
 AC Q8C1J1;
 DT 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE C1c protein.
 GN Name=C1c;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whitey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strauberg R.;
 RN Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Strauberg R.;
 RN Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Contains 1 PH domain.
 DR EMBL; BC023775; AAH23775.1; -.
 DR EMBL; BC051165; AAH51165.1; -.

DR MED; MG1.105313; C1c.
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. . .; IEN.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEN.
 DR InterPro; IPR001180; C1c1on.
 DR InterPro; IPR005479; Cbp synth L_D2.
 DR InterPro; IPR002219; DAG_Pe-bind.
 DR InterPro; IPR001849; PH_Pe-related.
 DR InterPro; IPR011036; PH-related.
 DR Pfam; PF001130; C1_1; 1.
 DR Pfam; PF00780; CNH; 1.
 DR Pfam; PF00169; PH; 1.
 DR SMART; SMO0109; C1; 1.
 DR SMART; SMO0036; CNH; 1.
 DR SMART; SMO0233; PH; 1.
 DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
 DR PROSITE; PS00479; DAG_Pe BIND DOM_1; 1.
 DR PROSITE; PS50081; DAG_Pe BIND DOM_2; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR SEQUENCE 1032 AA; 116918 MW; 59ABDC9659DA33B CRC64;
 Query Match 48.2%; Score 5057.5; DB 2; Length 1032;
 Best Local Similarity 95.1%; Pred. No. 1.5e-137;
 Matches 982; Conservative 10; Mismatches 8; Indels 33; Gaps 4;
 Qy 1054 MEALKTCTMLEBOVMDLEALNDELKERQWEMARSVLGDKSGQFGRVRELQRLMDTE 1113
 Db 1 MEALKTCTMLEBOVMDLEALNDELKERQWEMARSVLGDKSGQFGRVRELQRLMDTE 60
 Qy 1114 KQSRARADORTESROVEALVKEHKAETLALQALKEQKAKSLSDKNDLKRKAML 1173
 Db 61 KQSRARADORTESROVEALVKEHKAETLALQALKEQKAKSLSDKNDLKRKAML 120
 Qy 1174 EMNARSLOQKLETERELKORLLBEQAKLQOQMDLOKNHIFLITQGLQALDRADLKTTER 1233
 Db 121 EMNARSLOQKLETERELKORLLBEQAKLQOQMDLOKNHIFLITQGLQALDRADLKTTER 180
 Qy 1234 SDLEYOLENTIOVLVSHKVKVMEGTISQOTKILIDFLQAKMDQPAKKK----- 1280
 Db 181 SDLEYOLENTIOVLVSHKVKVMEGTISQOTKILIDFLQAKMDQPAKKK----- 240
 Qy 1281 --VLOVNEKLALKEKRCARCAELEALQKTRIELRSAREAAHKAATDHPSTPATAR 1338
 Db 241 TVPLQVNEKLALKEKRCARCAELEALQKTRIELRSAREAAHKAATDHPSTPATAR 300
 Qy 1339 QQIMSAIVSPHEQHPAMSLAPSSRRKSSSTPEFSRLKRMHNIHPRFVGLAM 1398
 Db 301 QQIMSAIVSPHEQHPAMSLAPSSRRKSSSTPEFSRLKRMHNIHPRFVGLAM 360
 Qy 1399 RATCAVCLDTVHFGROASKLEQVCHPCSTCLPATGCLPAEYATHFEACRDKMN 1458
 Db 361 RATCAVCLDTVHFGROASKLEQVCHPCSTCLPATGCLPAEYATHFEACRDKMN 420
 Qy 1459 SPGLQTEPSSSLHLEGMMKVPKRNKKGQOQMDKRYIVLESKYLIDNEAREKQRPVE 1518
 Db 421 SPGLQTEPSSSLHLEGMMKVPKRNKKGQOQMDKRYIVLESKYLIDNEAREKQRPVE 480
 Qy 1519 EPELCLPDGDVSIHGAVGASGLANTAKADVYILKMESHPTTCMPGRTLYLAPSPDX 1578
 Db 481 EPELCLPDGDVSIHGAVGASGLANTAKADVYILKMESHPTTCMPGRTLYLAPSPDX 540
 Qy 1579 QRWTALESVAVGGRVREKAKADA-----KLGNLSLLKLEGGDRDLDMNC 1623
 Db 541 QRWTALESVAVGGRVREKAKADA-----KLGNLSLLKLEGGDRDLDMNC 600
 Qy 1624 TLPPSDOVVLTGTEBGLYALNVLKNSLTHVPGICAVQIYIIKOLEKYLMAAGEBALCL 1683
 Db 601 TLPPSDOVVLTGTEBGLYALNVLKNSLTHVPGICAVQIYIIKOLEKYLMAAGEBALCL 660
 Qy 1684 VDVKKVQSLAQSLPAPOPDISPVIPEAVKGCFLFGAGKLENGLCICAMPKSVVILRYN 1743
 Db 661 VDVKKVQSLAQSLPAPOPDISPVIPEAVKGCFLFGAGKLENGLCICAMPKSVVILRYN 720
 Qy 1744 ENLSKCYCIKKEIETSEPCSIHFTNYSILIGTNKFEYIDMKOYTLBEFLDKNDHSLAPAV 1803

Db	721	DNLSXYCIRKELETSEPCSTHPIFNYSLLIGTNKFYEIDMKQYTLDEFLDKNDHSLADAV	780
QY	1804	FAASNSFPVSIYQVNASAGOREEYLLCCHFEQVFDVSYGRSRITDLMKSRLLPLAFAYRE	1863
Db	781	FASSNSFPVSIYQVNASAGOREEYLLCCHFEQVFDVSYGRSRITDLMKSRLLPLAFAYRE	840
QY	1864	PYLPYTHNSLAEVIEIYQARSSAGTPARAYLDIPNRYIGPAISSGATYLAASSYODKLRVI	1923
Db	841	PYLPYTHNSLAEVIEIYQARSSAGTPARAYLDIPNRYIGPAISSGATYLAASSYODKLRVI	900
QY	1924	CKKGLVYSGEHNHRGPTSRSSSNKKGPPTYNHITKRYAASSPAPRPGESHPEPSTP	1983
Db	901	CKKGLVYSGEHNHRGPTSRSSSNKKGPPTYNHITKRYAASSPAPRPGESHPEPSTP	959
QY	1984	HRYY--REGRTELRDKSDPGRPLEREKSDPGRILSTRERSPARLPEDSSRGLPAGAVTTP	2041
Db	960	HRYYREGRTELRDKSDPGRPLEREKSDPGRILSTRERSPARLPEDSSRGLPAGAVTTP	1019
QY	2042	LSQVKKVWDQSSV 2054	
Db	1020	LSQVKKVWDQSSV 1032	

DR	06XUH8	PRELIMINARY;	PRT;	482 AA.
ID	06XUH8			
AC	06XUH8;			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	Cltrcn Rho-interacting kinase short form.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Mao Y., Xie Y., Wu Q.;			
RL	Submitted (JAN-2003) to the EMBL/Genbank/DBJ databases.			
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
DR	EMBL; AY209000; AAP43922.1; -.			
DR	HSSP; P05132; IATP.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0006468; F:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR011009; Kinase like.			
DR	InterPro; IPR000961; Kinase C.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	InterPro; IPR008271; Ser_thr_kin_AS.			
DR	InterPro; IPR001245; Tyr_kinase.			
DR	Pfam; PF00069; Pkinase; 1.			
DR	Pfam; PF00433; Pkinase C; 1.			
DR	Prodom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00220; S_TKC; 1.			
DR	SMART; SM00133; S_TK_X; 1.			
DR	SMART; SM00219; TyKc; 1.			
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.			
DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
SO	SEQUENCE 482 AA; 54353 MW; 4f02a6a32c73bae CRC64;			
QY	Query Match	23.7%;	Score 2492;	DB 2; Length 482;
	Best Local Similarity	99.4%;	Pred. No. 2.2e-64;	
	Matches 477; Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
DB	1 MLKFTYGARNPLDAGAEPIASRSASRLNLFQKGKPEFTOOMSPLSREGILDAFLVFE 60			
	1 MLKFTYGGARNSDGAEPIASRSASRLNLFQKGKPEFTOOMSPLSREGILDAFLVFE 60			

QY	61	EC	S	P	A	L	M	K	I	K	V	S	N	F	V	K	R	S	T	T	I	A	E	O	L	O	S	A	D	F	E	R	S	L	V	G	C	H	A	B	V	O	V	R	E	K	A	G	120								
Db	61	EC	S	P	A	L	M	K	I	K	V	S	N	F	V	K	R	S	T	T	I	A	E	O	L	O	S	A	D	F	E	R	S	L	V	G	C	H	A	B	V	O	V	R	E	K	A	G	120								
QY	61	EC	S	P	A	L	M	K	I	K	V	S	N	F	V	K	R	S	T	T	I	A	E	O	L	O	S	A	D	F	E	R	S	L	V	G	C	H	A	B	V	O	V	R	E	K	A	G	120								
Db	61	EC	S	P	A	L	M	K	I	K	V	S	N	F	V	K	R	S	T	T	I	A	E	O	L	O	S	A	D	F	E	R	S	L	V	G	C	H	A	B	V	O	V	R	E	K	A	G	120								
QY	121	D	I	A	K	W	K	K	A	L	A	O	E	V	S	F	F	E	E	R	N	L	S	R	S	T	S	M	I	P	O	L	O	A	F	O	D	K	N	L	Y	L	M	E	O	P	G	180									
Db	121	D	I	A	K	W	K	K	A	L	A	O	E	V	S	F	F	E	E	R	N	L	S	R	S	T	S	M	I	P	O	L	O	A	F	O	D	K	N	L	Y	L	M	E	O	P	G	180									
QY	181	D	L	S	L	N	E	Y	E	D	O	L	E	N	L	I	O	F	Y	L	A	E	L	I	L	A	V	S	V	H	L	M	G	Y	H	R	D	I	K	P	E	N	I	L	V	D	R	T	G	H	I	K	L	V	D	F	240
Db	181	D	L	S	L	N	E	Y	E	D	O	L	E	N	L	I	O	F	Y	L	A	E	L	I	L	A	V	S	V	H	L	M	G	Y	H	R	D	I	K	P	E	N	I	L	V	D	R	T	G	H	I	K	L	V	D	F	240
QY	241	G	S	A	A	M	M	S	N	K	W	N	A	L	P	I	G	T	P	D	Y	A	B	E	V	L	T	Y	M	N	G	G	K	G	T	G	L	D	C	M	S	V	G	A	Y	A	E	M	I	Y	E	R	300				
Db	241	G	S	A	A	M	M	S	N	K	W	N	A	L	P	I	G	T	P	D	Y	A	B	E	V	L	T	Y	M	N	G	G	K	G	T	G	L	D	C	M	S	V	G	A	Y	A	E	M	I	Y	E	R	300				
QY	301	S	P	E	A	R	G	T	S	A	R	T	F	N	N	I	M	N	F	O	R	L	K	F	P	D	D	K	V	S	D	F	D	L	I	O	S	L	I	C	G	O	K	E	R	I	K	F	E	G	L	C	H	P	P	F	360
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QY	361	S	K	I	D	M	N	N	I	R	N	S	P	P	V	P	T	L	K	S	D	D	T	S	N	F	D	E	P	E	K	S	W	S	S	P	C	O	L	S	P	S	G	F	S	G	E	L	P	V	G	S	420				
Db	361	S	K	I	D	M	N	N	I	R	N	S	P	P	V	P	T	L	K	S	D	D	T	S	N	F	D	E	P	E	K	S	W	S	S	P	C	O	L	S	P	S	G	F	S	G	E	L	P	V	G	S	420				
QY	421	Y	S	K	A	L	I	G	I	R	S	B	S	V	S	G	L	D	S	P	A	K	T	S	S	M	E	K	K	L	I	K	E	L</																							

ID	088937	PRELIMINARY;	PRT;	494 AA.
AC	088937;			
DT	01-NOV-1998	(TREMBLrel. 08, Created)		
DT	01-NOV-1998	(TREMBLrel. 08, last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, last annotation update)		
DE	Rho/rac-interacting citron kinase short isoform.			
GN	Name=Cit; Synonyms=Crik-8k;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99009084; PubMed=9792683; DOI=10.1074/jbc.273.45.29706;			
RA	Di Cunto F., Calautti E., Hsiao J., Ong L., Topley G., Turco E.,			
RA	Docto G.P.;			
RT	"Citron rho-interacting kinase, a novel tissue-specific ser/chr kinase			
RT	encompassing the Rho-Rac-binding protein Citron."			
RL	J. Biol. Chem. 273:29706-29711(1998).			
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
DR	EMBL; AF086823; AAC72822.1; -.			
DR	HSSP; P31751; IMRV.			
DR	MGD; MGI:105313; Cit.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR011009; Kinase_C.			
DR	InterPro; IPR000961; Kinase_C.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	InterPro; IPR008271; Ser_thr_kin_AS.			
DR	Pfam; PF00069; Kinase; 1.			
DR	Pfam; PF00433; Kinase_C; 1.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SMO0220; S_TKc; 1.			
DR	SMART; SMO0133; S_TK_X; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			

SQ SEQUENCE 494 AA; 55742 MW; 2C60D2294B28A185 CRC64;
 Query Match 20.7%; Score 2175.5; DB 2; Length 494;
 Best Local Similarity 88.2%; Pred. No. 2.6e-55;
 Matches 413; Conservative 25; Mismatches 29; Indels 1; Gaps 1;
 QY 1 MLKRYGARNPLDGAAPIASRASRLNLFQGRPPPTQOQMSPLSEGLDALFVLE 60
 DB 1 MLKRYGARNPLDGAAPIASRASRLNLFQGRPPPTQOQMSPLSEGLDALFVLE 60
 QY 61 ECSOPALMKIKHVSNFPRKYSDDTIAEIOELQPSAKDFEVSILVCGHFAEYQVVERKATG 120
 DB 61 ECSOPALMKIKHVSNFPRKYSDDTIAEIOELQPSAKDFEVSILVCGHFAEYQVVERKATG 120
 QY 121 DIYAMKVMKKKALLAEOQVSPFEEERNILSRSTSPMIPOLOAFQDKNHLVMEYQPG 180
 DB 121 DIYAMKVMKKKALLAEOQVSPFEEERNILSRSTSPMIPOLOAFQDKNHLVMEYQPG 180
 QY 121 DVMAMKIMKKKALLAEOQVSPFEEERNILSRSTSPMIPOLOAFQDKNHLVMEYQPG 180
 DB 121 DVMAMKIMKKKALLAEOQVSPFEEERNILSRSTSPMIPOLOAFQDKNHLVMEYQPG 180
 QY 181 DLSLNRYEDQDENIIOFYLAELILAVSHVLMGVHRDIRENILLVDRTHIKLVDF 240
 DB 181 DLSLNRYEDQDENIIOFYLAELILAVSHVLMGVHRDIRENILLVDRTHIKLVDF 240
 QY 241 GSAAKNNSNMVNAKLPFGPDYAPVLYTMNGDGKGTGLDCDMNSVGVAYEMVYGR 300
 DB 241 GSAAKNNSNMVNAKLPFGPDYAPVLYTMNGDGKGTGLDCDMNSVGVAYEMVYGR 300
 QY 301 SPFAEGTSARTFNINMFORFLKPPDPKVSDFDLIOQLCGQKRLKEGICHPFF 360
 DB 301 SPFAEGTSARTFNINMFORFLKPPDPKVSDFDLIOQLCGQKRLKEGICHPFF 360
 QY 300 TPFEGTSARTFNINMFORFLKPPDPKVSDFDLIOQLCGQKRLKEGICHPFF 359
 DB 300 TPFEGTSARTFNINMFORFLKPPDPKVSDFDLIOQLCGQKRLKEGICHPFF 359
 QY 361 SKIDMNNIRNSPPFVPTLKSDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 420
 DB 361 SKIDMNNIRNSPPFVPTLKSDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 420
 QY 360 ARTDMNNIRNSPPFVPTLKSDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 419
 DB 360 ARTDMNNIRNSPPFVPTLKSDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 419
 QY 421 YSKALGILGRSESVSGLDSPAKTSMEKLLIKSKELQDSODCHXK 468
 DB 421 YSKALGILGRSESVSGLDSPAKTSMEKLLIKSKELQDSODCHXK 467
 RESULT 10
 088527 PRELIMINARY; PRT; 448 AA.
 AC 088527;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Cyttron-K kinase (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Madanave F., Eda M., Matanabe N., Fujisawa K., Matsunaka T., Bito H.,
 RA Ichizaki T., Narumiya S.;
 RT "Role of Cyttron kinase as a target of the small GTPase Rho in
 RT cytolysis";
 RL Nature 0:0-0(1998).
 CC -1- SMILARITY: Belong to the Ser/Thr protein kinase family.
 CC EMBL; AF070065; AAC27932.1; -.
 DR HSSP; P31751; IMRV.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase_Like.
 DR InterPro; IPR000961; Kinase_C.
 DR InterPro; IPR000719; Prot. Kinase.
 DR InterPro; IPR002290; Ser. Thr. Kinase.
 DR InterPro; IPR008271; Ser. Thr. Kinase.
 DR Pfam; PF00069; Kinase_Like.
 DR Pfam; PF00433; Kinase_C; 1.
 DR ProDom; PD000001; Prot_Kinase; 1.

DR SMART; SMO0220; S_TK_X; 1.
 DR SMART; SMO0133; S_TK_X; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00101; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00106; PROTEIN KINASE ST; 1.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER
 SQ SEQUENCE 448 AA; 50650 MW; 548CA5A8EA46394 CRC64;
 Query Match 20.6%; Score 2160.5; DB 2; Length 448;
 Best Local Similarity 91.1%; Pred. No. 6.3e-55;
 Matches 409; Conservative 20; Mismatches 19; Indels 1; Gaps 1;
 QY 1 MLKRYGARNPLDGAAPIASRASRLNLFQGRPPPTQOQMSPLSEGLDALFVLE 60
 DB 1 MLKRYGARNPLDGAAPIASRASRLNLFQGRPPPTQOQMSPLSEGLDALFVLE 60
 QY 61 ECSOPALMKIKHVSNFPRKYSDDTIAEIOELQPSAKDFEVSILVCGHFAEYQVVERKATG 120
 DB 61 ECSOPALMKIKHVSNFPRKYSDDTIAEIOELQPSAKDFEVSILVCGHFAEYQVVERKATG 120
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 DB 121 DIYAMKVMKKKALLAEOQVSPFEEERNILSRSTSPMIPOLOAFQDKNHLVMEYQPG 180
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 DB 181 DLSLNRYEDQDENIIOFYLAELILAVSHVLMGVHRDIRENILLVDRTHIKLVDF 240
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 DB 241 GSAAKNNSNMVNAKLPFGPDYAPVLYTMNGDGKGTGLDCDMNSVGVAYEMVYGR 300
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 DB 241 GSAAKNNSNMVNAKLPFGPDYAPVLYTMNGDGKGTGLDCDMNSVGVAYEMVYGR 299
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 DB 300 TPFEGTSARTFNINMFORFLKPPDPKVSDFDLIOQLCGQKRLKEGICHPFF 359
 QY 361 SKIDMNNIRNSPPFVPTLKSDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 420
 DB 361 SKIDMNNIRNSPPFVPTLKSDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 420
 QY 360 ARTDMNNIRNSPPFVPTLKSDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 419
 DB 360 ARTDMNNIRNSPPFVPTLKSDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 419
 QY 421 YSKALGILGRSESVSGLDSPAKTSMEK 448
 DB 421 YSKALGILGRSESVSGLDSPAKTSMEK 448
 RESULT 11
 09VTY8 PRELIMINARY; PRT; 1854 AA.
 AC 09VTY8;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE CG10522-PA.
 GN ORFNames=CG10522;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoekstra R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champs M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 RA Bailey R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benoit P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahler C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.U., Wei M.H., Ibegwan C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira K., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusekern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen T.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C.D., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgerger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frishe E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Taber P.E., Man K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminler J.S., Bergman C.M., Krommiller B., Carlson J., Svirkas R.,
RA Patel S., Frishe E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminler J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu U., Betman B.P.,
RA Bellocourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB003541; AAFA9907.2; -.
DR HSSP; P31751; IMRY.

DR Intact; Q9VY78; -.
DR FlyBase; FBgn0036295; CG10522.
DR GO; GO:0000910; P:cytokinesis; IMP.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000961; Kinase C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00433; Kinase_C; 1.
DR SMART; SM00109; Cl_1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PSS0081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PSS0107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PSS0108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1854 AA; 211323 MW; 93E5B69FB63DEBD CRC64;

Query Match 17.4%; Score 1822; DB 2; Length 1854;
Best Local Similarity 26.7%; Pred. No. 1.1e-44;

Matches 556; Conservative 406; Mismatches 646; Indels 474; Gaps 72;

QY 18 EPIASRASRLNLPFGQKP-----PMTQOQMSPLS-----REG 50
DB 6 EPIASVARTARLNMLILKKGAGVCAKPAAGSASGSGIPASTRSIRYVSTTSAVAEALICREG 65
QY 51 IIDLAFVLPBESQAPALMK-IKHVSFVKRYSDTIAELOPSADQFEVRSIVGCGHRA 109
DB 66 IIDLAFCLIVBECCKDITLKRDRIAIEFVKFRPIIETRTLRNADDFIKILIGGYRG 125
QY 110 EYGVASEKATGDIYANKWKKKALLAQEQVSPFEERNTLSRSTSWIPLOLYAFQDKXN 169
DB 126 NVHLVVERQNDIYANKKIKKSVVTSQ-----VKESRDWISIRNSMLNLQAFQNDN 181
QY 170 LYLWMEYOPGGDLSLNLNRYEDQDLENLIQFYLAELILAVSHVHLNGVYHARDIKPENTLV 229
DB 182 LYLWMEYMGDGLSLMSRSH-GPFDEDLARFYLAELITVLAHLTHENGVYHARDIKPENTLV 240
QY 230 DRTGHIKLVDFSGAAMNSKRNVAKLPIGTDPYNAEVLVTWNGD-GKITYGLDCDWM 287
DB 241 DRTGHIKLVDFSGAALNDRDGHVLSLSPVGTPIYIPELQITSLYKLSKSMHDSVCDTW 300
QY 288 SVGVIVYEMITGSGPPAEGTSARTENNIM-----NFGRIKPPDDPKYSDFLILQSL 341
DB 301 SWGIIIGYELICETTPHEDNVHETYSKILSHCBESHLKELISFPADLKVSVNRNLIESL 360
QY 342 LCGQKERLKEBGLCHPFFSKIDMNNIRNSPPFVPTLKSDDTSNFD-----PERN 394
DB 361 VYMSKRLSYERIKNHPFSEIPWGSIRGOVPIITVYASDDTSNFDGIRHKTRREG 420
QY 395 SWVSSPPQQLSPBGSFGEELPYVGSYKALGILGRSESVSGLDSPATSSMEKLLIK 454
DB 421 VAKKSLTTWKKSDIFSGKDLPIFGYSFVH-----MEKSAISATDETLQOR 466
QY 455 SKS-----LQDSQCKHKMQEMTRLH---RVSEVAVYLSQKEVELKASSETQSLLEQL 507
DB 467 LKELIOLKLTREIEISMLKODILRAQOSLRKTDNKSQVADAMEIK-KLQOIIKEKTM 524
QY 508 ATYITECSSLKSLSE-QARMEVSQEDKALQLLHDIREQSRKLQETK---EOEYQAOVBE 563
DB 525 E-LTTCKQIKTLQGSAKIDEEMSKKATITDLRLRKQRYEKKIKSBOQRYEQQLAD 582
QY 564 MRLMNNQLBEDLVASARRSDLYSESLRBSRLAAEFKRAATEQOR---KLRAKQCKPE 620
DB 583 KK-----QELASTIQKLDAREL-----EFNAKFECKHSLMKIYQKDWLQOI 625
QY 621 VGEYATLEKIKNAEQULKIOELQKLEKAVKASTAEATELLQNTROAKE---PARELEKIO 677

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Db 626 KEONLKSEPTNHEBOQRQMAELIYEQ-----KLTDRKKVRSQDTNRBMTEIKEIR 676
Qy 678 NREDESSBICRIKVLVEA-----BERRHSLEKVKLETMERRENRKIDDIQYSSQIQ 729
Db 677 TELDESISSKSTOBAKNATERNIEILRLNEIASNNIEIAEKVKLETQLKENETQ 736
Qy 730 QMAKILELEKHEEAQVSAHLEVHLKQKQHYE-----EKIKVLDNQIKD-LADKE 782
Db 737 EVRAECHRLELOLAECRCQLAESSLATQVSPYETAPGSLTELNALIDQLRADILAKE 796
Qy 783 T-----LENNMORHEEAEHKKGLISEOKA-----MINAMDSKIRS 818
Db 797 SENHQKGRADOLQTLVTKLEOMLERFNGQSLSPTKSHSRKQOEGEVTADMLERQNEKIED 856
Qy 819 -----LEQRIVLESEANKLANSSILFQRRNKAQOEEMISE--LRQOKFYLETQAGKLEA 870
Db 857 KLAABRQMIYERQAAAR--TANLSIM--KVEKQLEALSEKKLARRELTEDRLTKKQVN 912
Qy 871 QNRKLEBOLEKISHQSDSKRRLLELETRL-----REVSLEH-----EQQLLEKRLQLTE 920
Db 913 ASDAQORMLKTSQEBTRORESRIEELKQELAAAKRDVLKEHROWEKAEQOEHRMKCKSEIIE 972
Qy 921 LQLSIORESQUTALQAAABALLESOLROAKTELEBTTAEABEIOALTANHDEIOKPKDA 980
Db 973 HLANVHLEQOETEIR-----QKRLQISRFEGVTILEQNTTIRELOEERKSKRANKD- 1024
Qy 981 LRNSCTVITDLEBOQLTJEDNAILNNQNFYLSKQLEASGANDIYOLRSEVHLRREI 1040
Db 1025 ---SCLV---LQKELKQLTID-----NF--QRLKACGSTITDS-----QL 1054
Qy 1041 TEREMQLTQOKQOTMEALKTTCTMLEBOVMDEBALNDELLEKEROMEAMRSVLGDEKSOFE 1100
Db 1055 TEVTMTLKSSEBERKRSOKS-----QJDTLHEKIRENDQ----- 1088
Qy 1101 CRVELORMJLDTKOSRABADQ---ITESQVVELAVKEHKAELILQOALKXEOKLKAE 1157
Db 1089 --LTLDRKQLTVESSEKRLAEQRAQVLASETIDELRLNKEQOKCVLAQDQQLVEQ---- 1141
Qy 1158 SLSDKLDNLEKXGAMLE-MNARSLOQKLETERELKORLLEBOAKLQOQMDLQKNHIFL- 1215
Db 1142 --TVALFATQORABILQGNQNNYEAQTPADSREWVS--LKENANILISLFPKKEBVGNTQ 1198
Qy 1216 --TQGLQALDRADLLKTERSDLEYQLENIQVLYSHEKVKMEGTSIQOTKLIDFLQAKM- 1272
Db 1199 AEIRIGLESAA-QAN-LHAIEDISLQDTLAEKQFYQORDIKSNATLAQHKKIDVLIQKVE 1255
Qy 1273 DQPAKKKKV-----PLQVNEKLALKEKARCAELEALQKT 1309
Db 1256 DLSAKKKKTLADKLPGSSHTNKENVSPNDVSSITLYRLAKELREBQKMSLKEQLAQ 1315
Qy 1310 R--TELRSABEAAHRAKATDHPHPSTPATARQOIAMSAIVSPHPQPSAMSLAPSSRR 1367
Db 1316 NGRTILASPRAKSAVANDSDAP-----KQRPVSIALPSPKQOOP--LKRITTSQV 1365
Qy 1368 KESSTPEEPFSRRLKERMHNIIPHPFNVL--NNRATKCAVCLDTVHFGRQASKCLEQV 1424
Db 1366 ELKTTAKPTKVTIENQAH--HRFELALQSKYDAVAVCVCEKAVVAGSPFMCKECKD 1422
Qy 1425 MCHPKCCTCLPATQGLPAEYVITHTEAFCRKQKMSPGIQTEPSSSLHLEBGMVAPRRNK 1444
Db 1423 VTHRKCASNVOHSG-----STKPTA----- 1443
Qy 1485 RGQOGMRKYVILEGSKVLIYDNEAREAGQRPVEEFELCLPDGVSJHGAVALANTYA 1544
Db 1444 -----PSAD----- 1447
Qy 1545 KADVPIYLKMHSHPTTCWPGRTLYLLAPSPDKORWTALASV--VAGGRVSRKABADA 1603
Db 1448 --DLSSIQSVSS-----LTLDSVDVAGGTSS-----GG 1473
Qy 1604 KLGNSLKLKEGDD-----RLDMNCTLPFSD-QVIVNGTEBGLYALANVLKNSLTHVIGIG 1657
Db 1474 EYIGSLVYSSDGAEDQARKEIEVCAFEVAEQIILLGCGNTGLAYHLDQRLVHISGLE 1533

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Qy 1658 AVFOIYIITKLEKLMT--AGEERALCLVDYKVK---QSLAQSHLPAPQDIS-----PN 1707
Db 1534 SVSCMSICKRLAKAIMVGTQEKLYOC--DYROLESRCQSSSSCHKPVLRTSALELPPAN 1591
Qy 1708 IFEAVKGCCHLEFACKITNGU--CICAMPASVULIRVNMENSKYCIRKEIFTEPSCGII 1765
Db 1592 RTPEBKMLVLIISBAEALDSVAIAATSTIVLTKLDLKHMFEPVALDTATPVTISIF 1651
Qy 1766 FTNYSILIGTNKFPYEDIMKQYTLLEFLDKNDHSIAPAVFAASNSFPVSIQVNSAGORE 1825
Db 1652 FTRHSALVSSDPKFEILDNDNAEFPVLSKSM-----ESTACQPLTAVRIS-----RQ 1702
Qy 1826 EYLICFHEPGFVVDSYGRSRSTDDLKMSRLPLAPAYREPVLFTHPNSLEVIET----- 1879
Db 1703 EYLICFAEYGVFVDFECRSRPYDLNWWYAPTGFVYNDPFLFIHSYGQVQIIRLHRSFSK 1762
Qy 1880 -----QARSSAGRP--ARAVLDPNPRYLGPAL-SSGAYIL 1912
Db 1763 EMASGDNASENSESPELQRYVL---PHYMSTLLANSQDVNL 1800

RESULT 12
ID 054874 PRELIMINARY; PRT; 1732 AA.
AC 054874;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Myronic dystrophy kinase-related Cdc42-binding kinase.
GN Name=NRCK;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98078670; PubMed=9418861;
RA Leung T., Chen X.-Q., Tan I., Manser E., Lim L.;
RT "Myronic dystrophy kinase-related Cdc42-binding kinase acts as a
RT Cdc42 effector in promoting cytoskeletal reorganization.";
RL Mol. Cell. Biol. 18:130-140 (1998).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL: AF021935; AAC02941.1; -.
DR PIR: T14039; T14039.
DR HSBP; P31751; IMRY.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0004674; F:Protein serine/threonine kinase activity; IEA.
DR GO: GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0007242; P:intracellular signaling cascade; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR002219; DAG_Pe-Bind.
DR InterPro: IPR001180; Citron.
DR InterPro: IPR002219; DAG_Pe-Bind.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR000095; PAKbox/rhoBindng.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000961; Kinase_C.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR002290; Ser Thr kinase.
DR InterPro: IPR008271; Ser_Chtr_pkin_AS.
DR Pfam; PF00130; Cl_1.1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00008; DAGPDOMAIN.
DR PRODOM; PD0000001; Prot_kinase; 1.
DR SMART; SM00109; Cl_1.
DR SMART; SM00036; CNH; 1.

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DR SMART; SM00285; PBD; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00220; S TK; 1.
 DR SMART; SM00133; S TK X; 1.
 DR PROSITE; PS00108; CRIB; 1.
 DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN_1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 1732 AA; 197062 MW; 65f62f7872ACCD3B CRC64;

Query Match 14.5%; Score 1524.5; DB 2; Length 1732;
 Best Local Similarity 24.8%; Pred. No. 3.5e-36;
 Matches 523; Conservative 335; Mismatches 667; Indels 599; Gaps 76;

QY 36 PFMTQOQMSPLSRGILDAFLVEECSQPALMKIKVSNFVRKYSDTLAELOQSPAK 95
 DB 18 PAQINGQC--FSVETLIDILICLYDECNNSPLRKNIKLELWAKPFTSKVMRLHRE 75
 QY 96 DFEVRLVGGCHPAEYQVVRPKATGDIYAMKVMKKKLLAEOQVSPFEERENILSRSTP 155
 DB 76 DFEILKVIIGRAFGAEVAVVKKLNADKVFAMKIINKMEMLKKAETACREERDVLVNGDSK 135
 QY 156 WIPOLQAFODKNIYVMEYOPGDDLILNRYEDQDENTLIQVLAELIIVASHVM 215
 DB 136 WITTLHAFFODNNILYVMDYVGGDLITLTSKEDLPEEMARFYLAEMWIALDSYHQL 195
 QY 216 GYVHRDIKPNILVDRTGHI KLVDFGSAIKNSKRNVAKLPIGTDPYMAEVLTVANGD 275
 DB 196 HYVHRDIKPNILVDRTGHI KLVDFGSAIKNSKRNVAKLPIGTDPYMAEVLTVANGD 254
 QY 276 GKGTGYGDCWMSVGVIAEMITIGRSPABGTSAKTENININPGRFLKFPD -PKVSDP 334
 DB 255 GKRGYGECCWMSVGVICMYEMLYGETPFYAESLIVETYGKIMNHKRPQFPQVTVSENA 314
 QY 335 LDILOSLLCGQKELKEFGL---CCHPFFSKIDNNINRNSPPPLTKSDDDTSNDEP 391
 DB 315 KDILRLICREHRLGONGIEDFKGHPFSGIDMDNINRNCARFYIPEVSSDTDSNDDVD 374
 QY 392 E---KNSWSSPQCLSPSGFSGELPFVGFYSKALGILGRS-----ESV 434
 DB 375 DDCLKNSGEMTPP---THTAFSGHHLPFVGFYTSVCLVSDRGLRYAGPTSLDLVNV 431
 QY 435 VSGIDSPAKTSSMEKLLIISKELQDSODCKHKEOENTRLHRYSE---VEAV-LSQK 489
 DB 432 QRTLDNNIATEAVERRI-----KRLKEOERLELTRKLOESTOTVQALQYSTV 477
 QY 490 EVELKASETRQSLLEOPLATYITECSSIKSLLEOARMEVSOEDKALQLLHIDINEQSKL 549
 DB 478 DGPITLTA---KDL---EIKSLKEITEKRLQVAVEN----- 507
 QY 550 QEIKGEYOQAVEEMRLMMQLEEDLVASRRRSDLYSELEESRLAAEFGRKATTECOHK 609
 DB 508 -----HLEQGLEE---ANSVREILDAPRQIKAFEQIKTLQOEERBELINKELVQVSR 557
 QY 610 LIAKADQKPEVGVATLEKINAEOQLKIQLOELKEKAVASTAETALNTITQAKERA 665
 DB 558 L---KNSK-----ELKDAHCOCKLAMOFMEINERLTETLHQOKLTAHVADKKEEV 607
 QY 670 ERELKEQNMEDSEGIIRKULVEABERRHSLENVKVLJETMERERENLKODIQKSOQIQ 729
 DB 608 DLVWQK-----AESIRQELRRAERAKELVETTEALIAASOKRKLREGRSRIYSQLE 660
 QY 730 QMADKILEBEKREAOVSAQHLEVHLKQKQHYEBEKIKVLDNO-----IKDLADKETL 784
 DB 661 N-----ELE-----GLKQKQISYSPGICSEIHQOBITKKTDLKKSIF 699
 QY 785 ENMMQRHEEAEHKGKLLSEQKAMINAMDSKIRSLRQRIYELSTANKLANSSIFTORNM 844

DB 700 -----YEEETSRREGIHA-----SEINLUKKEELHND -SEGQOLANKKEIMV----- 738
 QY 845 KAOEEMISELROQKFFLETQAGKLEAQNKRLEBOLEKISHQSDSKNRLLLETLREVS 904
 DB 739 -----LKDKEK-----TR-RESQ 751
 QY 905 LHEBEQKLEIKRQUTLQSLQREESQUTLQAAABAASQLAQAQTELEETTAABEEI 964
 DB 752 SEREEFENERKQO-----YEREVYL----- 771
 QY 965 QALTARDEIQRFADLRNSCTVITDLBEQANQLTEDNEMANNQNFYLSKQLDASGAND 1024
 DB 772 -----LTENKUL----- 780
 QY 1025 EIVQLSREVLDHREITEREMQUTSQKQVMEALKTCTMLEBOVMDLEALNDELKERQ 1084
 DB 781 -----SELD-----KLTSS---LYESISLRNQHLEEVKDLA---DKKESVAV 816
 QY 1085 WEAMRSVLDGKSQFECRVRELQRMIDTEKQSRARADQRTESRQVVELAVKEHKAELIA 1144
 DB 817 WEA-----QITEIILQWVSDERDARG-----YIOLALA 842
 QY 1145 LQOALKEOKLKAESLSDKLNDEL---KKHAMLEMNAR-SIQOKLETERELKORLLEQAK 1200
 DB 843 SKATTEBELALRNSLSIGTRATDMQMKRRPRAKLDMASARLEIQSLADAEIRAKQALQBELNK 902
 QY 1201 LQOQMDLQKNHIFRLTQGLQELADRADLLETESDLEYLEQENIQVLYSHEKVMGTTISQ 1260
 DB 903 VK-----ASNITTECKLKDKSEKKNLEISEIQLIKDTELESEKGVH 946
 QY 1261 QTKLIDFLQAKMQPRAKKKVPLOVNEIKALEKEKARCALEBALQKRIELRSAREEA 1320
 DB 947 RDSQSEFL-AFLWTP-----DADQEE--RS----- 970
 QY 1321 AHRKATDHPHS--TPATARQOIAMSAIVSRSEHQPSAMSLAPPSRRKESSTPEERSR 1379
 DB 971 -----PSTCPAKGRRIADSAFL--PVNTPL-----RKKCCPASAGPPK 1009
 QY 1380 LKERMEHNIIPHRNVLGNMKAATCAVCLD-TVHFGQASKCLEQVWCHPKSTCLPATC 1438
 DB 1010 RK-----THQFVFSFAPATKCHQCTSLMVLGIRQSCCEVGSCHITCVNAKAPTTG 1062
 QY 1439 GLPAEYATHTFAFCDDKNSPGLQTER-----SSSLHGGMKVPPNNKRG-QQGW 1490
 DB 1063 PVPE-----QTKGPIGIDPQKGVGTAYVGHVRIK-PAGVKGW 1101
 QY 1491 DRKYIVLESGKVLIDYNEAREAGO-RPVEEFELCLPDGVSIHGAVASLANTAKADVP 1549
 DB 1102 QRALAVVCPKFLYLIDABGASQPSYSIQVIDKDEPFSV--SSVLASDVHIASRKDIP 1160
 QY 1550 YILKMB---SHPTTCWPGRTYLLAPSPDDKQWVTALAESVAVAGRVSRKAADAKL 1605
 DB 1161 CIFRYVASQULSAPSDK-----STLMADSETERSKNVGVLSL---HKVLKKNKFRDRSV 1213
 QY 1606 LQNSLKLQGDDBLDNACTLP-----PSDQVVLVTEBEGYALANVLKNSLTHVPG 1655
 DB 1214 ---YVPKEAYD-----STLPILKTTQAAIIDHERVALNENEGFLVAVHTQKELIIRVG 1264
 QY 1656 IGAVFOIYIILKLEKLMINGEERALCLVDVKVQKSLAQSHLPAOPDISPIFEAVKGC 1715
 DB 1265 NKKHQLELPSQOLVAVLSGRNRHVALFPMSALYDRETFYKLA-----TKGC 1314
 QY 1716 HLFQAGKIENGL--CICAMPKRVILRYVENLSKYCIRKEIBTSEPCSIHFTNVS--I 1771
 DB 1315 QTLAAGVHRGALSCICVANKRQVLCVELPQSTRHKKFEIQV--PCNVQMAIFSEHL 1372
 QY 1772 LIGTNKFEYIDMKQYTL-----EPLDKDHLAPVPAASNSPVSIVQVNSAQORE 1825
 DB 1373 CVG---FQSGFLRYPLNGRSPCNMLHSDHTLA---FITTHQPMALCAVEISN---K 1421
 QY 1826 EYLLCFHEPQVFDVSGRGRSRTDLDKMSRLPLFAVAREPLFPTHFNSLVIEVIOARSSA 1885
 DB 1422 EYLLCFSSISITVDCQGRSRQOELMMPANPSSCTNAPLISYSENAVUIDPVNSHWEI 1481

QY 1886 GTPARAYLIDIPNRYLGPATSSGAIYLAASYQDKLRYVCKGNLVKES-----GTEHHRG 1940
 Db 1482 QT-----LPLEKVR-----PLNTGSLINLLG--LETRILRYFNKRAEGDELVPETSDNSR 1531
 QY 1941 PSTSRSSPNKR-----GPPTYNE-----HI 1960
 Db 1532 KQVKNINNNKRRYFRVPEERMOQRNMLDPEKRNKLINPTVFNHIAHMGPGDGIQT 1591
 QY 1961 TKRVASSPAPPEG-----PSHPREPSTPHRYEGRTLE--RRDKSPGRPLEREKS 2008
 Db 1592 LKQIPMNPPESESTVSGSVISITKSRPEPGRSMASAGLSARSAQNGSLAKHEFS 1651
 QY 2009 PGRILSTRERKSPARLFEDSSGRPLPAGAV 2038
 Db 1652 GGS-YNTKROPMP-----PSEGLSSGCV 1675

RESULT 13
 Q86XX3
 ID Q86XX3 PRELIMINARY; PRT; 1719 AA.
 AC Q86XX3;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE CD042 binding protein kinase alpha (DMPK-like).
 GN Name=CD042BPA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Wilkinson S., Marshall C.J.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 CC -1- SIMILARITY: Contains 1 PH domain.
 DR EMBL; AJ518975; CAD57745.1; -.
 DR HSSP; P31751; IMRY.
 DR GO; GO:0016030; C:membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR001180; Citron.
 DR InterPro; IPR002219; DAG_PE-bind.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR01304; Lectin_C.
 DR InterPro; IPR003345; M repeat.
 DR InterPro; IPR000095; Pakbox/Rhoindng.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR000961; Kinase_C.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF00130; Cl_1; 1.
 DR Pfam; PF00780; CNH; 1.
 DR Pfam; PF02370; M; 1.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00433; Pkinase_C; 1.
 DR PRINTS; PR00006; DAGPEDOMAIN.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00109; Cl_1.
 DR SMART; SM00036; CNH; 1.
 DR SMART; SM00285; PBD; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00133; S_TK_X; 1.
 DR PROSITE; PS50108; CRIB; 1.

DR PROSITE; PS00615; C TYPE LECTIN 1; UNKNOWN 1.
 DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50003; PH DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 1719 AA; 195949 MW; DB15FA8611D9871 CRC64;

Query Match 14.2%; Score 1489; DB 2; Length 1719;
 Best local similarity 24.1%; Pred. No. 3.6e-35;
 Matches 523; Conservative 330; Mismatches 628; Indels 666; Gaps 76;

QY 36 PFMTQQQMSPLSREGILDALFVLEFECSPALMKIKVSNFVRKYSPTIAELQELQPSAK 95
 Db 18 PAQTNQGC--FSVETLLDILICLYDECNNSPLREKNILEVLWAKPFTSKVQKMRHRE 75
 QY 96 DFEVRSLVGCGHFAEVOVREKATGDIYAKVKKKKLLAQOVSFFEEENIISRSTP 155
 Db 76 DFEILKVIYGRGAFGEVAVVVKLNADKVFAMKILKWEMLKRAETACREERDVLVNGDNK 135
 QY 156 WIPQLOVAFQDQKHLVIMVEYQPGDLSLIRYEDQDENTLIQFYLAELILAVSHYLM 215
 Db 136 WITTLHYAFQDDNNLYVMWDIVYGGDLTLTLSTKFEDELPEDMARFYLAEMVTAIDSVHQL 195
 QY 216 GYVARDIKPENILVDRGTGHTKLVDFGSAAKNSKNVNAKPLIGTPDYMAPEVLTVMNGD 275
 Db 196 HYVARDIKPENILMDNMGHRLADFGSCCLKMEGTQSSVAVGTPDYISIELIQANE-D 254
 QY 276 GKGTYGLDCPMWSGVVIAIYENTYGRSPABSTARTNNINNFQRLKFPDD-PRVSSDF 334
 Db 255 GKGRYGPECDMWSLGVCMYELVGETPFYASLVEYGIKIMNHKRRQFPQAVTDVSENA 314
 QY 335 LDILQSLCCQKRETKREGI---CCHPEFSKIDMNNIRNSPPVPVPLKSDDDNSPPEP 391
 Db 315 KDILRLRISREHNLGONGIEDFKHPFFSGIDMDNIRNCEAPYIPEVSSPTDTSNFPVD 374
 QY 392 E---KNSWVSSPCQLSPSGSGEELPFVGSYKALIGRS-----ESV 434
 Db 375 DDCLAKSETPPP---HTTAFSGHILPFVGFYTTSSCVLSDRSLRTAGTSLDLQNV 431
 QY 435 VSGLDSPAKTSMEKKLLIKSKELQSDQCHKNGQEMTRILHRVSE---VEA----- 484
 Db 432 QRTLDNNLATEAVERRI-----KRLEGKELSRKLGSTQVQALQYSTV 477
 QY 485 ---VLSQKEVELKASETQSLLE--QDLATYITFESSLSLSEQARNEVQEDDKALQL 539
 Db 478 DGPLTASKDLERIK-----NIKEIETLRQVYESSHLEQOLEBAN-AVRQELDDAFRQI 530
 QY 540 HDIREGSRKLOETKEQEVQAVEEMRLMMNQLEEDIVSARRSDLYESLRESRLAABF 599
 Db 531 KAYEKQIKTLQERE-----DLNKELVQASERLKNQSKELKDA----- 568
 QY 600 KRAVECOHKLAKAQGKEVEGYALTEKINAEQQLKIOELQKLEKAVASTATEEL 659
 Db 569 -----HCQRK-----LAMQEPMEINRLTEIHLHQXKLA 597
 QY 660 QNIRQAKERARELEKIQNRDSESGIRKKLVAAEERHSLKNVYKLETMERENRLKD 719
 Db 598 RHVADKEEVDLVQKV-----ESLRQELRTERAKKELEVTEALAAEASDRKLR 650
 QY 720 DITQSQIOQWADKILEEKIRREAQVSAQHLEVLKQKQHYEEKIKVLDNQ-----I 774
 Db 651 QSEHYSKQLEN-----ELE-----GLKQKQISYSPVCSIEHQDEITKL 689
 QY 775 KQLADKETLENNQRRHEEAHKGKILSEQKAMINAMDSKISLEQRIYELSEANKLAA 834
 Db 690 KTDLEKKSIF-----YEE-----LSKREG-IHA-NEIKVLKKEHLND-SEGQQLAL 732
 QY 835 NSSLFTQRMKAQEMISSELROQKFIYLETQAGKLEAQRNKLQEBLEKISHQSDSKRLL 894
 Db 733 N-----KEIMI-----LKQLEK----- 745

QY	895	ELERLEBEVLSHEHQKLELKROLTLEQSLQSEBSQUTALQABALLESQLRQAKTELE	954
Db	746	---TR-RSOSEREFEBSFPOQREBEVYLTEENKLTLS	781
QY	955	ETTAAEBEITALTANHDEIQRKFDALNSCTVITDLEBQNLQTE--DNAELNNQNFYL	1012
Db	782	-----ELDKLTLYENLSJHNO	798
QY	1013	SKQDDEASGANDEIVQLRSEVDHLRELTTEBEMQLTSCQOMELAKTCTMLEBQWMDLE	1072
Db	799	-----OLEEBVQDLA	808
QY	1073	ALANDELLEKEROEWAMRSVLDGEKSQFECRYELQBMIDTEKOSRARADQRTESRQVYE	1132
Db	809	---DKESVAHMEK-----QTEIIQWSDSKDARG-----	836
QY	1133	LAVKHKAETIALLQALKEQKLEKESLSDKLNDE--KHAIMEANAR--SLQOKLETFR	1188
Db	837	-----YLQALASKMTBELBALRMSLSQTRATDMPWKRRAPRAKIDMSARLEQASALDAE-	889
QY	1189	ELKQRLIEQAKLQOQOMDLOKNHIFRLNQGQZALDRADLLKTERSDEYQLENIQVYLS	1248
Db	890	-----IRAKAIOBELN-----	901
QY	1249	HEKVMEGTISQOTLIDLOAKMDQPAKKKVPLOYNELKLALKEKARCALDEEALQK	1308
Db	902	---KYASNIIT--ECKLKD-----SEKONLEL-----LSEIHOILKD	934
QY	1309	TRIELRSAREZAAHKAATDH--PHSPFAPARAQOJMSALVRSBEPHPSAMSLAPRSS	1365
Db	935	TE-BIRS--EKGIEHDSQHSFLAFLNPTDLOQF-----ETVDSPTLSVHPETL	982
QY	1366	RKESSTPEEFSRRLKERMHNNIPIHRFVNGIMNBRATKCAVCLD--TVHGRQASKLECOV	1424
Db	983	RKKCGPGSTGFPKPK-----THQFPVKSFTPTTKHQCTSLMWGLIRGCGCEVCGF	1035
QY	1425	MCHEKCTCLPATGCLPAEYATHTFEAFCRDRMNSPGLQTEP-----SSLHLBGM	1477
Db	1036	SCHTTCVAKAPETTCVPE-----QTGPGIGIDPQKQIGTAYEBHV	1076
QY	1478	KVPNNNRKG--QOGMDRKITVEGSKVLTYDNEARAGORPV-----EEFELCLPD	1526
Db	1077	RIPK--PAGVKKGMORALAIYCDFELFLYDIAEGASPSVYISQVIDMRBBSV----	1130
QY	1527	GDVSIHAGVASELANTAKADVPLYLKE-----SHPTTCMPERTLYLLASFPDKORV	1582
Db	1131	-----SSVLASDVTHASRKDIPCFIFRYTASQLSASNNKC-----SILMLATENEKNMV	1180
QY	1583	TALESVAVAGGKVRSEKADAKLJGNSLXLKEGDRL-----DMNCILP-----	1626
Db	1181	GVLSH-----LHKILIKONFRRDSYVVPKEAVDSTPLPLIKTTQAAI	1222
QY	1627	FSDQVVLVTEEGYALNLVNLKNSLTHYPGIGAVFOIYIYIKLEKLMTJAGERALCT--	1683
Db	1223	IDHERIALGNBEGFLVHAVTDEIIRVGDNNKINHIELIPNDQVAVISGNRRHVRLEPM	1282
QY	1684	-----VDVKKVQOSLAQSHLPAOPDISPNIPEAVKCGHLFGAKITENG--LCI CAAMP	1734
Db	1283	SALDGERETDFYKLSET-----KGCQTVTSKVRHGAITCLCVAMK	1322
QY	1735	SKVYLIRANENLSKCIKEIETSPGCIHPTNYSILIGNKFEIDMKQYLTE-----	1789
Db	1323	KOVLCTYELFQSTTRRRKREIOVPYNOVMMAIFSQQLCVG---FQSGFLRPLPLANGBNP	1378
QY	1790	-EFLDKNDHSLAPAVFAASNSPFSIYOVNASAGOREBYLLCFHEFVGVDSYGRSRSTD	1848
Db	1379	YSMLHSNDHTLS--FIHQPMDAICAVEIS-----KEYLLCFNSIGIYTCQOGRSRHQ	1431
QY	1849	DLKSRRLPLAARYREPFYFTHFNSLEVIETQASBSAGTPARAYIIDIPIPRYLGPALISS	1908
Db	1432	ELMPFANSSCCYANPYLSYSENAVDLFDVNSMWMIOF-----LPLKVR--PLNNEG	1483

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OY      1909 AIVLASSYQOKRVCCKGNLVKES-----GTEHHRRPSTRSRSPNKR-----1954
           ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1484 SLNLGG--LETRILRIYFKMKABEDELVPETSDNSRKQWVRINNKGRISFVPEEREM 1541
           |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY       1952 -----GPPTYNE-----HITKEVASSPAPEEG-----1973
           :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1542 QQRREMLRDPEMNKNKLSNPTNFNIHAMGPGDGIQLTKLDPMNPFRQEASRTVFGSGSVSI 1601
           ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY       1974 PSHPREPSTPHRRREGTEL--RDKSPPGPLEREKSPGAILSTRRRRSARLFEDDSRG 2031
           ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1602 PSLIKSRPEPRGSMSASSGLSARSASAQNGALKRFEFGGS-YSAKRPMPMS-----PSEG 1655
           ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY       2032 RLPAAGAV 2038
           ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1656 SLSSGGM 1662
           ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 14
O9ULUS PRELIMINARY; PRT; 1760 AA.
ID O9ULUS
AC O9ULUS;
DT 01-MAY-2000 (TREMBLrel_13, Created)
DT 01-OCT-2001 (TREMBLrel_18, last sequence update)
DT 01-OCT-2003 (TREMBLrel_25, last annotation update)
DE KIAA1124 protein (Fragment).
GN Name=KIAA1124;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Ctenidta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039618; PubMed=10574461;
RA Hirotsawa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.;
RT "Characterization of cDNA clones selected by the Genemark analysis
   from size-fractionated cDNA libraries from human brain." ;
RL DNA Reel. 6:329-336(1999) .
CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB032950; BAA86438.2; -.
DR HSSP; P31751; IMRY.
DR GeneW; HGNC:1738; CDCA2BPB.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0005083; F:small GTPase regulatory/interacting protein. . ; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006458; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002119; DAG_PE-bind.
DR InterPro; IPR001180; Citron.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; PAKbox/RhoBindg.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Kinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00130; Cl_1.1.1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Kinase; 1.
DR Pfam; PF00433; Kinase_C; 1.
DR PRINTS; PRK00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0109; Cl_1.
DR SMART; SMO0036; CNH; 1.
DR SMART; SMO0285; PBD; 1.
DR SMART; SMO0233; PH; 1.
DR SMART; SMO0220; S_TKC; 1.
DR SMART; SMO0133; S_TK_X; 1.
DR PROSITE; PS50108; CRIB; 1.

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DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
 DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
 DR PROSITE; PS50083; PH_DOMAIN; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; kinase; Serine/threonine-protein kinase; Transferrase.
 PT NON_TER 1 1
 SQ SEQUENCE 1760 AA; 199208 MW; 3A1CA9A7A4BF5FA3 CRC64;
 Query Match 13.7%; Score 1440; DB 2; Length 1760;
 Best Local Similarity 24.4%; Pred. No. 9,4e-34;
 Matches 512; Conservative 336; Mismatches 668; Indels 584; Gaps 76;
 QY 44 SPLSREGILDALFVLFEECSQPALMKI KHVSNFVRKYSDTIAELOPSAKDFEVSILV 103
 DB 72 SALSVETLIDVLVLYTEGSHSLRDKYVAELFEMAKPFTQYKEMQHLREDEILKVI 131
 QY 104 GCGHFAVOYVREKATGDIYAMKMKKALLAQEVSFFEEENITLSRSTSPWIPOLQYA 163
 DB 132 GRGAFGEVAVVKNMTERIYAMKLIKMKEMIKRAETACFEEERDVLVNGCOWITALHYA 191
 QY 164 FODKNHLYLWVEYOPGGDLILNRYEDOLDENICQYLAELIAYVSHLMGVHRDIK 223
 DB 192 FODENHLYLVMDYVGGDLITLSKEDKLPEDMARFYIGEMVALADSIHQHLHYHRDIK 251
 QY 224 PENILVDRTHIKLVDFGSAAKNSNMVNAKLPITGPDYMAPFVLTVMNGDGKTYGLD 283
 DB 252 PDVILVDVNHGIRLADFGSCGLKNNDDGTQSSVAVGTDPYISPIILQAME-DGNGKKGPE 310
 QY 284 CDWWSGVLIYEMITYGSPFAEGTSARTFNINMFOFLKPPDD-PRVSSDFLDLIQSL 342
 DB 311 CDWWSLGVCMYEMLYGETPFYASLIVETYGKIMNHEERFQPSHVTQVSEAKDLIRLI 370
 QY 343 CGGKERLKEFGL---CCHPEFSKIDMNNIRNSPPFPVTLKSDDDTSNPEPE---KNSM 396
 DB 371 CSERIRLQNGIDIEFKGHAFFEGGLMNIENIRLNPAPYIPDVSSBDSITSPVDVLTNTE 430
 QY 397 VSSSPCLSP---SGFSGEELPFVGFYSKALGILGRSESVSGJDSPATSSMEKLLI 453
 DB 431 I-----LPPGSHGFGSLHLPITGTFPT-----TESCFSS--DNGSLKSIQSTLT 474
 QY 454 KSKELQDSQDKCHKMEQEMTLHRVSEVAVLSQKEVELKASGTQSLLEQDLATYTE 513
 DB 475 KDEDVQ--RDLEHSLQME--AYERRI----- 496
 QY 514 CSSLKLKSLQARMEVSGEDDKALQDLHDIQESRKLOET--KEQETQAQVEEMLMNQLE 572
 DB 497 ---RRLEQEKLELSKLOESTQTVOSLHGSSPALNSNRDKIKLNEIERLKAKIA 551
 QY 573 EDLVASARRSDIYESLEESRLAAEFKRAKATECOHLLAKADQKPEVGEVANKLEKINA 632
 DB 552 D-----SNRLEROL-EDTVALLRO-----EREDS 573
 QY 633 EQQLKIQLQELKEKAVKASTATELLQNIROAKERAERLEKLQNRNEDSEGIKKVLVE 692
 DB 574 TQRLRGLEKQHRV-----VROKEER-----LHQGLVE 600
 QY 693 AERRRISLEKVKRLLETMERENRLKDDITQTSQOIQAMDKLLELEKREAVQVSAQHL 752
 DB 601 ASER-----LKSQAKELKDAHQOKRLALQEFSS---ELMERNAEELRAQOKV 643
 QY 753 EYHLKQKQEHYEKIKVLDNQIKKDLADKETTLENNQORHEEAHEKGIUSEOKAMINAM 812
 DB 644 SRQLRKEEMEVATQVND-----AMQENKRAE-----KLKKELEA 680
 QY 813 DSKIRLEQRIIVLSSEANKLAANSSLETOONMKAQEEEMISLRQOKFYLETQAGKLEAON 872
 DB 681 -----QDDDAVABASKEKRLREHSENF-----KQMESELEALKV---KQSGRGAGAT 725
 QY 873 RKLBEQLEKISHQDHSKRNRLLELTRLEVSLLEHEQKLELQKQLTLOLSQERSSQL 932
 DB 726 LEHQOEISIKIS-----ELEKKV---LFYEE---ELVREASHVLEKYNKKEV 768

QY 933 TALQAPAALESOLQAKTELEETTAABEEIQALTARDEIQKFDALRNSCTVITDLE 992
 DB 769 HDSHSHQALQKETIMLKDKLEKSKRRHRNHEBAVG-----TIKDKYE 812
 QY 993 EQNLQLTEDMAELNNQNFYLSKQDEASGANDLIVQLRSEVDHLRREITEREMQLTSGQ 1052
 DB 813 RERAMLFDENKKJLTAENEKLCSPVD-----KLTJANR 844
 QY 1053 TMEALKTTCMTLEQVNDLEALNDELKEKROMEAMRSVLGDEKSOFEQCRVREIQRMIDT 1112
 DB 845 -----QLEBEDDLAAKK-----ESVAHNEA-----QIAELTIQWSD 876
 QY 1113 EKOSRARADQRTESRQVVELAVENKAEIITALQALKEOKLKAESLSDKLNDEKHAM 1172
 DB 877 EKD--ANGYLOALASKVTEEL-----EALRSSLSGRTL-DPLMKV-RRSQK 919
 QY 1173 LEKMAR-SLOQKLETEBELKQRLLEQAKIQ-QMDIQKNIHFKLTGLOEALRADLLK 1230
 DB 920 LDMASARLELOSALEAETIRAKQLVOEELRYKVDANLTLESK-----LK 961
 QY 1231 TERSDLETOLENIQVLSHKKVMKEGTISQOT--KLIDPLQAKMDQPAKKKVPLOYNEL 1288
 DB 962 DSEAKRRELLEMEITL---KKKMEKFRADTGKLDPDQDSIPE-----YENYA 1007
 QY 1289 KLALKEKAKCAELBEALQKTRIELRSAREEAHRKATDPHPS-----TPATAQQIAM 1343
 DB 1008 PLAMD-----LFRITSASEGTQAPKPEASPSWVAASEQEDM 1047
 QY 1344 SAIVRSPHOPSAMSLAPSSRRKESSTPEEFSRLKEKMHNIPIRFVGLNMRATKC 1403
 DB 1048 A---RPPQRPSAVPL---PTQALALAGKPKXA-----HQFISKSPSSPTQC 1088
 QY 1404 AVCLD--TVHGRQASKLEQVWCHPKCSCTLATGSLPAEYATHFPEARCRDQNSPGL 1462
 DB 1089 SHCTSLMGLIRQYALCEVCSFACHVSCKQGAPOVCTIPE----- 1129
 QY 1463 QTKEP-----SSSLHLEGMKVPRNNKRGQOQDMRYIVLESGKYLIYD-NEAREAGQ 1514
 DB 1130 QSRPLGVQDQRGIGTAYKGVAVPKPT-GVKKGWQAVAVVCDCKLFLVLDPEGKSTQ 1188
 QY 1515 RYVEEFELCLPDGDVSIHGAVASLANTAKADVPIYLKNEH---PHTTWCGRITLYL 1570
 DB 1189 GVIASQVLDLRDEDFSV--SSVLASDVVHATRPDIPICFIRVYASLIGAPSKT---SSLLI 1243
 QY 1571 LAPSFDKQWNTALE---SVVAGRYSREKADAKLNSLLKLEGGDRLDNNCTLPF 1627
 DB 1244 LLENENEKKKXVGLLEGLQSLIHKNRLRNQVHVPLEAYDSSLPL---KALITTAIVD 1299
 QY 1628 SDQVVLVGTGEGLYALNVLKNSLTHVPGIAGVFOIYIKLEKLMJAGEBALCLVDVK 1687
 DB 1300 ADRIA-VGLEEGLYVLETRDVIYRAADCKKNQIELAPREKIVILLGNNH----- 1350
 QY 1688 KVKQSLAQSHLPAOP---DISPITE---AVKGCHLFGAGKIEGLCTCAAMPKSVI 1739
 DB 1351 -----HVHLXYPWSSLDGAGSFDIKLPETKGCQMLMATATLKRNSTGCLFAVAVRIL 1401
 QY 1740 LRYNENLSKCIKKELETSEPCS--CIHFTNYSILIGTKNFYELDMQYTLF-----EF 1791
 DB 1402 LCYEIORTKPEHKKNEIYVAGSVQCLAVLRDLQVGS---YSGFCLLSIQGGQPLNL 1457
 QY 1792 LDKNDLSLAPVAPAASSNFPVSIIVQNSAGQREBYLLICGHEFGVFDYSIGRSRTDMLK 1851
 DB 1458 VNPNDPSLA---PLSQOSPALCAVELBS---EYILLCSHHGGLYVDPGRRARARQELM 1510
 QY 1852 WSRPLPLAFA-----YREPYLVTHNSLEVIE-----IQARSGAGT-----PAR 1890
 DB 1511 WPAAPVACSCSPHVVYVSYBGVDVDRTEMVQITGLRIRIPLNSEGTLNLCPPR 1570
 QY 1891 -----AYIDINP-----RYL-----GPAISSG 1908
 DB 1571 LIYFKSKFGSGLAVNVDTSDNSKKQMLRTSKRRFVQVPEERLQORREMLRDLPELRSK 1630

QY 1909 ATYASSYQ-----DKLRVICKGNLVKESGTEHHRGPSTSRSSPNKRGPTTNE-- 1958
DB 1631 MISNPTFNHVAHMGPDGMVLDLPLSAVPPSQEERRPGFAPNTLA---RQPSRANKPY 1687
QY 1959 -----HITKRVASSPAPPPGSHPRRPPSTPHR 1985
DB 1688 ISWPSGSGSEBPSVTVPILRSMSPDPQDFDKEDPSDSTGH--STPSNSSNPSGPPSPNSPHR 1745

RESULT 15
ID Q9Y5S2 PRELIMINARY; PRT; 1711 AA.
Q9Y5S2
AC Q9Y5S2;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE CDC42-binding protein kinase beta.
GN Name=CD42BPB;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=99216425; PubMed=10198171; DOI=10.1006/geno.1999.5769;
RA Moncreiff C.L., Bailey M.B., Morrison N., Johnson K.J.;
RT "Cloning and chromosomal localization of human Cdc42-binding protein
kinase beta."
RL Genomics 57:297-300(1999).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR HSSP; P31751; IMRY.
DR GO; GO:0005856; C:Cytoskeleton; TAS.
DR GO; GO:0004672; P:protein kinase activity; TAS.
DR GO; GO:0007163; P:establishment and/or maintenance of cell po. .; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR001180; CItcon.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000095; Pakbox/rhoindng.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00130; Cl_1; 1.
DR Pfam; PF00780; CNH; 1.
DR Pfam; PF00786; PBD; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00109; Cl_1.
DR SMART; SM00036; CNH; 1.
DR SMART; SM00285; PBD; 1.
DR SMART; SM00223; PH; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00133; S_TK_X; 1.
DR PROSITE; PS00108; CRIB; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW SSOURCE 1711 AA; 194356 MW; 3A3731D40A363497 CRC64;

Query Match 13.7%; Score 1438; DB 2; Length 1711;
Best Local Similarity 24.4%; Pred. No. 1e-33; Mismatches 668; Indels 584; Gaps 76;
Matches 512; Conservative 336; Mismatches 668; Indels 584; Gaps 76;

QY 44 SPLSRGCIIDALVTLFEESQPLMKIKVNSNVRKXSDTIALQELQSAKDFEVRSLV 103
DB 23 SALSVELTLDVLCLYTECHSALRRDKYAELENAKPTQLVKEMQJREDDEFELIKVI 82
QY 104 GCGHFAEVQVRRKAGDIIYAMKVMKKKALLAEOVSFFPEERNILSRSTPMIPOLOYA 163
DB 83 GRAPFGEVAVAKKNTERTIYAMKILNKEMTKAEFTACFEERDVLVNGCCOITALTHYA 142
QY 164 FQDKNHLVLMVEYQPGDLSLNLRYEDQDENIIOFYLAELLIAVNSVHLMGVHARDIK 223
DB 143 FQDENHLVLMVDVYVGGDILLTLKPEDKLPEDMARFYIGENVLAIDSIHQHLYVRDIK 202
QY 224 PENILVDRTGHILVDFGSAKNSNMKNNAKPIGTPTDMAEVLVWNGDGKGTGLD 283
DB 203 PDVVLVDVNHIRLADFGSLCKNNDDGTVOSSVAVGHPDIYSBEILQAM--DMGKKGP 261
QY 284 CDMAVGVLAEMITVGRSPPAEGTSARTENNINFORFLKFPD--PKVSSDFDLIOSL 342
DB 262 CDWMSIGVCMYEMLYGETPYAESLVETTYGKLNHERRFOFPHVYDVSEAKDILORLI 321
QY 343 CGOKERLKEFGL---CCHPPFSKIDWNININSPPVPTLKSDDTSNDEPE---KNSW 396
DB 322 CSRERRLGQNGIDPFKHAFFEGGLNMENIRNLAPYIPDVSSPSDTSNFDVDDVLANTE 381
QY 397 VSSSPCOLSP---SGRSGEELPVGFSYSKALGILGRSESVSGLDSPATSSMEKKLLI 453
DB 382 I-----LPPSGHTGSGHLPTIGFTT-----TESCFS--DRGSLKSIQSNLTLT 425
QY 454 KSKELDSDQCKHMOEMRHLHRRVSEVAVLVSKVELKASGTORSLLEQDLATYITE 513
DB 426 KDDVQ--RDLEISLQNE--AYERRI----- 447
QY 514 CSSLKSLEQARMEVSOEDDKALQLHDIREQSKLQEI--KEQGYAOVEEMLMNQL 572
DB 448 -----RLREQKLELRKLGQESTQVQSLGSSRALSNSRDEIKKLNIEIRLNKXIA 502
QY 573 EDIVSARRSDLYESLESRSLAAEFKPKATCQHKLKAKQOGKPEVGYAKLEKINA 632
DB 503 D-----SNRLEROL--EDTVALARQ-----EREDS 524
QY 633 EQLQKIOELQEKLVKASTATELLQNTROKERAERLEKQLQNRNDSSEGRKKLVE 692
DB 525 TORRLGLEKHRR-----VKQKEE-----LHKQIVE 551
QY 693 AERRRSLNKVRLKLEMERRENRKLDIQTKSQOIQOMADKILDEKHEAQAQVSAQHL 752
DB 552 ASER-----LKSQAELMDAHOQRKALQEPS-----ELNERVAELRAQOKQV 594
QY 753 EVHLKQEQHYEEKIKVLDNQIKDLADKETLENMQRHEEBAHEKKILSEOKANINAM 812
DB 595 SRQLRKEEBEVAATQVD-----AMRQEMRRAE-----KLRKELEA----- 631
QY 813 DSKIRSLQKIVLELSEANKLAANSILPTQRMKAQOEMISLQOKPYLETQAGKLEAQN 872
DB 632 -----QDDVAVASRKRKRREHSENF-----KQMSSELALKV---KQGRGAGAT 676
QY 873 RLKEOLEKISHODSDKNLLELETRLREVSLEHEQKLELRQUTLEQLSQAEBESQ 932
DB 677 LEHQEISIKKS-----ELKKV---LFYEE---ELVRREASHVLBYKVNKKEV 719
QY 933 TALQAPAALESQRLQAKTELEETVBAEETIGALTANRDEIQRKDALRNSCTVITDLE 992
DB 720 HDSESHQALQKQELIMLKQDLKESKBERHNEBEAVG-----TIKQYE 763
QY 993 EQNLQITENDAEILNNQNFYLSKQLDASGANDIYQLRSEVDHLRREITEREMQLTSQK 1052
DB 764 REEAMLPDEKKKLLAEKEKLCSTVD-----KLTQKQR 795
QY 1053 TMEALKTCTMEEQVMDLEALNDELLEKERQWEAMRSVLDGKESQFECHVRELQRMEDT 1112
DB 796 -----QLEDELQDLAAKK-----ESVAHWEA-----QIABLIQWVSD 827
QY 1113 EKOSRAPADQRITESSQVVELAVKEHKAETILALQALKEQKLKAESLSDKLNDLEKKHAM 1172

Db 828 EKD--ARGVIALASKMTEEL-----EALRSSISIGSRTL--DPLMKV-RRSQK 870
QY 1173 LEMNAR-SLOOKETERELKORLLEEQAKLOO-QMDLOKNHI FRLTQGLQALDRADLLK 1230
Db 871 LDMGARLELOALAEIRAKOLOVEELKRVANDANLTLESK-----LK 912
QY 1231 TERSDLEVOLENIQVLSHEKVKMEGTISOOT--KLIDFLOAKMDQPAKKKKVPLQYNEL 1288
Db 913 DSEAKNRELLBEMELT-----KKMEBEKFRADTGLKLPDFODSIFE-----YFNTA 958
QY 1289 KLALEKEKARCALEBEALQKTRIELRSAREBAHRKATDHPHS-----TPATAQOIAM 1343
Db 959 PLADH-----LTPRTSSASEQETQAPKPEASPSMSVAASEQEDM 998
QY 1344 SAIVRSPHOPSAMSLAPSPSRKESSTPEPSRRLKERMHNHLPFRFVNLMBRATKC 1403
Db 999 A-----RPPQPSAVPL-----PTTQALVLAGPKKA-----HOFSTKSFSSTQC 1039
QY 1404 AVCLD-TVHFGROASKLEQCMCHPKSTCLPATCGLPAEYATHTFAFCRDKXNSPGL 1462
Db 1040 SHCTSLMWGLIRQYACGVCSGACVSCGDGAPQVCPIRPE----- 1080
QY 1463 QTKEP-----SSSLHEGMMKVPRNNKRGQOGWDRKIYVBEGSKVLID-NEAREAGQ 1514
Db 1081 QSKRPLGVDVORGIGTAYKGVKVPKPT-GVYKGVQRAYAVVCECKLFLYDLPEBKSTOP 1139
QY 1515 RPVEFEFLCPDGDVSHGAVGASELANTAKADVYLLKMSH-----PHTCWPGRTYL 1570
Db 1140 GVILASQVLDLRDDEFSV--SSVLASDVHATRDIPCFRTVASLIGAPSKT-----SSLLI 1194
QY 1571 LAPSPDKORWVTALE---SVVAGGRVSRERAEADAKLIGNSLLEEGDDRLDMNCTLPF 1627
Db 1195 LTBENENEXKXVGLIEGLQSLHKRLNQVHVPLBAVDSLPLI---KAILTAIVD 1250
QY 1628 SDQVVLVTEBGLYALANVKNSLTHVPGIGAVFOYIITKLEKLIMAGEERALCLVDK 1687
Db 1251 ADRIA-VGLEBGLYVIEVTRDVIYAADCKVHQIETLAPREKIVILLCGRNH----- 1301
QY 1688 KVKQSLAQSHLPAOP---DISPNIIE---AVKGCILFGAKIENGCLICAMPKSVI 1739
Db 1302 -----HVHLYPWSLDAEGSFDIKLPETKGCQMLATATLKRNSGTCLFVAVKRLI 1352
QY 1740 LRYNENLSKYCIKKEIETSEPCS--CIHFTVYSILIGTNKFEIDMKQYTL-----EF 1791
Db 1353 LCYEIQRTKPRHRKNEIYVAGSVQCLAVLRDLCTVG---YPSGFCULSIOGDOGPINL 1408
QY 1792 LDKNDHSLAPVFAASSNSFPVSIQVNSAGQREBYLLCFHEFGVFDVSYGRSRRTDLC 1851
Db 1409 VNPNDPSLA---PLSQQSFALCAVELS---BEYLLCFSHMGLYVDPQGRARAQELM 1461
QY 1852 WSRLLPLAFA-----YREPYLFTHNSLEVIE-----IQARSSAGT-----PAR 1890
Db 1462 WPAAPVACSCSPRTHTVYSEYGVDFVTRTWEMVQTIGLRIRPLNSGTLNLNCEPDR 1521
QY 1891 -----AYLDIPND-----RYL-----GPAISSG 1908
Db 1522 LIYFKSKSGAVLNVPTSDNSKCOMLRTSKRRFVFPVEBERLOQRREMLRDELSK 1581
QY 1909 AIYLASSYO-----DKLRYICCKGNLVKESGTEHHRGPTSRSSPNKRGPPTYNE-- 1958
Db 1582 MISNPTNHNVAHMGPGQGMQVLMDLPLSAVPPSQEBRGPAPTYLA---RQPERNKPY 1638
QY 1959 -----HITKVASPAPPEGSHPRESTPHR 1985
Db 1639 ISWPSGSGSEPSVTYPLRSMSPDQDFDKPPDSSTKH--STPSNSNPSGPPSPNSPHR 1696

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 16:32:13 ; Search time 63 Seconds
(Without alignments)
3136.972 Million cell updates/sec

Title: US-10-791-666-2

Sequence: 1 MLKFKXGANNPLDAGAAEPI.....AGAVRTPLSQVKNKVMDOSSV 2054

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7935	75.6	1597	2	citron - mouse
2	1524.5	14.5	1732	2	protein kinase (EC
3	1419.5	13.5	1702	2	protein kinase (EC
4	1283.5	12.2	1548	2	hypothetical prote
5	1275.5	12.2	1354	2	serine/threonine-s
6	1263.5	12.0	1388	2	serine/threonine-s
7	1260	12.0	1354	2	serine/threonine-s
8	1250.5	11.9	1388	2	serine/threonine-s
9	1126.5	10.7	1173	2	hypothetical prote
10	888.5	8.5	624	2	protein kinase (EC
11	872	8.3	557	2	serine/threonine-s
12	761	7.3	1356	2	hypothetical prote
13	751	7.2	1286	2	hypothetical prote
14	728	6.9	1256	2	hypothetical prote
15	721	6.9	522	2	protein kinase r51
16	715.5	6.8	479	2	protein kinase (EC
17	710	6.8	441	2	myotonic dystrophy
18	710	6.8	474	2	myotonic dystrophy
19	710	6.8	516	2	myotonic dystrophy
20	707	6.7	756	2	probable protein k
21	701	6.7	526	2	protein kinase PKT
22	700	6.7	469	2	serine/threonine-s
23	697	6.6	596	2	probable protein k
24	696	6.6	569	2	hypothetical prote
25	676.5	6.4	443	2	probable protein k
26	676.5	6.4	475	2	protein kinase [im
27	674.5	6.4	465	2	protein kinase (EC
28	670	6.3	500	2	protein kinase (EC
29	660.5	6.3	483	2	protein kinase F41

30	639	6.1	545	2	T01288	protein kinase F27
31	636.5	6.1	665	2	S70706	probable protein k
32	636	6.1	480	2	T47255	serine/threonine k
33	636	6.1	598	2	T47254	serine/threonine k
34	636	6.1	620	2	S22711	probable protein k
35	631.5	6.0	412	2	T78395	myotonic dystrophy
36	608	5.8	908	2	T25035	hypothetical prote
37	604	5.8	1099	2	A56155	tumor suppressor p
38	591.5	5.6	1909	2	A45592	liver stage antiag
39	580	5.5	1410	1	A57013	early endosome ant
40	574	5.5	2139	2	T18296	myosin heavy chain
41	573.5	5.5	1738	2	T14667	interaptin - slime
42	567.5	5.4	1790	2	S67593	transport protein
43	550.5	5.2	2442	2	T08621	centrosome associa
44	549.5	5.2	624	2	T41341	probable serine-ch
45	548	5.2	607	2	S62556	probable serine/ch

ALIGNMENTS

RESULT 1

S68420
citron - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S68420

R/Madaule, P.; Furuyashiki, T.; Reid, T.; Ishizaki, T.; Watanabe, G.; Morii, N.; Narumi,

FEBS Lett. 377, 243-248, 1995

A/Title: A novel partner for the GTP-bound forms of rho and rac.

A/Reference number: S68420; MUID:96128238; PMID:8543060

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-1597 <MAD>

A/Cross-references: UNIPROT:P49025; EMBL:U039904; NID:G1079733; PIDN:AACS2341.1; PID:G107

C/Keywords: alternative splicing

F/911-979/Domain: protein kinase C zinc-binding repeat homology <K22>

Query Match 75.6%; Score 7935; DB 2; Length 1597;

Best Local Similarity 98.2%; Pred. No. 3e-204; Mismatches 10; Indels 2; Gaps 1;

Matches 1561; Conservative 16; Mismatches 10; Indels 2; Gaps 1;

QY	468	MEQEMTRLHRRVSEVAVALSQKEVELKASETORSLEQDIATYITTECSSLKRSLEQARME	527
DB	9	MEQEMTRLHRRVSEVAVALSQKEVELKASETORSLEQDIATYITTECSSLKRSLEQARME	68
QY	528	VSQEDDKALQLHDIREQSRKLOEIKQEQYQAVEEMRLMMNQLBEDLVASRRSDLYES	587
DB	69	VSQEDDKALQLHDIREQSRKLOEIKQEQYQAVEEMRLMMNQLBEDLVASRRSDLYES	128
QY	588	ELRESRLAEEPRKATKTEOHLKAKKDOGPVGEVAKLEKTNARQOLKIOLEQELK	647
DB	129	ELRESRLAEEPRKATKTEOHLKAKKDOGPVGEVAKLEKTNARQOLKIOLEQELK	188
QY	648	AVASTATEATLQINIQAKERARELEKLNREDSSEGRKCLVEAEERHSLENKVKRL	707
DB	189	AVASTATEATLQINIQAKERARELEKLNREDSSEGRKCLVEAEERHSLENKVKRL	248
QY	708	ETMERRENRLKQDIQYKSQOIQMADKYLEEKHREDAVSAQLEVLHKKQEHYEKI	767
DB	249	ETMERRENRLKQDIQYKSQOIQMADKYLEEKHREDAVSAQLEVLHKKQEHYEKI	308
QY	768	KVLNDQIKKDLKQETLENNMQHEEAHEKGLISEQKAMINAMSKIRSLRQIVELS	827
DB	309	KVLNDQIKKDLKQETLENNMQHEEAHEKGLISEQKAMINAMSKIRSLRQIVELS	368
QY	828	EANKLAANSLFTQRMKAQEWISLROOKFLFTQAGKLEAQNKLREOLEKISHQD	887
DB	369	EANKLAANSLFTQRMKAQEWISLROOKFLFTQAGKLEAQNKLREOLEKISHQD	428
QY	888	SPKRLLELETRILEVSLHEEQKLEKRLTELQSLQERESQLTALQAAAPALESSQUR	947

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Db 429 SDSRLLEETRIREVSLEHEEQKLEKQUTLEQLSLQREBSQTLQAPARALBSQLR 488
Qy 948 QAKTELEETTAABEEIQAALTAHDEIQKRFDAIRNSCTVITDLEQALQJTEDNMLNN 1007
Db 489 QAKTELEETTAABEEIQAALTAHDEIQKRFDAIRNSCTVITDLEQALQJTEDNMLNN 548
Qy 1008 QNFYLSKQIDBAGANDEIVQASVNDHLREITEREMQUTSQQTMEALKTTCTMLEEQ 1067
Db 549 QNFYLSKQIDBAGANDEIVQASVNDHLREITEREMQUTSQQTMEALKTTCTMLEEQ 608
Qy 1068 VMDLEALNDELLEKEROMEAMRSVLGDEKSOFECEVRELQMLDTEKQSPARADQRTTES 1127
Db 609 VMDLEALNDELLEKEROMEAMRSVLGDEKSOFECEVRELQMLDTEKQSPARADQRTTES 668
Qy 1128 RQVVELAVKHEKAEITLALQALKEQKAKASLSQKNDLDEKQAMLEMANRSIQQKLETE 1187
Db 669 RQVVELAVKHEKAEITLALQALKEQKAKASLSQKNDLDEKQAMLEMANRSIQQKLETE 728
Qy 1188 RELKQRLLEQAKLQOQMDLQKNHIFRLTQGLQALDRADLLKTERSDLEYOLENTQVLY 1247
Db 729 RELKQRLLEQAKLQOQMDLQKNHIFRLTQGLQALDRADLLKTERSDLEYOLENTQVLY 788
Qy 1248 SHEKVMKEGTSIQOTKIDFLQAKMDQPAKKKVPLQYNELKJLAEKEXARCALEBERALQ 1307
Db 789 SHEKVMKEGTSIQOTKIDFLQAKMDQPAKKKVPLQYNELKJLAEKEXARCALEBERALQ 848
Qy 1308 KTRIELRSAREBAHAKRATDHPHPSTPATARQOJLMSAIVRSPEHQSAMSLAPPSSRR 1367
Db 849 KTRIELRSAREBAHAKRATDHPHPSTPATARQOJLMSAIVRSPEHQSAMSLAPPSSRR 908
Qy 1368 KESSTPEEFSRRLKERMHNIPIHFVNGVLMKATKCAVCLDTYHFGQASKLECYQWCH 1427
Db 909 KESSTPEEFSRRLKERMHNIPIHFVNGVLMKATKCAVCLDTYHFGQASKLECYQWCH 968
Qy 1428 PKSTCIPATCGLPABAYATHTFAFCDDKNSPQLQTKEPSSSLHLEGMMKVPRNNRGQ 1487
Db 969 PKSTCIPATCGLPABAYATHTFAFCDDKNSPQLQTKEPSSSLHLEGMMKVPRNNRGQ 1028
Qy 1488 QGMDRKXIVLEGSKVLTYDNEABAGQRPVEEFELCLPDDQVSIHGAVAGSELANATAKAD 1547
Db 1029 QGMDRKXIVLEGSKVLTYDNEABAGQRPVEEFELCLPDDQVSIHGAVAGSELANATAKAD 1088
Qy 1548 VPYTLKMEHPHTTQWPGRTLYLLABSPRDKQKWTLLAESVAGGRSREKAEADACLG 1607
Db 1089 VPYTLKMEHPHTTQWPGRTLYLLABSPRDKQKWTLLAESVAGGRSREKAEADACLG 1148
Qy 1608 NSLLKLEGGDRLLMNCTLPSPDOVLYLGTBEGLYALNVLKNSLTHVHGIGAVFOIYIKD 1667
Db 1149 NSLLKLEGGDRLLMNCTLPSPDOVLYLGTBEGLYALNVLKNSLTHVHGIGAVFOIYIKD 1208
Qy 1668 LEKILMAGEERALCLVDYKVKVQSLAQSHLPAQPDISPNIPFAVKGCHLFGAGKLENGL 1727
Db 1209 LEKILMAGEERALCLVDYKVKVQSLAQSHLPAQPDISPNIPFAVKGCHLFGAGKLENGL 1268
Qy 1728 CICAAMPKSVILIRYENLSKYCIKKEIETSEPCSIHFTNYSLIGTNGKFEIEMKOYT 1787
Db 1269 CICAAMPKSVILIRYENLSKYCIKKEIETSEPCSIHFTNYSLIGTNGKFEIEMKOYT 1328
Qy 1788 LEPEFLDNHDSILPAVPAASNSPVSIVQVNSAGQEEVYLCHHEGAVVDVSGRSRT 1847
Db 1329 LEPEFLDNHDSILPAVPAASNSPVSIVQVNSAGQEEVYLCHHEGAVVDVSGRSRT 1388
Qy 1848 DDLEKMSRLPLAFVREBYLFTVTHNSLEVEIQARSAGTPARAYLDIPRPLYGPAISS 1907
Db 1389 DDLEKMSRLPLAFVREBYLFTVTHNSLEVEIQARSAGTPARAYLDIPRPLYGPAISS 1448
Qy 1908 GAIIYASSYQDKLRVICCKGNLYKESGTEHHRGPTSSRSGPNKGPPTVNEHTKRVASS 1967
Db 1449 GAIIYASSYQDKLRVICCKGNLYKESGTEHHRGPTSSRSGPNKGPPTVNEHTKRVASS 1508
Qy 1968 PAPPEGSHREBPTPRY--REGRTLRBDKSGRGLERBKSGRLTISRREBSPARLF 2025
Db 1509 PAPPEGSHREBPTPRYRDRBGRTELRBDKSGRGLERBKSGRMLSTRREBSPARLF 1568
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Qy 2026 EDSRGRPLPAGAVRTPLSQVNNKWDQSSV 2054
Db 1569 EDSRGRPLPAGAVRTPLSQVNNKWDQSSV 1597

RESULT 2
T14039
protein kinase (EC 2.7.1.37), myotonic dystrophy-associated - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Sep-1999 #sequence_rev150n 20-Sep-1999 #text_change 16-Aug-2004
C:Accession: T14039
R:Jung, T.; Chen, X.O.; Tan, I.; Manser, E.; Lim, L.
Mol. Cell. Biol. 18, 130-140, 1998
A:Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector
A:Reference number: 217862; PMID:9807670; PMID:9418661
A:Accession: T14039
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1732 <LEU>
A:Cross-references: UNIPROT:O54874; EMBL:AF021935; NID:g2736150; PID:g2736151; PIDN:AACO;
C:Gene: MRCK
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase
F:75-343/Domains: protein kinase homology <KIN>
F:1013-1062/Domains: protein kinase C zinc-binding repeat homology <KZN>

Query Match 14.5%; Score 1524.5; DB 2; Length 1732;
Best Local Similarity 24.8%; Pred. No. 6.9e-34;
Matches 529; Conservative 335; Mismatches 667; Indels 599; Gaps 76;

Qy 36 PFMTQQMSPLSREGILDALFVLFEECSQPALMKTHVSNFVRKYSDTLAELOEPSAK 95
Db 18 PAQTNGQC--FSVETLLDILICLYDECNNSPLREKNIILEYEMAKPFSTKVQMBLHRZ 75
Qy 96 DFEVRLVGGHFAEYQVUREKATGDIYAMKKKALLAQEOVSFEERNILTSSTSP 155
Db 76 DFEILVILGAGAEVAVVKLKNADKYPAKKILINKKEMLRGAETACFRERDVLVNGDSK 135
Qy 156 WIPQLYAFQDKNHLVMEYQPGDILLNRYEPDQDENLQFYLAELILAVSHVLM 215
Db 136 WITTLTAHQDDNNILVNDYVGGDLITLISFEEDRLPEMARFVLAENVIAIDVHQ 195
Qy 216 GYVHARDIKPENILVDRTHIKLVDFGSAAKNSKNVNAKLPIGTDPYNAEVLTVMGD 275
Db 196 GYVHARDIKPENILVDMNGHRLADFGSCIKMDEGTQSSVAVGTPDYSPEILOAME-D 254
Qy 276 GKGTGLDCDQMSVGIAYEMITGRSPFAEGTSARFPNNIMNFORLKKRPDD- PKYSSDF 334
Db 255 GKGRYRPECQMSVLGYCMYEMLVGETRPFYAESLVETYGKIMHKERRPQPTQVTVSENA 314
Qy 335 LDILQSLCGQKRLKFEGL---CCHPFESKIDMNNIRNSPPFVPTLKSDDTNSFDEP 391
Db 315 KDLIRRLIGSREHRLQNGIEDPKRPFPSGIDMDIIRNCEALYIIEVSPPTDTSNPDVD 374
Qy 392 E--KNSWSSSDQSLPSGSGSEELPFVGFYSKALGILGRS-----ESV 434
Db 375 DDLCKNSEMTPEP---THNLFSGHNLPFVGFYTSSCVLSDRCLRTAGPTSLDIDVNV 431
Qy 435 VSGLDSPAKTSSNEKKLLIKSKELQDSQDKCHMGDEMTRLHARVE---VNAV-LSQK 489
Db 432 QRTLDNNLTAFAVERRI-----KLLDEKLELTAKLQSDSTQTVQALQSTV 477
Qy 490 EVELKASETQSLLEBDLATTITEGSSLKRSLEQAEWEVSQEDDKALQLLHDIRESQRL 549
Db 478 DGPLTAS-----KDL-----EIKSLKEIIRKLAKQAVNV-----507
Qy 550 QEIKEOEYQAVEEMELMNNQLEBDIVSARRSDLYESLRESRLAAEFKRAATECOHK 609
Db 508 -----HLBQQLBE-----ANSVREILDPAFRQIKAREKQIKTLQOREEELINKELVQASER 557
Qy 610 LLAQKQGRPEVGEYAKLEKINAEOQLKIOLEQKLEKAVKATENTELLQNIROAKERA 669
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Db 558 L-----KNSK-----ELKDHQCKRLAMQEFMEINERTELTHQKQALAHVNDKEEV 607
Qy 670 ERELEKLONRDESEGRKQLVEAEERHSLNKKVLETMERENRLKODIQKTSQOIQ 729
Db 608 DLVWQK-----AESLRQELRAERAKKEVHTHEALIASQDKRLREGSRHYSQLE 660
Qy 730 QMADKILEKREHBAOVSAQHLEVLKQKQHYBEKIKVLNDQ-----IKKDLADKEL 784
Db 661 N-----ELF-----GLKQKQISYSPGCSIEHQOETLYKLTDEKKSIF 699
Qy 785 ENMWQREBEAHEKGLISEQKAMINMDSKIRSELQRIVELSEANKLAANSLSLFTQRM 844
Db 700 -----YEBEISKEGJHA-----SEIKNLKKELDH-SGQOQALAKELMV----- 738
Qy 845 KAOBEMISELRQKQFYLETQAGKLEAQRKLEOLEKISHODSDKRLLELETRLEVS 904
Db 739 -----LKDLEK-----TR-RESQ 751
Qy 905 LEHEQKLELKRQLTQLTQLSLQERESQYALQAPRALESQRLQAKTELETTAEAEI 964
Db 752 SEREEFNEFEKQ-----YEREKVL----- 771
Qy 965 QALTANDEIQKRDALRNSCTVITDLEBOLQITEDNAELNQNPFYLSQDLBASGAND 1024
Db 772 -----LTERNKLT----- 780
Qy 1025 EIVOLRSEVDHLREITEREMQLTQOKQTEALKTCTQMLEBQVMDLEALNDELLEKRO 1084
Db 781 -----SELD-----KLTSS-----LYESLSLRQHLEEVKDLA-----DKKESVAA 816
Qy 1085 WEAMRSVLDGSKQFQECRVBELQMLDTEKQSPARADQRTESQVVELAKVHKAEILA 1144
Db 817 WEA-----QITEIILQWVSDEKQARQ-----YLQALA 842
Qy 1145 LQALQKQKLEKASLSKNDLE-----KXHAMLENNAR-SIQOKLETERELKORLEEQAK 1200
Db 843 SKRTEBELAERNSLSGTRATDMKMRKRFALDLMSALELOASALDAITRAKQALQOEILNK 902
Qy 1201 LQOQMDLQKNHIFRLTQLOALDRADILKTERSDLEYOLENIOVLASHEKMEGTISQ 1260
Db 903 VK-----ASNITTECKLXQSEKKNLBSIEBILJIDTEBELREKGEVH 946
Qy 1261 QTKLIDFLQAKMDQPAKKKKVPLQYNELKLALEKAKCAELBEALOKTRIELNSAREEA 1320
Db 947 RDSQHSPL-AFLNTP-----DALDQFE-----RS----- 970
Qy 1321 AHKATDHPHS--TPATARQOIAMSAIVRSPHOPSAJSLAPSSRKSSSTPEEFSR 1379
Db 971 -----PSCTRPAGKGRIRADSAPL--PVNTP-----RKKGCPASAGPPPK 1009
Qy 1380 LKERMHNIHPRFVGNLNRATKCAVCLD--TVHGRQASKLEQWCHPKCSCLPATC 1438
Db 1010 RK-----THQFVVSFTAPTKCHQCTSLMVGILRQGCSEVGCSCHTTCVNAKAPTC 1062
Qy 1439 GLPAEYATHTPEAFCRDKMNSPGIQTPE-----SSSLHLEGMKVPRNNKRG--COGW 1490
Db 1063 PVPE-----QTKPGIIGIDQKGVGTAVEGHVAPK--PAGVAKGW 1101
Qy 1491 DRKTYLESGKVLTYDNEAREAGO-RPVEBELCLPDGVSIHGAVGASBELANTAKADV 1549
Db 1102 QRALAVVCDPFLFLYDIAEGKASQSPSSVISOVIDMRDEFSV--SSVLASIVIHASRDIP 1160
Qy 1550 YILKME-----SHPHTCWPGRTLYLLAPSPDKQWTALESVAVAGRVREKAEADAKL 1605
Db 1161 CTRVAVASQLSAPSDK-----STIMLADSETERSKWGVSEL--HKVLKKNKFRRSV 1213
Qy 1606 LGSNLSLKEGDDRLDMNCTLP-----PSDQVVLVGTBEGLYALNVLKNSLTHVPG 1655
Db 1214 -----YVPEKAYD-----STLPILKTTQAAIIOHERALNBSGLFVYVHTKOEILRVGD 1264
Qy 1656 IGAVFQYIITKDLBKLMINGEBALCLVYVKVYKQSLAOSHLPAPDPDISPNIPEAVKGC 1715

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Db 1265 NKTIHQELIPSDOLVAVISGRNRHVLFFPMSALDGETDYKLA-----TKGC 1314
Qy 1716 HLFAGKIEKNGL--CICAMPKSVYLIRYENELSKYCIKEIETSEPCSIHFTYVS--I 1771
Db 1315 QTIAGKVRHIALSCLCVAMKQVLYCYELFQSKTRHKKFEIQV--PCNVQWMAIFSEHL 1372
Qy 1772 LIGNKVEYELDKOYTE-----EFLDKXDSLAPVAFVASSNFPVSIYQVNSAGRE 1825
Db 1373 CVG-----FQSGFLRPLPANGBSPCNMLHSDHTLA---FITHQPMDALCAVEISN---K 1421
Qy 1826 EYLLCFHEFGVAVDSYVRRSRTDCLKWSRLPLAVAREPVLFTVHFNLSLEVIEIQARBSA 1885
Db 1422 EYLLCFSSIGIYTDQGRSRQOELMPANBSSCTYAPVISTYSENAVDFVNSMEWI 1481
Qy 1886 GTPARAVLIDIPNPRYLPAISGAIYVASSYQDLARYICCKGNLVKES-----GTEHRRG 1940
Db 1482 QF-----LPLKVR---PLMTGSLNLG--LETRILIFYKNRAEGDELVPETSDNR 1531
Qy 1941 PSTSRSSPNKR-----GPPTYNE-----HI 1960
Db 1532 KQWVRNINNKRRYVFRVPEERMQRRMLRDEMRNKLISNPFNFHIAHMGDGIQI 1591
Qy 1961 TKRVASSPAPPEG-----PSHREPESTPHRYREGREL--RDKDSRGLEREKS 2008
Db 1592 LKDLPMNPRQESRTVFSVSIPSTIKSRPEPGRSMSSGSLARSQAONGALKRHS 1651
Qy 2009 PGRILSTRERSPARLFEDESSRGLPAGAV 2038
Db 1652 GGS-YNTKQPMPS-----PSEGLSSGCV 1675

RESULT 3
T14050
protein kinase (EC 2.7.1.37) beta, myotonic dystrophy-associated - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 16-Aug-2004
C:Accession: T14050
R:Leung, T.; Chen, X.Q.; Tan, I.; Manser, E.; Lim, L.
Mol. Cell. Biol. 18, 130-140, 1998
A:Title: Myotonic dystrophy kinase-related Cdc42-binding kinase acts as a Cdc42 effector
A:Reference number: Z17862; MIMD:98078670; PMID:9418861
A:Accession: T14050
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1702 <LEU>
A:Cross-references: UNIPROT:O54875; EMBL:AF021936; NID:g2736152; PID:g2736153; PIDN:AACO
A:Experimental source: brain
C:Genetics:
A:Gene: MRCK-beta
C:Superfamily: protein kinase homology
C:Keywords: ATP; phosphotransferase
F:74-342/Domain: protein kinase homology <KIN>
F:1027-1076/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 13.5%; Score 1419.5; DB 2; Length 1702;
Best Local Similarity 24.7%; Pred. No. 4.2e-31;
Matches 482; Conservative 310; Mismatches 623; Indels 533; Gaps 64;

Qy 44 SPLSRGILDALVYLEEGSCOPALMKIKVSNFYRKYSITTAIELOEQPSAKDFEVRSLV 103
Db 23 SLSLSEVTLIDVLCLYTECHSHALRRDKYVAEFLMAKKPTQVLKMDQLHREDEIIKVI 82
Qy 104 GCGHPAEVQVVRKATGDIYAMKVMKKKALLADQVSEFEERNIILSRSPWIPOLQYA 163
Db 83 GRGAPGEVAVVKNKNTERTIYAMKILNKWEMLKAELETAQFEERDVLVNQCQWITLALHYA 142
Qy 164 FQDKNHLIYVMEQPGDDLILNRYEDQDENLQFYLAELILAVSVHLMGGVHRDIK 223
Db 143 FQDENVLYVMQYVGGDDLITLTSKPEDKLPEMARARYIGEMVLADISIHQLHYVHRDIK 202
Qy 224 PENIYDRTGHITLVDFGSAAKNSKNVNAKPIGTPTDMAPEVLTVMNNGDGKGTYGLD 283
Db 203 PDNVLLDVNGHRLADFGSLKNNDDGTQSSVAVGTPDYISBEILOAME-DGWSKYGPE 261

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Db      19 NITWDG-----PSKPPALSTFTLIDSLICLYDECNSTLRKEKCIAPFESVKTIVLSKA 73
Qy      88 QELPQSAKDFEVSRLVCGHFAEVOVREKATGDIYAMKWKKKALLAQEQVFFEEERN 147
Db      74 KKLRLSDDFEVLKIKGAFGEVAVVRMGVGEIYAMKLIKEMKVRKATACFRERD 133
Qy      148 ILRSSTSPWIPQLOAFQDKNHLVMEYQPGDLSLNLREYDQDENTLIQFYALIEL 207
Db      134 VLVYGDRRMTITNLAYAFQDEKNLTFVMDYYIGDMLTLLSKFVDHIESMAKFYIAEMVL 193
Qy      208 AVHSVHMGVYVHDIKENITLVPTGHIKLVDPGSAKMSNMKNAKLPITGTDYAPPE 267
Db      194 AIDSLHRLGYVHRVDPKDVLLDMQGHILADFGSCRLIADGSAVNAVAGTDTYISPE 253
Qy      268 VLVYMGDQKGTGYLDCDMMVSVGIAYEMIYGRSPFAEGTSARTFNNINMFORLKPDD 327
Db      254 ILKAME-DGRGRYKCEDMWSLIGICMYEMLYGTTTFYSERLVDTYGIKIMSHQMDLPDD 312
Qy      328 P---KVSSDFLDLIQSLCCQKERLKEGLC---CHPFSKIDMNNIRNSPPRPVTLKS 381
Db      313 EIDMVVSEAKDLIRQLICSSDVAFGHNGLSDFQLHFPFEGIDMNTIRDSNPVPVYSS 372
Qy      382 DDDTSNDEPERKSWSSPQQLSP---SGFSEELPVGFYSKALGILGRESVVG 437
Db      373 PEDTSNDFDVCD-DFTPCETQPPRVLAFTGNHLPVGFYSYTHG-SLSDARSLTDE 429
Qy      438 LDBPAKTSMEKKLILSKELQSDQDKHMOEMTLHRRVSEVAVELASQEVETLASE 497
Db      430 IRLAIQCGQDAELMEKSV-----GPMLENEKAEIVQKAKAQYITTIADHVAENRSE 484
Qy      498 TQSLLEQDLATYITTECSSLRSLSEQARMEVSQEDYALQILHIREQSRLOEIKOEY 557
Db      485 EDEN-----YESTIAQK-----497
Qy      558 QAQVEEKRLMNQLEEDLVGARRRSDLYESGLRESRLAABEFKAKTECOHKLKADQG 617
Db      498 ---DEQIINKKLEDEL-----AQOQO 517
Qy      618 KPEVGEYAKLEKINAEQOLKIOELOELKAVKASTATELLQNIQAKRABERELKQ 677
Db      518 KPK-----DEYVASEKKLEKELKERNKQV-----MEKSEIQLELNNIN 556
Qy      678 NREDSSEGIKKVVEAERHSHLENKYRLTETMERENRKLKDIQTSQOIQWADKILE 737
Db      557 DHD-----QVLYEKATVVGQR---DMQA---ELADGDSLL- 588
Qy      738 LBEKHAEOVSAQHLVHLKQKQHYEKKIKVLDNQIKDLADKETLENMQRHEBAHE 797
Db      589 -----TEKDSVKRLQDEA-E 602
Qy      798 KGLILSQKAMINAMDSKISLRQIYELSEANKLANSSLFTORNMKAQEMISELRQ 857
Db      603 KAL-----KQVADFEKLEKEL-ETEKIAL-----IKKBEVITEAR- 637
Qy      858 KFYLETQAGLEAONRKLSEOLEKISHQDSDKNRILETRLEVSLEHEEQKLELRQ 917
Db      638 -----KSEVETDHL-----SEEVVAKNT 656
Qy      918 LTELQSLQERESQTLAQARAALASQLROAKTELETTAAEETIQTALTARHDEIQK 977
Db      657 IASLQATNERETEIKLK-----QRMDEERASHTAQSQHOKQLEAHYERAKM 706
Qy      978 FDLARNSCTYITLLEBQNLQTEDMALNNQNFYLSQDL--EASGANDETVOYRSVDH 1035
Db      707 -----LQDVEQNNVENRGLRDEITELQSOOMALPRGILNEQ--QIHEIFNW 751
Qy      1036 LRRE-ITEREMOLTSQKQT--MEALKTCTMLLEQVWDLRLANDELLEKROMEAWSVL 1092
Db      752 VSEKATREEMENITRKITGEVSLKNNSPITTSNYI-----QNTBSGWS-- 797
Qy      1093 GDEKQFECREVLQRN--LDTEKQSPARADQRTTESRQVVELAVKHKAEITIALQOALK 1150

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Db      798 -----RMMNVARQDGLDQROLAELIDAK-----LKLKAEK 830
Qy      1151 EOKIKAESLSDKLNDEKKHAMLEMARSLQOKLETERELKQRLLEQAKLQOQMDIQ-- 1208
Db      831 NSQEQVLTSAARLDDTEKMA-----SLMREVAAMLKQCKNIENS 869
Qy      1209 KNIIFRLTQGLQEAADLADLKTRESDLEYQLENTIQLVYSHKVKMEGTSIQQTKLDFL 1268
Db      870 SDSAFSSTWG-----RGDLMTSMNND--YEMSN-SSLMQEMISROSTPSEYENAIL--- 917
Qy      1269 QAKMDQPAKKKKVPLQYNEILKLALEKAKCABELEALQKTRILRSAREBAARKATDH 1328
Db      918 -----LHDQVFKRVDLRY--KQKPM-----937
Qy      1329 PHSTPATARQOIAMSAIVSPHQPSAMSLAPSSRRKSSSTPEEFSSRLKERMHNI 1388
Db      938 ---KTASGISPYSISMERG--HNFRMKIKTP-----966
Qy      1389 PHRPVGLNRAIKCAVCLD-TYHFGQASKCLCEQVMCHPKSTCLPATCGLPABEYATH 1447
Db      967 -----TKCGHCTSIILIGLDRQGLFCQSCQYACHVSCAERYSQCPVEE--- 1010
Qy      1448 FTEAFCDKNNSPGLQTKERSSSLHLEGMKVPNNNRGQGMQRKXIVLEGSVLLYDN 1507
Db      1011 -----ERRPLGMITR--AEQNMQOVKN 1031
Qy      1508 EAREAGQPVVEEFELCLPDGDSIHGAVGASELANTAKADVYLKMA-----ESHPT 1560
Db      1032 EIR-----LVDMRDDEFTVCG--VSEADVIHQKGIPIKFRYTTQILNSSSEYS 1081
Qy      1561 TCPMGRTYLLADSPFDQKQWNTALLESVAVAGRVSRKADAKLGNLSLKLEGGD-- 1617
Db      1082 SSKFYTLLF-MAETEEKRKVVVALSELKT---LRRSKLADR--AFVKEVPVVT 1133
Qy      1618 ---RLDMCTLPSPQVVLVGTBEGLYALNVLKNSLTHYPGIGAVFOIYIKLEKLTLM 1673
Db      1134 LPSIRVAQCCAILIDRSKIVIGFSDHGYCIEISRQLLIPVG-----EK-- 1177
Qy      1674 IAGEERALCLVDYKVKVQSLAQSHLPAQ-----DISPINEAVKCHLFG 1719
Db      1178 -ENKQRCVETVEYDEBAQOLMIVGPAKDRHVRVPSAALDGRLLKIKVNDTIGCHLLA 1236
Qy      1720 AGKIENG---LCICAMPKSVILRYNENLSKYCIRREIETSEPCSIHFTNYSILGTN 1776
Db      1237 VGTNNPGRAGPAVAFKKSVTIFQIDRSEKHKWDLMPGPQSIATFNGLYVGS 1296
Qy      1777 KFYEI-----DMKQYTLF--EFLDKNDHSLAPVAFASNSFPVSVQVNS 1820
Db      1297 HSFRRWSLVGVDSPVGSGDASGAVLQHISLVNMEDTSLQ---FLNQOTSYEAKLI-VNV 1352
Qy      1821 AGQREYILCFHFGVGVDSYGRSRRTDILKWSRLPLAFAYRBPYLVPTHFNSLEVIEI 1879
Db      1353 PGSBDEYLVFNMTIGLVNEMGRSRLLPEVMFPQAKFYAHBYFLVFSENEVDIFNV 1411

RESULT 5
S74244
serine/threonine-specific protein kinase (EC 2.7.1.-) isoform I, Rho-associated - mouse
C/Species: Mus musculus (house mouse)
C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 16-Aug-2004
C/Accession: S74244
R/Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Saito, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A/Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein
A/Reference number: S74244; M01D:96368048; PMID:8772201
A/Accession: S74244
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1354 <NAK>
A/Cross-references: UNIPROT:P70335; EMBL:U58512; NID:g1514695; P1DN:AACS3132.1; P1D:g1514
C/Superfamily: protein kinase homology
C/Keywords: coiled coil; phosphotransferase; serine/threonine-specific protein kinase
F/74-338/Domain: protein kinase homology <KIN>

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F:1229-1283/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 12.2%; Score 1275.5; DB 2; Length 1354;

Best Local Similarity 25.7%; Pred. No. 2.3e-27;

Matches 388; Conservative 276; Mismatches 439; Indels 409; Gaps 47;

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QY 44 SPISREGIDALVYLFECCQPALMTKHYSNFPRKTSDDTIAELOQPSAKDPEVNSLV 103
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 23 SEVNSDCLDLGDLALVYDLDFPALRKKNKINDNPLSRKYDINKRDRIMAEDEVKVI 82
QY 104 GCGHFAVQVVRKATGDIYAMKVMKKKALLAQOVFPFEERIIISRSTPMIPOLQYA 163
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 83 GRGAFGEVQVLRHKSTKRYAMKLSKFEMIKSDSAFPEBERDIAMFANSPWVQVLFYA 142
QY 164 FQDKMHLVLMVYQPGGLSLINRYEDQDENLQFYLAELILAVSHLMGVYHRDIK 223
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 143 FQDDRYLYMMETWPGDLYNMISNYD--VPEKKARYTAEVVALALAIHSMGFIHNDVK 200
QY 224 PENILVDRTHIKLVDFGSAARNSNKNVNAKLPIGTPDYMAPVLTVMNGDGKTYGLD 283
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 201 PDNMLDKSGHLKLADFGTCMKMKKEGMVRCDTAVGTPDIYSPREVLKSGQGD--GYGGE 258
QY 284 CDMMSVGVIAVEMTYGSPPAEGTSARTFNINMFOFLKPPDPKYSDFDLIQSLIC 343
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 259 CDMMSVGVFLYEMLVGDPFYADSLVGTYSKIMHKNSLTFPDDNDISKAKNKLICAPLT 318
QY 344 GQKERLKEFG--LCCHPFPSKID--WNINRNSPPPVPTLKSDDDTNSFDEPKNSWVS 398
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 319 DREVRLGRNVEELKRLFFKNDQMAWETLRDYAPVPPDLSIDTDSNDDLEEDGDE 378
QY 399 SS--PCQSPSGSGEELPVGFSYSKALGILGRSESVSGIDSPAKTSMEKKLLISKE 457
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 379 ETEPII--PRAFVGNQLPFGVFTYYSNRYL-----PSANASERSSSNVDKS 423
QY 458 LQDS--QDKCKMGCEMRLHRVSEVAIVSQKEVELKASFTQ---SLLEQD--LATYIT 512
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 424 LQESLQCTTYKLEBQL-----HNEMQLKDEMEQCRISNLIKDKIMELD 468
QY 513 ECGSLKRSLEQAMVMSQEDKALQLDLHIREQSKLOEIKQEYQAOVE--EMRLMNNQL 571
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 469 EBNQNRNLESA---VSQIEKEKLLQHRINEYRKVEQ--ENKRNINENVEVSTLMDQL 523
QY 572 EEDLVASRRSDLYESELRESRLAEEPRKRYATECQHKLLKAKDQKPEVETAKLEKIN 631
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 524 E-----DLRKASQTSQLANEKLTLQKQLEBANDLRTESPTVAIRLKSH 568
QY 632 AEOQLKQELQEKLEKAVKASTEITELLQNRQKKEARELEKQ-----NRDSS 683
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 569 TEMSKSTISQL--ESLNRELQ--EENRILLEN--SKSQADKQYVLOAVLEARRDRGHDS 621
QY 684 E--GIRKKLVEAERHSHLENKYKRL-----TWERRENLKDDIQTKSQOIQ 729
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 622 EMIGDLOARTISLOEBVYKHLKHLIERVEGRKEAQMNLNSEKKNLLEIDANKLSIQ 681
QY 730 QMADKILEBEKREAOVSAQHLEVLKQKQHYEKKIKVLDNQIKDLDKLETLNMQ 789
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 682 Q-----RLRQEVNHEKVT---KARLTDKHQSIEFAKSYMCMEMEKUL----- 720
QY 790 RHREBAHEKKG--IISQKAMINAMDSKIRSRQRIIVELSEANKLAANSSLFTQSNMKAQ 848
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 721 KEERBAEAKENRVETEKQSMLDVLIKOSQOKLEHILTE--NKRMEDV---NQLALQL 776
QY 849 EMTSELR---QOKYLFEOAGKLEAONRK--LEQDLEKISHQDHDKRLLELFTLREVS 904
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 777 EQSNKRLILQNE--LKTQA--FEADNIKGLEKQMKQ-----EINTLLFAK--RLLEFE 824
QY 905 IEHEBQKLEIKRQUTTELQSLQERESQUTLQAARALBSQRAKTELEBTTAEAEERI 964
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 825 L-----AQLLKQVNGMGQWRELQDDLEAQYSTLYKQVQKLEIEBKRENENLRKI 878
QY 965 QALTARHDEIQRKDALRNSCTVITDLBEQNLQUTEDNAELANNQFLISKOLDASGAND 1024
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 879 QELQSEKRTISTOLD-----LAETKAESEQLA--RGILIEQYFELTQESKKAARN- 927

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QY 1025 EIVQLASVDHLRREITEREMQULTSQQYMEALKTCTMLEEQVMDLEANDLEKERQ 1084
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 928 -----ROEITDXD-----HIVSRLEETNSVLTQKQIEMLRKNEEINEMWRT 968
QY 1085 WEAMRSVLGDKEKQGFEPERVRELQRMLDTEKQSRADQRITSEQVVELAVKHEKAEILA 1144
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 969 AE----- 970
QY 1145 LQOALKQKLAESLSDKNDLEKHAMLEMANRSLQOKLETRELRKQRLLEQAKIQOQ 1204
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 971 -----EYKTKKE--EELNNLK-----AAREKNISTRTLLKTAQVNNKLAETMNR 1012
QY 1205 MDIQKHIFRLTQGLQALDRADLLTERSDLEYOLENTQVLYSHEVNMKEGTTISQTKL 1264
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1013 KDFKIRKKRANTQ-----DLRKEKENRKLQLE-----LNOERKQNQVYVHKQKE 1058
QY 1265 IDPLQAKMQDPARKKKVPLQVYNELKLALKEKARCQLELEBQALQKTRIELRSAREEAHRK 1324
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1059 LNDMQQQLVEECTHR-----NELQML-----ASKESDITQLRAKLDDSD----- 1099
QY 1325 ATDHPSTPATARQOIAMSIVRSPHOPSAWSLLAPSSRRKESSTPEFRRRLKERM 1384
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1100 -----SIVASFPESADEFTDGLPES----- 1119
QY 1385 HNNIPHRFNVLNMRATKCAVCLDYHFRQASKCLCEQVMCHPKSTCLPATGLPAEY 1444
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1120 ----- 1119
QY 1445 AHTFTEAFCDKNNSPGLQTKERPSSILHEGMKVPNNNRGGQGMQRKYIVLEGSVLI 1504
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1120 -----RLBGMLSVPRNGIKRYGMKKQYVVSCKILF 1152
QY 1505 YDNEAREAGQRP 1516
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 1153 YNDEQDKQESSP 1164

```

RESULT 6

serine/chreonine-specific protein kinase (EC 2.7.1.-), Rho-associated - bovine
 N/Alternate names: Rho-associated protein kinase
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004
 C/Accession: S70633; S77694
 R/Matsumi, T.; Amano, M.; Yamamoto, T.; Chihara, K.; Nakafuku, M.; Ito, M.; Nakano, T.; Oki
 EMBO J. 15, 2208-2216, 1996
 A>Title: Rho-associated kinase, a novel serine/chreonine kinase, as a putative target for
 A/Reference number: S70633; MUID:96208507; PMID:8641286
 A/Accession: S70633
 A>Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 1-1368 <MAT>
 A/Cross-references: UNIPROT:Q28021; EMBL:U036909; NID:g1326077; PIDN:AA048567.1; PID:g132
 A/Accession: S77694
 A/Molecule type: protein
 A/Residues: 1-18;30-34;36-44;58-64;133-140;248-252;291-295;297-305;327-347;350-360;366-3
 -1070 <MAT>
 C/Superfamily: protein kinase C zinc-binding repeat homology; protein kinase homology
 C/Keywords: ATP; phosphotransferase; serine/chreonine-specific protein kinase
 F/90-354/Domain: protein kinase homology <KTN>
 F/98-106/Region: protein kinase ATP-binding motif
 F/1261-1315/Domain: protein kinase C zinc-binding repeat homology <KZN>

Query Match 12.0%; Score 1263.5; DB 2; Length 1386;

Best Local Similarity 24.4%; Pred. No. 4.9e-27; Indels 443; Gaps 41;

Matches 382; Conservative 274; Mismatches 466; Indels 443; Gaps 41;

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QY 15 GAAPRIA---SRASRLNLFQGKPPFWTQOQMSPLREGGIIDLFLVFECCQPALMKIK 71
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 12 GAPEAVSGDQAGSR-----QRKLEALIRDPRIPIVNESLIDGLNPLVLDLPFPAKKNK 66
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 72 HVSNFVRKYSDDTIAELOQPSAKDPEVRSLVGCGHFAVQVVRKATGDIYAMKVMKKK 131

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Db      67 NIDNPLNRKYKIVKIGKIGLOKAKEDYDVYKVGIGAGEVOLVNHKKSOKYAAKLLSKF 126
Qy      132 ALLAQEVSPFEEERNILSRSTSPWIPOLQYAFODKXHLYLWMEYOPGDDILSLNRYED 191
Db      127 EMIKRSDSAFWEERDIMAFAFNSPWVQLFCAFODDKLYLWMEYMGDDVNLMSYND- 185
Qy      192 QLDENLIQFIYLAELILVAVSHLMGYVHRDIKPEINILVDRTHGHIKLYDFGSAAKNSNM 251
Db      186 -VPEKMAKFFYTAEVVLLDALHSMGLIHRDVKPDMMLDKHGHIKLDLFGTCMKQIDEGM 244
Qy      252 VNAKLPICGTPDYMAPEVLTWVNGDGKGYGLDCDMWSGVYAYEMITGRSPFAEGTART 311
Db      245 VHCDAVGTIDYISPEVVKSGQGD--GYTGRECDMWSGVYLFEMLVGDTFFVADSLVGT 302
Qy      312 FNNIMNFORFLKFPDDPKVSSDFLDLIQSLICGQERLKKEG--LCCHPFPSKIDNN-- 366
Db      303 YSKIMDKHNSLCPEDEAIEISGAKNLIICAPLTREYVLRNGVBEIQHPFFKNDQNMWD 362
Qy      367 NINSPPPYPTLKSDDDTSNFDEPEKNSM-VSSPCQLSPGSGEELPFVGFYSKAL 425
Db      363 NIRETAPVVPBELSSDIDSNFDDIEDKGVETFPF--PKAVVGNQLPFGFTYYREN 419
Qy      426 GILGRSSVVGSLDSPA--KTSSMEKKLLIKSKELQSDQKCHQEQEMTRHHRVSEVE 483
Db      420 LLSS-----DSPCKENDSTQSR--KNESQEIQKLYLLEHLS----- 457
Qy      484 AVLQKEVELKASETQSLLEQDLATYITECSSLKRSLLEQARMVNSQEDKALQLDHIR 543
Db      458 -----TEIOAKE-----LEQ-----KCKSVNTLEKAKALEEITLRKINVESTLR 499
Qy      544 --EQRKLOEIKEOQYQAVEKRLMMQLEEDIVSARRSDVSELRRESRLAAEEFKR 601
Db      500 QLRERKALLOHKAQAEYORKADHEADKRNLENDVNSILKQLEDDKKNQNSQISTE---- 555
Qy      602 KARECHOKLLKADQCKREYGVAKLEKIAEQOLKIOELO-----K 644
Db      556 KVNQLOQDLQDETVALLTESDTPARLKRKTQESSKQIOLESNNRDIQDKNCLETAKLK 615
Qy      645 LEKAVKASTATELLQNIROAKERAERELEKQNR-----EDSSEG--IRKLVFAEERRH 698
Db      616 LEKEP---INLOSVLEBERDRTHGSEIINDLQIRISGLEBDVNGKILAKVLEKQOL 672
Qy      699 SLENKVRLETERRENRLKADIQTSQOIQOMADKILLEEKREARQVSAOHLEVHLKQ 758
Db      673 Q-----ERTDLEKEKNMEIDMTYQLKVIQOS-----LEQEBETHKA-----TKARLAD 717
Qy      759 KEQHYE-----EKIVLNDQIKKDLADKXTLENMQRHE-----EAAHEKGI 801
Db      718 KNKIYESIEBAKSEAMKEMERKULSEERTLKQKVENLLEAKKCSILDCDLKQSOQKINE 777
Qy      802 LSBOKAMINMDSKIRLSIORIVLESEANKLAANSLSFTQRMKAGOEIMISLRQCKFYL 861
Db      778 LKQKQVLA--EDVRLUTKIEGETQKCI-----TQNDLMQIQOVNTILMS----- 823
Qy      862 ETQAGKLEAQRKLEQLEKISHODSDKNRLLELTRLEVSLEHEQKLEKQKLTTEL 921
Db      824 -----EKQLKQ-----ENHILEMKSL-----EKQNAELRKEKQDA 855
Qy      922 QLELOERESULTAQARALLESQLOKATELEETT--AAEBEIOALTANDEIORKF 978
Db      856 DQGMKEIQDQLEAQYFSTLYKTOVRELKECEKEKYLCKELOQKQKQELDERISLAQL 915
Qy      979 DALRNSGTIVTDLLEQOLNOLTEQNAELANNQNFYLSKQLEASGANDSIVOLRSVDHLRR 1038
Db      916 E-----ITLTKADSEQLARSTIAEBQYSDLEKEKIMKE-----LEIKEMMARHKQ 959
Qy      1039 EITEREMQLTQSQOTMEALKTCTCMLEEQVMDLEALNDELLEKRCQWEARSVLGD-- 1095
Db      960 ELTEKQATIASLETNRTTLTSVAVLANL--EKELNNKLEKAQEQ-----LSRLKBEIS 1012
Qy      1096 ----KQFERVAVELQRMMDTEKOSRARADQRTTESQVAVELAVKEKAEILALQALKE 1151

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Db      1013 AATAKQFE-----KQLTE 1027
Qy      1152 QKLKAEISLSDKLANDLEKKHMLENNARSLOQKLETERELKQRLLEEQAKLOQOMDLOKMH 1211
Db      1028 RLTKQAVNNKLAELMNRKEPEVKRGNDDTVRKEKENRKLHMLSEKREKLTQOM----- 1081
Qy      1212 IFRLLQLEALDADLILKTERSDLEQLENIQVLYSHEKVKMEGTISQOTKLIDFLQAK 1271
Db      1082 -----AKYQELNEMOQAIAESQI----- 1101
Qy      1272 MDQPAKKKKVPLQYNEMLKALEKEKARCABELEALOKTRIELRSAREBAARKATDHPH 1331
Db      1102 -----RIELQMLTDSKOSDIEQLRSQLOALHIGLDS----- 1133
Qy      1332 STPATARQOIAMSAIVSPHEQPSAMSLAPSSRRKSSSTPEEFSSRLKERMHNIPHR 1391
Db      1134 -----SIGSGPGTLEADDGPES----- 1151
Qy      1392 FNVGLNRAIKCAVCLDTPHFGRQASKLECQVMCHPKCSTCLPATGCLPAEYATHFTEA 1451
Db      1152 ----- 1151
Qy      1452 FCRDKKMSPGLOTEKPESSSLHLEGMMKVPRNNKRGQGGWRKYTVLESGSKYLYDNEARE 1511
Db      1152 -----RLBGMLSLPVRNNTYKKGWVKYIVSSKILFYDSEQDK 1191
Qy      1512 AGQRP 1516
Db      1192 EQSNP 1196

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RESULT 7
S69211
serine/threonine-specific protein kinase (EC 2.7.1.-), Rho-associated - human
C:Species: Homo sapiens (hmn)
C>Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 16-Aug-2004
C:Accession: S69211, S71910
R:Ichikaki, T.; Maekawa, M.; Fujitaawa, K.; Okawa, K.; Iwamatsu, A.; Watanabe
EMBO J. 15, 1885-1893, 1996
A:Title: The small GTP-binding protein Rho binds to and activates a 160 kDa Ser/Thr prot.
A:Reference number: S69211, MIMD:96203110, PMID:8617235
A:Accession: S69211
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1354 <ISH1>
A:Cross-reference: UNIPROT:Q13464; EMBL:U03195; NID:g1276900; PTDN:AB02814.1; PTD:g1276;
F:1229-1287/Domain: protein kinase C zinc-binding motif
F:1229-1287/Domain: protein kinase C zinc-binding repeat homology <KZN>

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Query Match      12.0%; Score 1260; DB 2; Length 1354;
Best Local Similarity 26.3%; Pred. No.5.9e-27;
Matches 400; Conservative 293; Mismatches 531; Indels 296; Gaps 53;

Qy      44 SPLSREGILDALFVLEECGQPALMKIKHVSNFVAKYSDTIABLOELQPAKDEFEVSLV 103
Db      23 SEVNSDCLDLDGLALVYLDLPALRKKNIDNLFSLRYKDTINKRIDRMKAEDVEYVKVI 82
Qy      104 GCGHFAEVQVVRKATCDIYAMVKMKKALLAQEQVSFFEEERNILSRSTSPWIPOLQYA 163
Db      83 GRAFGEVQVLRKRSRKRYAMKLSFEEMIKKSDSAFWEERDIMAFAFNSPWVQLFETYA 142
Qy      164 FQDKNHLVLMVEYOPGDDLSLNRYEDQDENLIQFIYLAELILVAVSHLMGYVHRDIK 223
Db      143 FQDDRYLYMMEIMPQGGDLVNLMSYND--VPEKMAKFFYTAEVVLLDALHSMGTHRDVK 200
Qy      224 PENILVDRTHGHIKLYDFGSAAKNSNMKNVNAKLPIGTPDYMAPEVLTWVNGDGKGYGLD 283

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Db 201 PDNMLDKSHLKLADFGTCMKKKEGMVRCDTAVGTPDITISPEVYLKSGGD--GYTGRE 258
Qy 284 CDWMSVGVIAIYEMLYGRSPPAEGTSARTFNINNFQRLFKRPDDPKVSDFLDIQSLC 343
Db 259 CDWMSVGVIFLYEMLVGDPFYADSLVGTYSKINHKNLSLFPDDNDISKEAKNLICAFLT 318
Qy 344 GQERLKFEG--LCCHPFSKID--WNINRSPPPVPTLKSDDTDSNDEPKSVWS 398
Db 319 DREVRIGRNVEBELKRIHFKNDQWAWETLRDTVAPVPDLSIDITSNDLEEDGEE 378
Qy 399 SS-PCQSPSGSGEELPFVGFSSKALGLIGRESVSGLDSPAKTSMEKLLIKSKE 457
Db 379 KTFPT--PRAFYGNQLPFVGFTT-----YSNRYYLSANPNDNRISN-----ADKS 423
Qy 458 LODS-ODCKHMEQEMTRLHRRVSEVAVLQKEVELKASGTOR---SLLEOD-LATYIT 512
Db 424 LQESLQITIKYLEQL-----HNEMQKDEMEQCRISNLIKDKIMELD 468
Qy 513 ECSSLKRSLEQARMVVSQEDDKALQLHDIRESRKLOETKEQYQAOVE-ENKLMNQ 571
Db 469 EENGORNLST--VSQIEKEKMLQHRINEYORKAQO--ENKRNVEVEVSTLQDL 523
Qy 572 EBDLVASRRSDIYESELRSRLAABEFKGRKATECQHLKAKQOGKEVGEVAKLEKIN 631
Db 524 -EDLKVSQNSQL-----ANF--KLSQLOQLBANDLRTESDTRVRLKSH 568
Qy 632 AEOLKIQLOEKLEKAVKASTATELLONIRQAKERARELEKQNRDESSGIRKLV 691
Db 569 TEMSKTSIQ-L-ESLNRELQ--EENRLTEN--SKQTDQDYQLQ-----AIL 610
Qy 692 EAEBRHSLENNKRYLETMERENRLKDIQT--SQOIQOMADKILEKHEKRAQV 747
Db 611 EAERRDG-----HSEMIQDQARTISLOEVEKHLKHLMEKVEGERKEAQD 657
Qy 748 SAQHLEVHLKQXQHVEKIKVLDNQKKQLADETLENNQORHEBAHE---KGLIS 803
Db 658 MNHSE--FEK-----NNLEIDLNRY--LKSQOQREOVNHEKVTAKALT 700
Qy 804 EOKAMINAMDSKTRSEORIVELSEANKLANSSLFTQNMKAQOEINIS-ELRQOKVYLE 862
Db 701 KHQSIKSAKSVANCMEMKIKLEKEKRAKXENRV---QIRQCSMLVDVLKQSOQKLE 756
Qy 863 TOAGKLEAQRKLEBQLEKISHQDHSKRLLELETRLEVSLEHEBOK----- 911
Db 757 HLGNKKE--RMEDVIGNLTQLQESNKRLLQNLQETQAFRADMLKGLKQKOEIN 812
Qy 912 --LEIKQLTQLQS-----LQRESQLTQLQARALBESQLAQATLEET 957
Db 813 TLEBARK-LLEFELAQTQKQYRGNEGQMRLEQDLQLEAQYFSTLYKQVKELEKEIEKN 871
Qy 958 AEAEBEIQALTARHDEIQRKFDALRNSCTVITDLEBQNLQTEDNALNNQNFYLSKQLD 1017
Db 872 RENUKTIQELQNEKETLATQLD-----LAETKASEQLA--RGLLEQYFELTQESK 921
Qy 1018 EASGANDEIVQLSEVDHLREITEREMQUTSQKQTMALKTCTMLBEOVMLEALNDE 1077
Db 922 KAASRN-----RQETIDKD-----HTVSRLSEANSMLTKDIEILRRENEE 961
Qy 1078 LLEKERQWEAMRSVLGE-----KSQFECVRELQRMVLDTEKQSRADQRITESQVVE 1132
Db 962 LTERMKKAESEYKLEKEEISNLKAPE-----KNINTERLTKTQAVNKLAIMNRKD 1014
Qy 1133 LAVENKAEIITALQOALEKQK--LKAESLSDKLNLEKQAMLENNARSIQQLFETERE 1189
Db 1015 FKIDRKKAANTQDLRKKEKERNKQLELQNEREKFNQWVXK-----QKEL--ND 1061
Qy 1190 LKORLLEBQA--KLQOQMDLQKNHIFRLTQQLQALDRADLL-----KTERSDLEYQL 1240
Db 1062 MQQQLVEECAHRELQWQLASKSDIEQLAKKLIDLSSTVSASFPSADETDGMLPESRI 1121
Qy 1241 ENIQVLSHREKVMGEGTISQ---QTKLIDFLQAKMDQPAKKKVPVQLQNELKALAEK 1296
Db 1122 EGMVLSVNRGNIKRYGWKQYVVSXKILFYNDQDQKQSNPSMVLIDIKL----- 1173

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Qy 1297 ARCAELEALQTRIELRSAREBAHRKATDHPHPSTPATARQOIAMSAIVRSEHPSA 1356
Db 1174 -----FHVRRPTQGDVYRAET-----EELPKI 1195
Qy 1357 MSLLAPSSRRKESSTPEESRRLKERMHNIPIHRFVGLNMBATKCAVCLDTVHFGROA 1416
Db 1196 FQILYANEGECRQDVEHEPVQAEKTNFQNHKEHEFPTLYHFRPANCDAKAPLMVFKP 1255
Qy 1417 SKCLQCVMHCPKCS-----TCLPATCGIPAEYATHTPEAFGRDRXNSPGIQTKE 1466
Db 1256 PPALEOCR-RCHVACHDHLDKEDLLC-----PCQVSYDVSTA--RDMILLACSGDQ 1305
Qy 1467 PSSSLHLEGMMKVPNNKRG 1486
Db 1306 KKWVTHLV--KKIPKNPPSG 1323

RESULT 8
S74245
serine/threonine-specific protein kinase (EC 2.7.1.-) isoform II, Rho-associated - mouse
C/Species: Mus musculus (house mouse)
C/Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 16-Aug-2004
C/Accession: S74245
R/Nakagawa, O.; Fujisawa, K.; Ishizaki, T.; Salto, Y.; Nakao, K.; Narumiya, S.
FEBS Lett. 392, 189-193, 1996
A/Title: ROCK-I and ROCK-II, two isoforms of Rho-associated coiled-coil forming protein
A/Reference number: S74244; WUID:96368048; PMID:8772201
A/Accession: S74245
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1368 <NA>
A/Cross-references: UNIPROT:P70336; EMBL:U58513; NID:G1514697; PID:AA053133.1; PID:G151.
A/Supfamily: protein kinase C zinc-binding repeat homology; protein kinase homology
F/Keywords: phosphotransferase; serine/threonine-specific protein kinase
F/90-354/Domains: protein kinase homology <KIN>
F/1261-1315/Domains: protein kinase C zinc-binding repeat homology <KZN>

Query Match 11.9%; Score 1250.5; DB 2; Length 1388;
Best Local Similarity 24.1%; Pred. No. 1.1e-26;
Matches 365; Conservative 284; Mismatches 489; Indels 379; Gaps 35;

Qy 32 QKRPPTQQMSPLSBEGLDMLFVLFECSQPALMKIKNVSNFPAKYSDDTAELEQL 91
Db 27 QRLKELAIRDPRSPINVESLIDGLNSLVLDLDPALRKNNQINDPILRYEKIYKJRLQ 86
Qy 92 PSAKDEPVRSVLCGCFPAEVQVVRKATGDIYAMKWKKKALLAQEVSFEEERNLISR 151
Db 87 MKKEDVDVAVVIGRGAEGEVQVRHRAQKQVAMKLSKFEEMTKRSDSAFFWEERDIMA 146
Qy 152 STSPWIPQLQYAFQDKNHLYLVMEYQPGDLSLNRYPEDLDENLQFYLAELIYAVHS 211
Db 147 ANSPFWVQLFCATQODRILYLVMEIYMPGDLVNLMSYD--VEPKNAKFYTAEVYALDA 204
Qy 212 VHLMGVHRDIKENTILVDRTHIKLVDPGSAAMNSKNVNAKLPIGTVDYAAPEVLT 271
Db 205 IHSMGILHRDVKEDNMLDKHGHLKLADFCTCKMKMETGVAHCDTAVGTDTYISPEVLKS 264
Qy 272 MNDDGQGTVGLDDCMDSVGVIAIYEMLYGRSPPAEGTSARTFNINNFQRLFKRPDDPKV 331
Db 265 QGGD--GYTGRECDWMSVGVIFLYEMLVGDPFYADSLVGTYSKINHKNLSLFPDDNDIS 322
Qy 332 SDFLDLIQSLQCGQERLKFEG--LCCHPFSKIDWN--NINRSPPPVPTLKSDDTDS 386
Db 323 KXAKNLICATLTREYVRLGNGVBEIKQHPFFKNDQNMNINETAAPVPELSSDIDS 382
Qy 387 NFDEPEKNSW-VSSSPQQSPSGSEELPFVGFSSKALGLIGRESVSGLDSP--AK 443
Db 383 NFDDIEDDKGDTVETPL--PKAFVGNQLPFIQTYFRRENILIS-----DSPPCRE 430
Qy 444 TSMMEKLLIKSELDQSDQCKHMEQEMTRLHRRVSEVAVLQKEVELKASGTORSL 503
Db 431 NDAIQTR--KSEBSQEIQKLYALEHLS-----SEVQA--KEELEOK----- 469

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QY 504 BODLATYITBSSSLKRSLEQARMEVSQEDDKALQDLHDIR--EBSRKLQITKEQBYQAOV 561
Db 470 -----CKSINTREKTAKELEBEITLRKGVESTLRQLEBKALQHKNAEYORKA 519
QY 562 EEMRLMANQLEEDIVSARRSDLYESSELRESRLAAEFKFKATSCQHKLTAKXQOQREV 621
Db 520 DHEADKGRNLENDVNSLKQDQLEDKKGNQSQISTE---KVNQOQDLBANMLLTRES 575
QY 622 GEYAKLEKINAEQOLKIQELQEKLEKAVKASTATELLQNIROKERAERELK-LONRE 680
Db 576 DTAIRLRKTOAESKQIQOLESN-----NRDLQDNGCLLETKLKEKEFINLQ 624
QY 681 DSSGIRKKLVAEERHSLNKKYKRLTMRERENRLKQDIQTSQOQLQOMADKILBEE 740
Db 625 SALESERDRTHSGEIIINDLOGRISGLEEDLTKTKALLAKELKROQ--EKLTLDEK 681
QY 741 KHRBAQVSAOH---LEVHLKQKE-OHYEEKIKYLD-NOIKQD--ADKETLEMMORHE 792
Db 682 EKSMELDMYQOLKVIOQSLQEBEAHKTKYARLADNKKIYESIEBAKSEAMKEMKKLL 741
QY 793 EEAHEKQKI--LSEQKAMINAMDSKIRSLERIVELSEANKLANSSLFTORNMKAQEE 849
Db 742 EERSLKQKVENLLLEAEKRGSIILDDCLKQSQOKLNEU-----LKQXDV 784
QY 850 MISLRQOKYLETQAGKLEQNRKLEBQLEKISHQDSKNRLLELTRLEVSLEHEE 909
Db 785 LNEBVRMLTLKIEBETQRCIMQNDLKMGTQOVNLTLMKSEK-QIKQENNHMEKMKYLEK 843
QY 910 QKLELQKQLELOSLQERESQUTALQAPRALESQURQAKTELEPT--AAEMEELQA 966
Db 844 QNTLRERODAQOMELQDQLEBQYFSTLYTVARELEKEBEKTKLCKELQOQKOD 903
QY 967 LTAHREIQRKFDALRNSCTVITDLBQNLQTEDNAELNNQNFYLSKQDLDEAGANDEI 1026
Db 904 LQDRSDSLAQLF-----ITLTAKDSEQLARSIAEQYSDLEKIKIME----- 947
QY 1027 VQLRSEVDHLRREITEREMQLTQOKQTEALKTTCMLBQVMDLEALNDELLEKEROWE 1086
Db 948 LEIEMMARHQBQELTEKDTTASLEETNRILTSDVANLAN--EKEELNNLKQSQOQ-- 1002
QY 1087 AMNSVLDG-----KSQFCRVRELQRMIDTEKQSRARADQRTITSRQVVELAVENK 1139
Db 1003 --LSKNDKEMSAARAIQAQFE----- 1021
QY 1140 AEIATLQALKECKLKAESLSDKLNDEKKHAMLENNARSLOQLETERELKQRLBEOA 1199
Db 1022 -----KQNLNERLTQAVVKLAELMNRKEPVKRGSDTVRRKEKENRKLHMLKSEBE 1075
QY 1200 KLOQOMDLQKNHIFRLTQGLQEALDRADLLKTERSDELEYOLENTQVLYSHEKVMEGTIS 1259
Db 1076 KLTOQM----- 1096
QY 1260 QQRTKLDFLOAKMDQPAKKKKVPLQVNEKLALKEKARCALEBALQKTRILERSAREE 1319
Db 1097 EBSOI-----RIELQWTLDSKQSDIEQLRSQALHIGMDS-- 1133
QY 1320 AAKRKATDHPSTPATARQOIAMSAIVRSEHPQSAISLAPPSRKSSSTPEERSR 1379
Db 1134 -----SISGSGDAEPPDGEPES----- 1151
QY 1380 LKERMHNIPIHRFNVGLNMBATKACVLDTVHFGRAQSKLEQCVMPKQSTCLPATCG 1439
Db 1152 ----- 1151
QY 1440 LPAPAYATHTFPAFCRDMNSBGLQTKPESSSLHLEGMMKYPRNNKQOQCKDRKYTYLEG 1499
Db 1152 -----RLLEGWLSLIPVRNNTKKFGWVKKYIVSS 1179
QY 1500 SKVLYIDNEARBAGQRP 1516
Db 1180 KKLIFDSEODKEQSNP 1196

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RESULT 9
T25539
hypochemical protein C10H11.9 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T25539
R/Dante, M.; Wambley, P.
submitted to the EMBL Data Library, February 1997
A/Description: The sequence of C. elegans cosmid C10H11.
A/Reference number: 220047
A/Accession: T25539
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1173 <DAN>
A/Cross-References: UNIPROT:P92199; EMBL:U88311; PDB:1AAB42348.1; GSPDB:GN00019; CESP:C1
A/Experimental source: strain Bristol N2; clone C10H11
C/Genetics:
A/Gene: CESP:C10H11.9
A/Map position: 1
A/Intons: 23/3; 51/1; 104/3; 343/1; 478/2; 868/3; 891/3; 970/3; 1027/3; 1114/1
C/Superfamily: hypochemical protein C10H11.9; protein kinase homology

```

Query Match 10.7%; Score 1126.5; DB 2; Length 1173;

Best Local Similarity 29.2%; Pred. No. 1.8e-23; Matches 294; Conservative 198; Mismatches 339; Indels 175; Gaps 30;

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QY 44 SPSRREGILDALFVLFEECSQPALMKIKHVSNFYRKYSDTIAEQLEQPSAKDFEVSILV 103
Db 15 SPINIESLDTITLNLVNDCKIPVLMRKYSVDNFSRERAVESLAALRMQADRLQKVI 74
QY 104 GCGFAEVOVVRKATGDIYAMKMKKALLAQOVSPFEERNILSRSTPMIPLQOYA 163
Db 75 GRGAFGVLHVRHRTNTVYAMKLNKDMDIKRADSAFFWEERIDIMAHANSEWIVRLQYA 134
QY 164 FQDKNHLXYLMEVQPGDILSLNRYEDQDENLQCYTLAELIYAVSHLMGVNHDIX 223
Db 135 FQDPRLHYMEVYMPGGDLVNLMTSYE--VSEKTRFYTAIEYALALSHMGVYIHDVK 192
QY 224 PENLVDRTHGKIKLVDSAAKMSNKNVNAKLPICGPDVMAAPVLTVMNGDGKGYGLD 283
Db 193 PDNKLISGHIKLADGTCVKNANGVRCSTNAGPDIYSFVLNQGODAE--FGKE 250
QY 344 GQKRL--KFEGLCHPFPFSKIDMN--NIRNSPPPVLPVLTSDDTSNFDEPKNSWVS 398
Db 311 AADRLGRNSVDIDIRNKKFVNDMEWTPATLRASPPVLPISLKSDDDTTFEEIETRDND 370
QY 399 SSPQQLSPSGFSGELPFGVFSYKALGILGRSESVSGLDSPAKTSMEK----- 449
Db 371 AGDFQL-PKTFNGQLPFIQFTYSNEYSV--KNLLKGAGAGSKQIGIEQHKQTVBQ 426
QY 450 -----KLLIKSKB-----LQDS-----ODKCHKEQEMTRLRARSEV 482
Db 427 PLTNGHAGVPEEKYAVNKELDSSKNREFELKDSIARNRIPAKMINENKNSLSTKISDL 486
QY 483 E-----AVLSQKEVFLKASEFORSILBEDLATYITCESLSKRSLEQAR 525
Db 487 ERELKONKDLRAGASDADAKYNEIYAVELRMSKEVNSMESELKFRDKCEQLKEDLRKS 546
QY 526 MEVSQEDDKALQDLHDIRQSRKLQELKEQBYQAOVEEMLMNMQLEEDIVSARRSDLY 585
Db 547 GELAQEKNEQVRFOQKQDDAEAPAEIKRDYELLQIRENEKSV-QLKAL-DEKKEGAY 604
QY 586 ESELRESRLAAEFKFKATECOHKLAKXQOQREVGEYAKLEKINAEQOLKIQELOEKL 645
Db 605 QQSVAKATDA--EMERKMGYFEKQLEHANDERKRE-----EQKRTAAEPQSR 650
QY 646 EKAVKASTAT-ELLQNIROAKERAERELEK-LQNRDSSBGRKKLVAEERHSLNKK 703

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Db	231	FARTHYRWPESTLPPDFISKPEFSKRRKAE	TWKRRBRAVAYSTVGPRDYIAEFVQ-	PNG	289
Qy	275	DKGTYGUDCDMWNSGVLA	YEMIVGSRSPAEGTSARTFNINNFQFLKPEPDPKXSSD	F	334
Db	290	-----YTWSCDMWMSGVIMTEMLIG	PPYPCSELPOETAKYKVINWOOTLVPSPVPISTIEA		344
Qy	335	LDLIOSLTCGQKBRLEKFEQ-----	LCCPFPSKJIDMNNIRNSPPEFVPTLKSDDDTSNF		368
Db	345	KATIRFPCCEARRKIRGNHGGDEIQOC--	PFYKIRDMNHIRRPPRIRTVIVSIDTISNF		402
Qy	369	DE-PEKN-SWSSSPCOUSPSPGSGEBEL	PVFGFSYK-----		423
Db	403	DDPPEDLTWPST--LIRPEQPRGRGEFVD	FTYKRFPGLTQOKRYILGWLFGEMLWYI		460
Qy	424	-----ALGILGRS-----	ESVGG---LDBPATSSMEKULLIKSKEL		458
Db	461	LSWGLVAVLCYFALNHLSTGTEAHTS	STFGSSGVANGVANGTHTSSGE-----WSNI		515
Qy	459	OD-SODCKHMEQEMTRLRRAVSEVAVLS	QCEVELKASETOSLSLEQOLATYITECSSL		517
Db	516	VSMLXSNHKKVAPAPDAMIKSINE----	AAKV---TSPTCEVULFEEGQGHSDVLQSP		567
Qy	518	KRSLEQARMEVSOEDDKALQLLHDI	REOSRKLOEIKEOEYOAQVEBMRIMNQLEBDVS		577
Db	568	K--ISNVREHGRPD-----	HLTVRSVHLPCYKRLVSSQRPBERMIVSNVDSYID		618
Qy	578	ARRRBDLYESELRESERLAAEFKRA	TECOHLYLAKOQKREVEGEYALTEKINAEQOLK		637
Db	619	LRG-----EVECRMCIANQULY-----	LMGCFSGREMIELINTDPNAYOVS		662
Qy	638	IOELOEKLEKAVKASTEATELLONT	IROAKERARELEKJONNEDSEGIKKYLVAEER		697
Db	663	IPWBEISIRCLISA-----VTNINLS	EBEME-----EUNTADITSRTIYNPPTH		709
Qy	698	HSLENKVKRLEETMERENRLKODI	QTKSQOIQOMADKILEEKHREAQVSAOHLVHLK		757
Db	710	PS-----GIMRSYNNYDTNINL	HVADYGTQ-----SSHRNSPBGDVPBEMFKX		751
Qy	758	QKEQHYEKIKVLDNQI	KDLADKETLENNMQHHEBAHEKIKLSEQAKAMINMADSKR		817
Db	752	LNESH-----	-----LISPSYNTNSIPNKXR		772
Qy	818	SLEGRIVELSEANKLAANSLS	FTQNMKAQOEEMISELROQKRYLETQAGKLEAOKRKEE		877
Db	773	-----IKVITASRLGREVS-----	-----QPFV-----NENDE		796
Qy	878	QLEKISHODSHDKRLLLELTR	REVSLEHBEQKLELKROLTLEOLSLOERESQULTALOQ		937
Db	797	PAOKYSTTKGINANPFME-----	ETFPDLTPATVEILFEIYEGNDKLHMMD		844
Qy	938	ARAALESOLROAKTELETTABE	BEIQALTAHDEIQ---RKDALRNSCTVYTDLEE		993
Db	845	-----EGFLGIAIVNFEIRSGE-----	TVHSIKLOGRPYRK-DATSGEITVYQDFEY		892
Qy	994	QUNQTEBDNAELNNQNFYLS	KOLDEASGANDIEVOLRESVNHLREITEREMQLTQOKOT		105
Db	893	DPNLLTS-----	GKLTDTYVKTNPNGSFPFETLITTHRRPITDPHDPNGHEPI		940
Qy	1054	MEALKTTCTMLEBOVMDEALN	DELLEKXEROMEAMRSVLDGEKQSFECRVEBELQMDTE		1113
Db	941	VPSKTTVT-----VKTVSQTLKEK--	PTIOSVHG-----SLENAVADPA		977
Qy	1114	KQSRARADQRTESROVELAV	KHEKAEITLALQALKEQYKAKESLSKDANLDEKGMIL		1177
Db	978	TQ-----KILDRQFKXHN-----	DKRTLELAK---L		1001
Qy	1174	EMNARSLOOKLETERELK-----	ORLBEQO--KLQOQMDLOKNIHFLTQOLQALDRA		1226
Db	1002	QSVASQMSASSTLDRPSKNGN	NGQYUHQTAAPREHNELDVROGR-----DKS		1044
Qy	1227	DLKTERSDELEYOLENIOVL	SYHEKVMKEGTISQOTKLIDFLQAKMDPRAKKKYVPLQYN		1286

Db 1050 KKAFTKRRDSF-----FGELKDRLSGRGRSÖK-----RSKSDVYENN 1088
Qy 1287 ELKALKEKARCALEBAL-----ÖKTRIELSGAREEAAKRTDHPHSTPATAR 1338
Db 1089 QL-----LEBAVSLPPSRDPSTRYAVASSNDKYRETHSVGSGESTKSLYQ 1335
Qy 1339 QQLMSAIVSPHEQPSMSLAPPSRRKSSPTPEPSRLK--ERMHNHPIPRFVGL 1396
Db 1136 H---STLIELDDDKQAKFLIPPAALNEPA-----SLMRKCKLHYNDHTF-VAV 1185
Qy 1397 NMR-ATCAVCLDTVH--FGROASKLECYWCHPKCSTCLPATCGPABEYATHF-TEAF 1452
Db 1186 KVKGGATCNCVQQRIRSSFSKQAVQCRCKVCHKTC-----HYKIDAF 1229
Qy 1453 C 1453
Db 1230 C 1230

RESULT 13
T16507
hypothetical protein F59A6.5 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16507
R/Nhan, M.
submitted to the EMBL Data Library, December 1995
A/Description: The sequence of C. elegans cosmid F59A6.
A/Reference number: Z18526
A/Accession: T16507
A/Status: preliminary; translated from GH/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1286 <NHA>
A/Cross-references: UNIPROT:Q21025; EMBL:U41994; NID:G1123047; PID:G1123050; PIDN:AAA834
A/Genes: CESP:F59A6.5
A/Intons: 35/3; 335/3; 685/3; 973/3; 1097/3

Query Match 7.28; Score 751; DB 2; Length 1286;
Best Local Similarity 21.64; Pred. No. 1.9e-13;
Matches 299; Conservative 289; Mismatches 583; Indels 214; Gaps 50;
Qy 640 ELDEKLEKAVKATREATELLONTROAKERARELEKQONREDSSEGIKKLVLEERRHS 699
Db 42 ESHEDLKRRV--LDAENITQDLKSRDALH--ETLVDAKAGLESV--TIEQSKAVST 92
Qy 700 LENKVKLETMERERENLKDDIQTKSQOIQOMADKILEEKREAOVSAQHLEVHLKQK 759
Db 93 QETRIYR-----RDVNLLEDLKHQSQIRILQKCKSTLEMEKQTLQETIQRAQDDCKET 147
Qy 760 EOHVE--EKIKVLDNO-----IKQDLADK-ETLENNMQRHEEAHEKGIISQ 805
Db 148 ETELESSRSRLHVLKELSAKANDIFMVTQDLHDKNELTSPMEYVTKLSEANR--EK 204
Qy 806 KAMINANDSKIRSLKQIVLSEANKLAANSLEPTQNMKAQEMISELQOQFYLE--T 863
Db 205 KA-----LEEKLEKTKNDMKENDRKSLELNQVTTQVLSLEVQLSAHFEFLT 253
Qy 864 QAGKLEAQNRLKEE--OLE-KISHQSD--KNRLP--ELETRLRVSVSEHEOKLEK 915
Db 254 PVRKNMSKIRELDYHQLSAKVIESMNDLKIKNETITKELSDGTBLVKNKNE--LEDL 311
Qy 916 ROLTELOLS-----LOERESQITALQA-----APAALESQLRQAKTELETTAA 959
Db 312 RQTTTASISGSEQATKYLHEENMKLTROKADIRCEILFAARKVEG-FDKLKOELKERD 370
Qy 960 AAEELQALTAHRDEIQKFDALRNSCTVITDLBEQNLQEDNALNNQNFYLSKQIDEA 1019
Db 371 ALADVQKIRVKNVEREQLSL--TSLMAERDQLE-----ELKTKMFSPFMIKKDH 420
Qy 1020 SGANDEIVQLRSEVDHIREITEREMQTSOKQMEALKTT-----CTMLEEQVWDL 1072
Db 421 ESKAKNELSRQEKLDQMKHILMADQOCSTFKSLKESABSGRRARALQCNEMVVRIDLQ 480

Qy 1073 ALNDELLEKERQWEANRSVLGDEKSGFEQRYRELQMLDTEKQSPARADQRTESQVVE 1132
Db 481 T-----SLESQR-----KVEQEVMLKAENSRQAKKLEFMEEBEOEVH 518
Qy 1133 LAVENKAEILALQALKEQ-----KLKAESIDKLNDLEKKHAMLENNARSLOQKLET 1186
Db 519 L---DYRQELSRLAETKTKGDEDADHRLTLISQSDSELRSKAKTIQEVKADNQVQMLVE 575
Qy 1187 ERELKORLLEEQAKLOQOQNDLOKNHIFRLTQGLQALDRADDLKTERSDLEYOLENIQVL 1246
Db 576 VRQHQEKILEENVRILRKGMADALAKILEYKRSVQNSQETCEERLESATKEDLDKLE-- 633
Qy 1247 YSHETKMEGTISQOQTKLIDFLQAKMDQPKKKVVLQYNELKLALEKKEKARCALEBAL 1306
Db 634 --BEQEKQOQIAESKELVYLHSQID--AKQTKP-----KGRNSTLSTVSE-- 679
Qy 1307 ÖKTRIELSGAREEA--HRKATDHPHSTPATARQOILMSAIVRSPHEQPSMSLAP 1363
Db 680 MDTSVYMRERAEVRALBQROL---MNLAEKRQ-----LVDSKKSQTANTTITVT 730
Qy 1364 SSR--KESTPEPSRRLKERMHNHPIPRFNV--GLNRAITCAVCLDTVHFGROASKC 1419
Db 731 TTTEISKSQSASLSLSNR-ÖGTWRHDI PKMKAFRHVGVLSMKCSLCFVGISAFAKAKC 789
Qy 1420 LECQWCHPKCSTCLPATCGPABEYATHTFEACRCKNNSPGLQTEPSSSLHLEGMMKV 1479
Db 790 SHCDVHVHASCARVNVNCGMPLOQAVYREN--HTTVSSSGV-----SEGMMNMLRV 841
Qy 1480 PRNNKRGQOQMDKYVILESGKVLIDYNEAREAGRPVEFEFLCPDGVSIIHAGVASE 1539
Db 842 YRDMTGST-NTASWAMMDLIRISFTYNDGADL-EKPFPSIDL-NMQVNLRTQGMPPD 898
Qy 1540 LANTAKADVPIYLKMSHPHTTCWPGRTLYLLASFPDKQVWVTALESVAVAGVRERKA 1599
Db 899 CDSWKNANNVLMTKM-----PRRCLYIILASQPSARRMAECLQTAQRKMMNLSKE 949
Qy 1600 EADAKLGNLSILKLEBDDLDNMCTLPSPDOVVLVTBEGVLYANLTK-NSLTHVGIGA 1658
Db 950 SSIAEF--TCLLVLNSPNNIKLIFKAYTIDW-ILFATQGLFPTSISQPNPRLIAPNS 1006
Qy 1659 VFQIYTIKDEKLMJAGEBALCLVDVKKVQKSLQSHLPAPDIPSPNIFEAVKCHLP 1718
Db 1007 VTSLEIMAEIKCYAMVANSQQLAMTPL-----DSLILMAQSTQPSIRPEILPEFEHVHM 1062
Qy 1719 GAGKIBNGLCICAMPKSVVILRYNENLSKYCIETSEPCSTHFTNYSILIGTNKE 1778
Db 1063 KYHQQNGQRFLLISDQTHLHVRYNATRDIFSQYAKFDVPEPISFIESAPSGIIFACDTE 1122
Qy 1779 YEIDMKQYTLBEFLDKNDLSLAPAVPAASSNRPVSIQVNSAGQBEVLLCTHNGVTV 1838
Db 1123 YVVALDHQT-----SSNVSAKLMSPKNRPFPSIAQMIN--QNEVLLAVQNGITV 1171
Qy 1839 DSYGRSRRTDQKSLPLAFAYREPLYFVTFHNSLEVEIQARSSAGTPA-RAYLDIPN 1897
Db 1172 NLHGQSRKNTIEMEMKPEFIYTSFPLYIYHDDSEIIEIESTSRITYLAERALPECVN 1231
Qy 1898 PRYLGAISSGALYLAASYQDKLRYICCKGNLVKESGTEHNR-----GPTSRSSPNKKG 1952
Db 1232 AHVIGRYGVALISVSN-----DSTEVHRSTATQKQKNVSKRRG 1274
Qy 1953 PPTYN 1957
Db 1275 ASPTN 1279

RESULT 14
T26101
hypothetical protein W02B8.2 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T26101
R/Slime, M.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 16:44:55 ; Search time 204 Seconds
(without alignments)
3363.442 Million cell updates/sec

Title: US-10-791-666-2
Perfect score: 10493
Sequence: 1 MLKFKYGARNPLDGAAPL.....AGAVRPLSQVKNKWDQSSV 2054

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10493	100.0	2054	US-10-028-946-2	Sequence 2, App11
2	10486	99.9	2054	US-10-415-011-21	Sequence 21, App1
3	10464.5	99.7	2055	US-10-618-941-67	Sequence 67, App1
4	10458.5	99.7	2053	US-09-964-956-11	Sequence 11, App1
5	10458.5	99.7	2053	US-10-262-511-2	Sequence 11, App1
6	10435.5	99.4	2066	US-09-964-956-9	Sequence 9, App11
7	10425.5	99.4	2066	US-10-262-511-14	Sequence 14, App1
8	10109.5	96.3	2055	US-10-017-216-4	Sequence 4, App11
9	10022.5	95.5	2053	US-10-017-216-2	Sequence 2, App1
10	10022.5	95.5	2053	US-10-325-430-12	Sequence 12, App1
11	10022.5	95.5	2053	US-10-757-262-52	Sequence 52, App1
12	9916	94.5	1958	US-10-028-946-4	Sequence 4, App11
13	8161	77.8	1641	US-09-964-956-40	Sequence 40, App1

14	8161	77.8	1641	13	US-10-017-216-5	Sequence 5, App1
15	7935	75.6	1597	11	US-09-964-956-41	Sequence 41, App1
16	7935	75.6	1597	13	US-10-017-216-6	Sequence 6, App1
17	7189	68.5	1441	15	US-10-412-897-3	Sequence 3, App1
18	6575	62.7	1286	11	US-09-964-956-38	Sequence 38, App1
19	6575	62.7	1286	13	US-10-017-216-7	Sequence 7, App1
20	5045	48.1	999	15	US-10-276-774-1487	Sequence 1487, App
21	4871	46.4	940	11	US-09-964-956-39	Sequence 39, App1
22	4601	43.8	883	11	US-09-964-956-37	Sequence 37, App1
23	4115	39.2	832	15	US-10-262-511-6	Sequence 6, App1
24	4097.5	39.0	847	15	US-10-262-511-8	Sequence 8, App1
25	3244	30.9	623	15	US-10-262-511-10	Sequence 10, App1
26	3226.5	30.7	638	15	US-10-262-511-12	Sequence 12, App1
27	3165	30.2	623	15	US-10-262-511-4	Sequence 4, App1
28	2440	23.3	497	14	US-09-804-471A-2	Sequence 2, App1
29	2440	23.3	497	14	US-10-238-709-2	Sequence 2, App1
30	2440	23.3	497	15	US-10-724-594-2	Sequence 2, App1
31	2435	23.2	497	15	US-10-311-034-7	Sequence 7, App1
32	2175.5	20.7	494	9	US-09-804-471A-4	Sequence 4, App1
33	2175.5	20.7	494	14	US-10-238-709-4	Sequence 4, App1
34	2175.5	20.7	494	15	US-10-724-594-4	Sequence 4, App1
35	1792	17.1	373	15	US-10-120-835-42	Sequence 42, App1
36	1655	15.8	319	15	US-10-412-897-2	Sequence 2, App1
37	1509.5	14.4	1770	15	US-10-433-794-19	Sequence 19, App1
38	1489	14.2	1719	15	US-10-288-798-2	Sequence 2, App1
39	1489	14.2	1719	15	US-10-362-892-2	Sequence 2, App1
40	1487.5	14.2	1732	17	US-10-679-366-2	Sequence 2, App1
41	1467.5	14.0	1738	15	US-10-210-130-100	Sequence 100, App
42	1465	14.0	1664	15	US-10-210-130-102	Sequence 102, App
43	1439	13.7	1711	17	US-10-781-581-206	Sequence 206, App
44	1438	13.7	1711	9	US-09-771-161A-219	Sequence 219, App
45	1438	13.7	1711	9	US-09-771-161A-220	Sequence 220, App

ALIGNMENTS

RESULT 1
US-10-028-946-2
; Sequence 2, Application US/10028946
; Publication No. US20020123622A1
GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Maricar
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-2

Query Match 100.0%; Score 10493; DB 13; Length 2054;
Best local similarity 100.0%; Pred. No. 0;
Matches 2054; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MLKFKYGARNPLDGAAPL...ASRSRLNLFQCGPPTMOQMSPLRREGILDLFVLF 60
QY ECGSOPALMKIKHVSNFYRKYSDTIAEQELQPSAKDFEVSIVGCGHFAEVQVVRERATG 120
DB ECGSOPALMKIKHVSNFYRKYSDTIAEQELQPSAKDFEVSIVGCGHFAEVQVVRERATG 120
QY 121 DTYAMKMKKALLAQGVSFEEERNITSRSPWIPOLQYAFQDNHLYLVMEYPPG 180
DB 121 DTYAMKMKKALLAQGVSFEEERNITSRSPWIPOLQYAFQDNHLYLVMEYPPG 180

Db 121 DIYAKVMKKALLAQEVSFEEBERNILSRSTSPWIPQLOVAFODKNHLYLVMEYOPGC 180
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 Db 181 DLASLNRVEDQDENLQFYLAELILAVSHVLMGVYHRDIKPBENILVDRTHGHIKLVDF 240
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 Db 241 GSAAKNSNKNVNAKLPIGTPDYMAPEVLYVMNGDGKTYGLDCDWMVGVYIAYEMTYGR 300
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 Db 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNFDEPKNSWVSSPCQSPSGFSEBELPFGFS 420
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 Db 421 YSKALGILGRSESVSGIDSPAKTSMEKULLIKSKELQDSQDYCKHMEQMTLHRRVS 480
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 Db 541 DIRQSRKLOEIKQEOYQAOVEENLMNQLBEDLVASARRSDIYSESLRESRJLAABEFK 600
 Qy 601 RKATECOHKLKAKDOQKPEVGEYAKLEKINAEOQLKIQELQEKLEKAVKASTATELILQ 660
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 Qy 781 KETLENNMQRHEEAHEKGIKLSQKAMINAMDSKINSLEORIVELSEANTLAANSILFT 840
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 Db 1021 GANDEIYQLRSEVHLRREITEREMQLTQKQWEMALKTTCTMBEQWMDLEANDLELLE 1080
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 Db 1801 PAVFAASNSFPVSIYVQVNSAGOREEYLLCFHEBGVFDVDSYGRSRRTDILKMSRLPLAFA 1860
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 Db 1861 YREBYLFVTHFNLSLEVEIQARSSAGTPARAYLIDIPRVLGPALISSGAYLASSYODKL 1920
 Qy 1921 RVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPTYNEHITTKVASSPAPBEGSHPREP 1980
 Db 1921 RVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPPTYNEHITTKVASSPAPBEGSHPREP 1980
 Qy 1981 STPHRYREGRTELRRDKSPERPLEREKSPGRILISTRERSPARLFEDESSRGRLPAGAVRT 2040
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 Qy 2041 PLSQVNVKVMDOSSV 2054
 Db 2041 PLSQVNVKVMDOSSV 2054

RESULT 2

US-10-415-011-21
 ; Sequence 21, Application US/10415011
 ; Publication No. US20040053394A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE CORPORATION
 ; APPLICANT: GURURAJAN, Rajagopal
 ; APPLICANT: BAUGHEY, Mariah R.
 ; APPLICANT: CHAWLA, Nandinder K.
 ; APPLICANT: ELLIOTT, Vicki S.
 ; APPLICANT: XU, Yuming
 ; APPLICANT: ARVIZU, Chandra S.
 ; APPLICANT: YAO, Montique G.
 ; APPLICANT: RANKOWAR, Jayalaxmi
 ; APPLICANT: DING, Li

APPLICANT: TANG, Y. Tom
APPLICANT: HAFALIA, April J.A.
APPLICANT: NGUYEN, Daniel B.
APPLICANT: GANDHI, Ameena R.
APPLICANT: LU, Yan
APPLICANT: YUE, Henry
APPLICANT: BURFORD, Neil
APPLICANT: BANDMAN, Olga
APPLICANT: TRIBOULEY, Catherine M.
APPLICANT: LAL, Preeti G.
APPLICANT: RECIPON, Shirley A.
APPLICANT: LU, Dyung Aina M.
APPLICANT: BOROMSKY, Mark L.
APPLICANT: THORNTON, Michael B.
APPLICANT: SWANNAKER, Anita
APPLICANT: THANGAVELU, Kavitha
APPLICANT: KHAN, Farrah A.
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PT-0262 USN
CURRENT APPLICATION NUMBER: US/10/415,011
CURRENT FILING DATE: 2003-04-18
PRIOR APPLICATION NUMBER: PCT/US01/47728
PRIOR FILING DATE: 2001-10-20
PRIOR APPLICATION NUMBER: US 60/242,410
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/244,068
PRIOR FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: US 60/245,708
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/247,672
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/249,565
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,730
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/250,807
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PERL Program
SEQ ID NO 21
LENGTH: 2054
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040053394A1 7484498CD1
US-10-415-011-21

Query Match 99.9%; Score 10486; DB 15; Length 2054;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2052; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKFKYARNPDLGAGAPLPSASRLNLPFGKRPMTQOQMSPLSREGILDALFLYLF 60
DB 1 MLKFKYGARNPDLGAGAPLPSASRLNLPFGKRPMTQOQMSPLSREGILDALFLYLF 60
QY 61 ECQOPALMKTKHVSNFVKRKTSDTIAELOEPSAKDEVSRLVCGHFAEYQVREKATG 120
DB 61 ECQOPALMKTKHVSNFVKRKTSDTIAELOEPSAKDEVSRLVCGHFAEYQVREKATG 120
QY 121 DIYAMKMKKALLAQOVSPFEERNILSRSTSPMIPOLQYAFQDKNHLVLYWEYQPG 180
DB 121 DIYAMKMKKALLAQOVSPFEERNILSRSTSPMIPOLQYAFQDKNHLVLYWEYQPG 180
QY 181 DLSLNRREYDQDENTLQYTLAEILIAVHSHVLMGVYHVDIKENILVDRGTGHIKLVDF 240
DB 181 DLSLNRREYDQDENTLQYTLAEILIAVHSHVLMGVYHVDIKENILVDRGTGHIKLVDF 240
QY 241 GSAAKMNSNMVNAKLPITPDVYAVRVLTYMNGDGKGTGJDDCMKSVGVIAEMTYGR 300
DB 241 GSAAKMNSNMVNAKLPITPDVYAVRVLTYMNGDGKGTGJDDCMKSVGVIAEMTYGR 300

QY 301 SPFAEGTSARTNNINMFORFLKFPDDPKYSSDLDIQSLCCQKRLKEGICCHPFF 360
DB 301 SPFAEGTSARTNNINMFORFLKFPDDPKYSSDLDIQSLCCQKRLKEGICCHPFF 360
QY 361 SKIDMNNIRNSPPFVFTLKSDDDTSNPDEEKXSWSSSPCOLSPSGSGEELPVVGS 420
DB 361 SKIDMNNIRNSPPFVFTLKSDDDTSNPDEEKXSWSSSPCOLSPSGSGEELPVVGS 420
QY 421 YSKALGILGRSESVSGIDSPAKTSMEKLLIKSKELQSDQCHKMGQEMTLHRVVS 480
DB 421 YSKALGILGRSESVSGIDSPAKTSMEKLLIKSKELQSDQCHKMGQEMTLHRVVS 480
QY 481 EYEAVLSQKVELKASTQNSLAEODLATTYTCSSIKRSIQARMEVSQEDYALQILH 540
DB 481 EYEAVLSQKVELKASTQNSLAEODLATTYTCSSIKRSIQARMEVSQEDYALQILH 540
QY 541 DIREQSRKLOEIKQOEYQAOVEEMRLMMNOLEEDLVARRSDLYESLRSRLAAEFK 600
DB 541 DIREQSRKLOEIKQOEYQAOVEEMRLMMNOLEEDLVARRSDLYESLRSRLAAEFK 600
QY 601 RKATECOHKLKAKDQCKPEVEYAKLEKINAEOQLIOELOEKLKRAVKASTATEBLIQ 660
DB 601 RKATECOHKLKAKDQCKPEVEYAKLEKINAEOQLIOELOEKLKRAVKASTATEBLIQ 660
QY 661 NIROAKERARELEKLNREDSSEGIKKLVAEERHSLBNKYKRLTERRERNRLKDD 720
DB 661 NIROAKERARELEKLNREDSSEGIKKLVAEERHSLBNKYKRLTERRERNRLKDD 720
QY 721 IQTSSQOIQOMAKKILEEKHREAOVSAHLEVHLKQKHQHEKIKVLDNQKKLAD 780
DB 721 IQTSSQOIQOMAKKILEEKHREAOVSAHLEVHLKQKHQHEKIKVLDNQKKLAD 780
QY 781 KETLENNMQHBEERAEHKKILSEQKAMINAMSKIRLSQRIYELSEANKLAANSLSFT 840
DB 781 KETLENNMQHBEERAEHKKILSEQKAMINAMSKIRLSQRIYELSEANKLAANSLSFT 840
QY 841 QRNMKAQEEMLSELROQKFLYLETQAGKLEAQRNRLKEQLEKISHQSDXNRLLLETRL 900
DB 841 QRNMKAQEEMLSELROQKFLYLETQAGKLEAQRNRLKEQLEKISHQSDXNRLLLETRL 900
QY 901 REVSLHEBEOKLELKQULTLOLSLOERESQTLQAARALBSQLQAQTELEETTAEA 960
DB 901 REVSLHEBEOKLELKQULTLOLSLOERESQTLQAARALBSQLQAQTELEETTAEA 960
QY 961 EEEIOALTARDEIORFDMALRNSCTYITDLEBOLNLTEDNAELNNQNFYLSQOLDEAS 1020
DB 961 EEEIOALTARDEIORFDMALRNSCTYITDLEBOLNLTEDNAELNNQNFYLSQOLDEAS 1020
QY 1021 GANDEIVQLRSEVDHLRREITEREMQLTSGQOTMEALKTTCTMLEQVMDLEALNDELLE 1080
DB 1021 GANDEIVQLRSEVDHLRREITEREMQLTSGQOTMEALKTTCTMLEQVMDLEALNDELLE 1080
QY 1081 KERQWEAMRSLVLDKESQFECRVRLEORMLDTEKQSAARADORTTESROYVELAVKHKA 1140
DB 1081 KERQWEAMRSLVLDKESQFECRVRLEORMLDTEKQSAARADORTTESROYVELAVKHKA 1140
QY 1141 EIALLOALKEQKQKAEESLSDKLNLEKKHAMEMNAARSLOQLTETREKORLLSEQAK 1200
DB 1141 EIALLOALKEQKQKAEESLSDKLNLEKKHAMEMNAARSLOQLTETREKORLLSEQAK 1200
QY 1201 LQOQMDLQKNHIFRLTQLOEALDRADLKTERSDLEYQLENTQVLSHEKVMEGTITSQ 1260
DB 1201 LQOQMDLQKNHIFRLTQLOEALDRADLKTERSDLEYQLENTQVLSHEKVMEGTITSQ 1260
QY 1261 QTKLIDFLQAKMDQPAKKKVPLOYNELKALKEKARCALEBALQKTRIEBLSAREEA 1320
DB 1261 QTKLIDFLQAKMDQPAKKKVPLOYNELKALKEKARCALEBALQKTRIEBLSAREEA 1320
QY 1321 AHRKATDHPHSTPATARQOIIASATVRSPEHQPSAMSLAPSSRKESSTPEEFSRRL 1380
DB 1321 AHRKATDHPHSTPATARQOIIASATVRSPEHQPSAMSLAPSSRKESSTPEEFSRRL 1380
QY 1381 KERMEHNIPIHFVGLNMRATKCAVCLDVHFGQASKLEECQVMGHPKCSGCLPATGCL 1440

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Db 1381 KERNHNI PHRFNVLNMRATKCAVCLDTVHFGOASKCLECYWCHPKCSTCLPATCGL 1440
Qy 1441 PAEVAHTEFAFCGDKNNSPGLQKPESSSLHSGMMKVPNNNRKGGQGMKRTIYVEGS 1500
Db 1441 PAEVAHTEFAFCGDKNNSPGLQKPESSSLHSGMMKVPNNNRKGGQGMKRTIYVEGS 1500
Qy 1501 KVLIVDEAREAGORPVBEFELCPDGDVSIHGAVGASELANTAKADVPIYLKMHESHPT 1560
Db 1501 KVLIVDEAREAGORPVBEFELCPDGDVSIHGAVGASELANTAKADVPIYLKMHESHPT 1560
Qy 1561 TCWGRGLTYLLABFPDKORWVTLYESVYAGGRVSRKAEADAKLGNLSLKLEGGDRLD 1620
Db 1561 TCWGRGLTYLLABFPDKORWVTLYESVYAGGRVSRKAEADAKLGNLSLKLEGGDRLD 1620
Qy 1621 MNCTLPSPDOVLVGTBEGYALNVLNKSLLTHVIGIGAVFOIYIIXOLEKMLMAGEBRA 1680
Db 1621 MNCTLPSPDOVLVGTBEGYALNVLNKSLLTHVIGIGAVFOIYIIXOLEKMLMAGEBRA 1680
Qy 1681 LCLVDVKKVQSLAQSHLPAOPDISPNI FEAVKGCJHFGAGKIBNGLCICAMPSTKVIL 1740
Db 1681 LCLVDVKKVQSLAQSHLPAOPDISPNI FEAVKGCJHFGAGKIBNGLCICAMPSTKVIL 1740
Qy 1741 RYNNENLSKYCIKKEIETSEPCSIHFTNYSILLIGTNKFEYIDMKQYTLIEEFLDKNDHSLA 1800
Db 1741 RYNNENLSKYCIKKEIETSEPCSIHFTNYSILLIGTNKFEYIDMKQYTLIEEFLDKNDHSLA 1800
Qy 1801 PAVPAASNSPVSIVOVNSAGOREEYLLCFHEGVFVDSYGRSRTDCLKMSRLPLAFA 1860
Db 1801 PAVPAASNSPVSIVOVNSAGOREEYLLCFHEGVFVDSYGRSRTDCLKMSRLPLAFA 1860
Qy 1861 YREBYLTVTHNSLEVIEIQARSSAGTPARAYLDIPNRYLGPAISSGATYLAASYODKL 1920
Db 1861 YREBYLTVTHNSLEVIEIQARSSAGTPARAYLDIPNRYLGPAISSGATYLAASYODKL 1920
Qy 1921 RVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPTYNHITKRVASSPAPPEGSHPREP 1980
Db 1921 RVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPTYNHITKRVASSPAPPEGSHPREP 1980
Qy 1981 STPRHYREGTELRDQSPGRPLEREKSPGRILSTRERSPARLPEDSSRGRLPAGAVRT 2040
Db 1981 STPRHYREGTELRDQSPGRPLEREKSPGRILSTRERSPARLPEDSSRGRLPAGAVRT 2040
Qy 2041 PLSQVNVKWDQSSV 2054
Db 2041 PLSQVNVKWDQSSV 2054

RESULT 3
US-10-618-941-67
; Sequence 67, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618, 941
; PRIORITY FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/3395, 632
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 67
; LENGTH: 2055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-618-941-67

Query Match 99.7%; Score 10464.5; DB 16; Length 2055;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2050; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
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Qy 1 MLKFKYGARNPLDAGAAEPFIASASRLNLFQGGKPPMTQOQMSPLSREGILDALFVLF 60
Db 1 MLKFKYGARNPLDAGAAEPFIASASRLNLFQGGKPPMTQOQMSPLSREGILDALFVLF 60
Qy 61 ECGQPALMKIKHYSNFPVRK YSDTIABELOLOQASADFEVRSLVGGCHFAEVOVVERKAT 119
Db 61 ECGQPALMKIKHYSNFPVRK YSDTIABELOLOQASADFEVRSLVGGCHFAEVOVVERKAT 120
Qy 120 GDYIYAMVMKKALLAOEQVSPFEERBNILSRSTSPWIPOLQYAFODKMLYLMEXOPG 179
Db 121 GDYIYAMVMKKALLAOEQVSPFEERBNILSRSTSPWIPOLQYAFODKMLYLMEXOPG 180
Qy 180 GDLLSLNRYEDQJDEMLIOFYLAELILAVHSVHMGYVARDIKPENILVDRGHIKLV 239
Db 181 GDLLSLNRYEDQJDEMLIOFYLAELILAVHSVHMGYVARDIKPENILVDRGHIKLV 240
Qy 240 FGSAAKNNSKMNNAKLPIGTPTYMAPEVLTWNNGGKGTYGLDCMWSVGLAYEMTYG 299
Db 241 FGSAAKNNSKMNNAKLPIGTPTYMAPEVLTWNNGGKGTYGLDCMWSVGLAYEMTYG 300
Qy 300 RSPFAEGTSARTFNINNFORFLKFPDDPKVSDFLDLIOSLLCGOKERLKFEGLCCHPF 359
Db 301 RSPFAEGTSARTFNINNFORFLKFPDDPKVSDFLDLIOSLLCGOKERLKFEGLCCHPF 360
Qy 360 FSKIDMNNINRSPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGEELPFVGF 419
Db 361 FSKIDMNNINRSPFPVPTLKSDDDTSNFDEPKNSWSSPCQLSPGSGEELPFVGF 420
Qy 420 SYKALGILGRSSSVYGLDSPAKTSMKKLILSKELODSODCKHMEQETRLHRRV 479
Db 421 SYKALGILGRSSSVYGLDSPAKTSMKKLILSKELODSODCKHMEQETRLHRRV 480
Qy 480 SEVEAVLSQKEVELKASETORSLLEODLATYITECSSLKRSLEQARMEVSOEDKALQIL 539
Db 481 SEVEAVLSQKEVELKASETORSLLEODLATYITECSSLKRSLEQARMEVSOEDKALQIL 540
Qy 540 HDIREOSRKLQETKEOEYQAOVEEMRLMNOULEEDLVASARRSDLYESELRESRLAAEF 599
Db 541 HDIREOSRKLQETKEOEYQAOVEEMRLMNOULEEDLVASARRSDLYESELRESRLAAEF 600
Qy 600 KRYATBCQKLLAKAQOGKEVGEYAKLEKINAEQOLKTOELODKLEKAVKATETELL 659
Db 601 KRYATBCQKLLAKAQOGKEVGEYAKLEKINAEQOLKTOELODKLEKAVKATETELL 660
Qy 660 QNIRQAKERARELEKLONRDESSSEGRKKLVABEERHSLKVKVRLIETMERERENLKD 719
Db 661 QNIRQAKERARELEKLONRDESSSEGRKKLVABEERHSLKVKVRLIETMERERENLKD 720
Qy 720 DIOTKSQOLQOMADKILLEEKHREAOVSAQHLVHLKQEHYEEKIKVLDNQIKKDLA 779
Db 721 DIOTKSQOLQOMADKILLEEKHREAOVSAQHLVHLKQEHYEEKIKVLDNQIKKDLA 780
Qy 780 DKETLENMQRHEBEAHEKGIISBOYAMINANDSKIRLSIQRIYVLSSEANKLAANSSLF 839
Db 781 DKETLENMQRHEBEAHEKGIISBOYAMINANDSKIRLSIQRIYVLSSEANKLAANSSLF 840
Qy 840 TORNMKRAQEMISELQOKFYLETQAGKLEAQRKLEBOLEKISHODSHDKNRLLEETR 899
Db 841 TORNMKRAQEMISELQOKFYLETQAGKLEAQRKLEBOLEKISHODSHDKNRLLEETR 900
Qy 900 LREVSLEHEQKLEKRLQELTOLSTOERESQUTALQAAAPALAESOLQOKATELEETJAE 959
Db 901 LREVSLEHEQKLEKRLQELTOLSTOERESQUTALQAAAPALAESOLQOKATELEETJAE 960
Qy 960 ABEEIQALTARDEIORKFDALNSCTVITDLBEOLNOLTEDNAELNNONFYSKOLDEA 1019
Db 961 ABEEIQALTARDEIORKFDALNSCTVITDLBEOLNOLTEDNAELNNONFYSKOLDEA 1020
Qy 1020 SGANDEIVOLARSVDHRRITERRMOQTSQOKTMAKTKTCTMLEBOVMDLEALNDEL 1079
Db 1021 SGANDEIVOLARSVDHRRITERRMOQTSQOKTMAKTKTCTMLEBOVMDLEALNDEL 1080
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1080 EKEROMEARSVLGDKEKQFECRVELEORMLDTEKQSRARADORTTESROVVELAVKREHK 1139
1081 EKEROMEARSVLGDKEKQFECRVELEORMLDTEKQSRARADORTTESROVVELAVKREHK 1140
1140 AEIILAOALKEOKLKAESLSDKLNDEKKAEMNARSLOQKLETEREIKORLLEBOA 1199
1141 AEIILAOALKEOKLKAESLSDKLNDEKKAEMNARSLOQKLETEREIKORLLEBOA 1200
1200 KLOOQMDLOKXNHIIFLTQGLQBALDRADLLKTERSDLEYOLENIQVLYSHEKVMKEGTIS 1259
1201 KLOOQMDLOKXNHIIFLTQGLQBALDRADLLKTERSDLEYOLENIQVLYSHEKVMKEGTIS 1260
1260 OOTKLIFLOAKMOPAKKKVPIQYNELKALEKAKRCALEBALKOTRIELRSABEE 1319
1261 OOTKLIFLOAKMOPAKKKVPIQYNELKALEKAKRCALEBALKOTRIELRSABEE 1320
1320 AAHRKATDHPSTPATRQOJAMSATVSRPEHOPSAMSLAPSSRRKESSTPEEFERR 1379
1321 AAHRKATDHPSTPATRQOJAMSATVSRPEHOPSAMSLAPSSRRKESSTPEEFERR 1380
1380 LKERMHNNIPHRFNVGLMRAATKCAVCLDTVHFGQASKLECOVMCHPKSTCLPATCG 1439
1381 LKERMHNNIPHRFNVGLMRAATKCAVCLDTVHFGQASKLECOVMCHPKSTCLPATCG 1440
1440 LPAEYATHTFAFCGDKKNSPGLQTKEPSSSLHEGMKVPNNKRGQGMKRYIVLEG 1499
1441 LPAEYATHTFAFCGDKKNSPGLQTKEPSSSLHEGMKVPNNKRGQGMKRYIVLEG 1500
1500 SKVLIVDNEARAGORPVEEFELCPDGDVSIHGAVGAELANTAKADVPYILIMKESRPH 1559
1501 SKVLIVDNEARAGORPVEEFELCPDGDVSIHGAVGAELANTAKADVPYILIMKESRPH 1560
1560 TTCWPGRTLYLLAASFPDKORWVTALESVAVGVRREKADAKLIGNSILKLEGGDRL 1619
1561 TTCWPGRTLYLLAASFPDKORWVTALESVAVGVRREKADAKLIGNSILKLEGGDRL 1620
1620 DMCNTLPPSDQVVLVGTREBGIYALANVLKNSLTHVPGICAVPQIYIIXDLEKLMIAEGER 1679
1621 DMCNTLPPSDQVVLVGTREBGIYALANVLKNSLTHVPGICAVPQIYIIXDLEKLMIAEGER 1680
1680 ALCLVDYKVKVQSLAQSGLPAQDPISPNIFEAUVGCHFGAGKLENGLCICAMPKSVYI 1739
1681 ALCLVDYKVKVQSLAQSGLPAQDPISPNIFEAUVGCHFGAGKLENGLCICAMPKSVYI 1740
1740 LRYNENLSKYCIKEIETSEPCSCIHFTNYSILIGTNKFYEDIMKQYTLBEFLDKNDHSL 1799
1741 LRYNENLSKYCIKEIETSEPCSCIHFTNYSILIGTNKFYEDIMKQYTLBEFLDKNDHSL 1800
1800 APAAVFAASSNSFPVSIQVNSAGOREEYLLCFHEFGVFPVDSYGRSRRTDLMKSRPLAF 1859
1801 APAAVFAASSNSFPVSIQVNSAGOREEYLLCFHEFGVFPVDSYGRSRRTDLMKSRPLAF 1860
1860 AYREPYLFVTHFNLELEIETIOARSSAGTPARAAYIDINPRILGPAISSGAIYLLASSYQDK 1919
1861 AYREPYLFVTHFNLELEIETIOARSSAGTPARAAYIDINPRILGPAISSGAIYLLASSYQDK 1920
1920 LRVYICCKGNLVKESGTEHHRPSTSRSSPNKGPPTYNENHTTKVASSPAPPEGSPHRE 1979
1921 LRVYICCKGNLVKESGTEHHRPSTSRSSPNKGPPTYNENHTTKVASSPAPPEGSPHRE 1980
1980 PSTPHRYREGRTELRDKSPGRPLEREKSPGRILSTRERSPARLFEDSSRGRLPAGAVR 2039
1981 PSTPHRYREGRTELRDKSPGRPLEREKSPGRILSTRERSPARLFEDSSRGRLPAGAVR 2040
2040 TPISQVNVKWDQSSV 2054
2041 TPISQVNVKWDQSSV 2055

RESULT 4
US-09-964-956-11
; Sequence 11, Application US/09964956
; Publication No. US20040043926A1

GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
APPLICANT: Gunther, Erik
APPLICANT: Ellerman, Karen
APPLICANT: Grose, William M
APPLICANT: Alsbrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Murailidhara
APPLICANT: Kerkuda, Rameesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A
TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
CURRENT APPLICATION NUMBER: US/09/964,956
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,631
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,633
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,808
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/237,434
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238,321
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,399
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/238,396
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/276,667
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/294,823
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: 60/304,868
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 2053
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-956-11

Query Match 99.7%; Score 10458.5; DB 11; Length 2053;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2049; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

1 MLKFKYGARPLDGAEPASPIASRASRLNLFPOGKPPMTQOQMSPLSREGILDLPLVLE 60
1 MLKFKYARNPDLGAAEPASPIASRASRLNLFPOGKPPMTQOQMSPLSREGILDLPLVLE 60
61 ECGSOPALMKIKHVSNFVRKYSDDTIAELQSLQPSAKDFEVSILVCGHFAEVQVVRKATG 120
61 ECGSOPALMKIKHVSNFVRKYSDDTIAELQSLQPSAKDFEVSILVCGHFAEVQVVRKATG 120
121 DIYAMKMKKKKALLAQOVSPFEERNTLSRSTSPMTPOLOVAFODKXNLVYVNEYPGG 180
121 DIYAMKMKKKKALLAQOVSPFEERNTLSRSTSPMTPOLOVAFODKXNLVYVNEYPGG 180

QY 181 DLSTLNRYEDQJDENTLOFYLAELILAVSHVMGVHDIKENTLINDRTGHIKLVDF 240
 DB 181 DLSTLNRYEDQJDENTLOFYLAELILAVSHVMGVHDIKENTLIVRTGHIKLVDF 240
 QY 241 GSAAKNNSNMKNVNAKLPITGPDYMAPEVLJVMNGDGKTYGLJDDMMNVGVIAEMTYGR 300
 DB 241 GSAAKNNSNMKNVNAKLPITGPDYMAPEVLJVMNGDGKTYGLJDDMMNVGVIAEMTYGR 299
 QY 301 SPFAEGTSARTFNNIMNPFORFLKPEPDDPKVSSDFLDLIQSLCGQKERLKFEGLCCHPFF 360
 DB 300 SPFAEGTSARTFNNIMNPFORFLKPEPDDPKVSSDFLDLIQSLCGQKERLKFEGLCCHPFF 359
 QY 361 SKIDMNNIRNSPPFVFTLKSDDDTSNPDEBEKNSWSSPCQSPSGSGSEELPFVGF 420
 DB 360 SKIDMNNIRNAPFPFVFTLKSDDDTSNPDEBEKNSWSSPCQSPSGSGSEELPFVGF 419
 QY 421 YSKALGILGRSESVSGLDSPAKTSMEKLLIKSKELQDSQDKCHQMEQMTLHRVS 480
 DB 420 YSKALGILGRSESVSGLDSPAKTSMEKLLIKSKELQDSQDKCHQMEQMTLHRVS 479
 QY 481 EWEAVLSQKEVELKASFTQSLBQDLATYITTECSSLKRSLEQARMEVSGEDDQALQLH 540
 DB 480 EWEAVLSQKEVELKASFTQSLBQDLATYITTECSSLKRSLEQARMEVSGEDDQALQLH 539
 QY 541 DIRQSKLOEIKQOEYQAOYEBEMLMNOLEBDLVARRSDLYESBELRESRLAAEFK 600
 DB 540 DIRQSKLOEIKQOEYQAOYEBEMLMNOLEBDLVARRSDLYESBELRESRLAAEFK 599
 QY 601 RKATECHOKLKKAKDOQKPEVGEYAKLEKINAEOQLIOELQELERQAVASTATBLQ 660
 DB 600 RKATECHOKLKKAKDOQKPEVGEYAKLEKINAEOQLIOELQELERQAVASTATBLQ 659
 QY 661 NIFQAKERARELEKLONREDSSGIRKKUVEABERHSHLENNVKLETFMERENRLKDD 720
 DB 660 NIFQAKERARELEKLONREDSSGIRKKUVEABERHSHLENNVKLETFMERENRLKDD 719
 QY 721 IQRSQOIOQMADKILLEEKHREAOVSACHLFTYHLKQKQHYBEKIKVLDNQKKDLAD 780
 DB 720 IQRSQOIOQMADKILLEEKHREAOVSACHLFTYHLKQKQHYBEKIKVLDNQKKDLAD 779
 QY 781 KETLENNMOHREBEAHEKGLISEOKAMINAMDSKISLEORIVELSEANKLANSSFLT 840
 DB 780 KETLENNMOHREBEAHEKGLISEOKAMINAMDSKISLEORIVELSEANKLANSSFLT 839
 QY 841 QRMNKAQEMISSELROQKFLYLETQAGKLEAQNRLKLEBQLEKISHQDSDKNRLLEETRL 900
 DB 840 QRMNKAQEMISSELROQKFLYLETQAGKLEAQNRLKLEBQLEKISHQDSDKNRLLEETRL 899
 QY 901 REVSLEHEBQLEKROLTIELQSLORRESQTLQARAALBESQLFOAKTELETTAA 960
 DB 900 REVSLEHEBQLEKROLTIELQSLORRESQTLQARAALBESQLFOAKTELETTAA 959
 QY 961 EBEIQTALTARDEIQRKFDALRNSCTVITDLEBQLOLTEDNAILNQNFFYLSKQDEAS 1020
 DB 960 EBEIQTALTARDEIQRKFDALRNSCTVITDLEBQLOLTEDNAILNQNFFYLSKQDEAS 1019
 QY 1021 GANDEIVOLRSEVDHLREITEREMOJTSQOKTWEALKTCTMLEBQVMDLEALNDELLE 1080
 DB 1020 GANDEIVOLRSEVDHLREITEREMOJTSQOKTWEALKTCTMLEBQVMDLEALNDELLE 1079
 QY 1081 KERQWEMRVSYLGRBKQOFERVALEORMLDTEKQSAARADORTTERROYVELAVKHKHA 1140
 DB 1080 KERQWEMRVSYLGRBKQOFERVALEORMLDTEKQSAARADORTTERROYVELAVKHKHA 1139
 QY 1141 EILALQOALKEOKUKAESSLSQKNDLLEKQAMLEMMNARSLOQKLETREBELKORLLEBQAK 1200
 DB 1140 EILALQOALKEOKUKAESSLSQKNDLLEKQAMLEMMNARSLOQKLETREBELKORLLEBQAK 1199
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 DB 1200 LQOQMDLQKNHIFRLTGLOALDRADULTKTERSDEYOLENTIOVLSHEKVKNEGTISQ 1259
 QY 1261 QTKLIDFLQAKMDQPAKKKVPLOYNVELKALEKAKRCALEBALQKTRIELRSAREEA 1320

DB 1260 QTKLIDFLQAKMDQPAKKKVPLOYNVELKALEKAKRCALEBALQKTRIELRSAREEA 1319
 QY 1321 ABRKATDHPHSPATAPARQOIJAMSAIVRSEHOPSAAMSLIAPPSSRRKESSTPEBSRRL 1380
 DB 1320 ABRKATDHPHSPATAPARQOIJAMSAIVRSEHOPSAAMSLIAPPSSRRKESSTPEBSRRL 1379
 QY 1381 KERMHNNIPIHRENVGLMRAITKCAVCLDPTHFERQASKLECOVMCHPKSTCLPATCG 1440
 DB 1380 KERMHNNIPIHRENVGLMRAITKCAVCLDPTHFERQASKLECOVMCHPKSTCLPATCG 1439
 QY 1441 PAEYATHTFAFCRDKMNSPGLQTKPESSSIHLEGMMKVPNNKRGQOGMDRKYIVLEGS 1500
 DB 1440 PAEYATHTFAFCRDKMNSPGLQTKPESSSIHLEGMMKVPNNKRGQOGMDRKYIVLEGS 1499
 QY 1501 KVLIIYNEAREAGQRPVEEFELCLPGDVSIHGAVASIELANTAKADVPIYILKMEHPHT 1560
 DB 1500 KVLIIYNEAREAGQRPVEEFELCLPGDVSIHGAVASIELANTAKADVPIYILKMEHPHT 1559
 QY 1561 TCMFGRTLYILASPFDKQWWTALLESVYAGRVSRKKAADAKLIGNSILKLEGGDRLD 1620
 DB 1560 TCMFGRTLYILASPFDKQWWTALLESVYAGRVSRKKAADAKLIGNSILKLEGGDRLD 1619
 QY 1621 MNCSTLPFSDQVNVGTEBGLYALNVLKNSLTHVPGIGAVFOYIIXDLKELMTAGEERA 1680
 DB 1620 MNCSTLPFSDQVNVGTEBGLYALNVLKNSLTHVPGIGAVFOYIIXDLKELMTAGEERA 1679
 QY 1681 LCLVDYKVKQSLAQSHLPAOPDISPNIFEAVKCHLFGAGKILENGCICAMPSSKVIL 1740
 DB 1680 LCLVDYKVKQSLAQSHLPAOPDISPNIFEAVKCHLFGAGKILENGCICAMPSSKVIL 1739
 QY 1741 RYNEENSKYICIRKEITSEBSCSIHFTNYSILIGTKKFEIMDKOYTLBEFLDKNHSILA 1800
 DB 1740 RYNEENSKYICIRKEITSEBSCSIHFTNYSILIGTKKFEIMDKOYTLBEFLDKNHSILA 1799
 QY 1801 PAVFAASNSFPYSIVQVNSAGOREEYLCFHEFGVFNVSYGRSRTDLMKSLPLAFA 1860
 DB 1800 PAVFAASNSFPYSIVQVNSAGOREEYLCFHEFGVFNVSYGRSRTDLMKSLPLAFA 1859
 QY 1861 YREPYLVTHFNSLEVEIEIOARSSAGTPARAYLDINPRYLGPAISSGAIYLAASYODKL 1920
 DB 1860 YREPYLVTHFNSLEVEIEIOARSSAGTPARAYLDINPRYLGPAISSGAIYLAASYODKL 1919
 QY 1921 RYVICKGNLVKESGTEHHGRPSTRSSPNKRGPTTNEHITTKVASSPAPBEPSPHREP 1980
 DB 1920 RYVICKGNLVKESGTEHHGRPSTRSSPNKRGPTTNEHITTKVASSPAPBEPSPHREP 1979
 QY 1981 STPHRYREGRTELRRDKSPGRPLERKSPGRILSTRERSPARLFESSSRGRPLAGAVRT 2040
 DB 1980 STPHRYREGRTELRRDKSPGRPLERKSPGRILSTRERSPARLFESSSRGRPLAGAVRT 2039
 QY 2041 PLSQVNVKVDQSSV 2054
 DB 2040 PLSQVNVKVDQSSV 2053

RESULT 5
 US-10-262-511-2
 ; Sequence 2, Application US/10262511
 ; Publication No. US20040038223A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Smithsonian, Glenda
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Peyman, John A.
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Ju, Jinfang
 ; APPLICANT: Li, Li
 ; APPLICANT: Guo, Xiaojia (Sasha)
 ; APPLICANT: Patuturajan, Meera
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Malysankar, Uriel M.

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? APPLICANT: Ort, Tatiana
? APPLICANT: Gorman, Linda
? APPLICANT: Zerhusen, Bryan D.
? APPLICANT: Anderson, David W.
? APPLICANT: Zhong, Mei
? APPLICANT: Catterton, Elina
? APPLICANT: Uj, Weizhen
? APPLICANT: Miller, Charles E.
? APPLICANT: Raetelli, Luca
? APPLICANT: Stone, David J.
? APPLICANT: Pena, Carol E. A.
? APPLICANT: Shenoy, Suresh G.
? APPLICANT: Shimkets, Richard A.
? APPLICANT: Rothenberg, Mark E.
? APPLICANT: Leach, Martin D.
? APPLICANT: Agee, Michele L.
? APPLICANT: Berghs, Constance
? TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
? FILE REFERENCE: 21402-462C
? CURRENT APPLICATION NUMBER: US/10/262,511
? PRIOR APPLICATION NUMBER: 2003-05-28
? PRIOR APPLICATION NUMBER: 60/326,483
? PRIOR FILING DATE: 2001-10-02
? PRIOR APPLICATION NUMBER: 60/373,815
? PRIOR FILING DATE: 2002-04-19
? PRIOR APPLICATION NUMBER: 60/327,917
? PRIOR FILING DATE: 2001-10-09
? PRIOR APPLICATION NUMBER: 60/381,642
? PRIOR FILING DATE: 2002-05-17
? PRIOR APPLICATION NUMBER: 60/328,029
? PRIOR FILING DATE: 2002-10-09
? PRIOR APPLICATION NUMBER: 60/381,038
? PRIOR FILING DATE: 2002-05-16
? PRIOR APPLICATION NUMBER: 60/328,056
? PRIOR FILING DATE: 2001-10-09
? PRIOR APPLICATION NUMBER: 60/373,260
? PRIOR FILING DATE: 2002-04-17
? PRIOR APPLICATION NUMBER: 60/373,826
? PRIOR FILING DATE: 2002-04-19
? PRIOR APPLICATION NUMBER: 60/327,435
? PRIOR FILING DATE: 2001-10-05
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 439
? SOFTWARE: Cuiaseq1ist version 0.1
? SEQ ID NO 2
? LENGTH: 2053
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-262-511-2

Query Match      99.7%; Score 10458.5; DB 15; Length 2053;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2049; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

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QY 301 SPFAEGTSARTENNINMFORFLKPPDDPKVSSDFLDLIQSLLCGQKERLKEGLCCHEFF 360
DB 300 SPFAEGTSARTENNINMFORFLKPPDDPKVSSDFLDLIQSLLCGQKERLKEGLCCHEFF 359
QY 361 SKIDMNNIRNSPPFPVFTLKSDDDTSNFDEPKNSWSSSPCCQSLPSGFSSEELPVPVGS 420
DB 360 SKIDMNNIRNAPFPFPVFTLKSDDDTSNFDEPKNSWSSSPCCQSLPSGFSSEELPVPVGS 419
QY 421 YSKALGILGRSESVSGIDSPAKTSMEKLLISKELODSQDCHMKOEQMTLHRVVS 480
DB 420 YSKALGILGRSESVSGIDSPAKTSMEKLLISKELODSQDCHMKOEQMTLHRVVS 479
QY 481 EVEAVLSQKEVELKASESTORSLLBQDLATYITTECSSIKRSLEQARMEVSQEDKALQLLH 540
DB 480 EVEAVLSQKEVELKASESTORSLLBQDLATYITTECSSIKRSLEQARMEVSQEDKALQLLH 539
QY 541 DIRQSRKLOEIKQOEYQAOVEEMRLMMNOLEBDLVARRRSDLYESBLRESRLAAEFK 600
DB 540 DIRQSRKLOEIKQOEYQAOVEEMRLMMNOLEBDLVARRRSDLYESBLRESRLAAEFK 599
QY 601 RKATECOHKLKAKDOGKPEVGEYAKLEKINAEOQLKIOELOEKLKAVKASTATELLO 660
DB 600 RKATECOHKLKAKDOGKPEVGEYAKLEKINAEOQLKIOELOEKLKAVKASTATELLO 659
QY 661 NIRQAKERARELEKLONRDSSSEGIKKLVEAEERHSLENKYRLTETMERRENRLKDD 720
DB 660 NIRQAKERARELEKLONRDSSSEGIKKLVEAEERHSLENKYRLTETMERRENRLKDD 719
QY 721 IOTKSQOIQOMADKILLEEKHREAOVSQOHLVHLKQKQOYBEKIKVLDNOIKKDLAD 780
DB 720 IOTKSQOIQOMADKILLEEKHREAOVSQOHLVHLKQKQOYBEKIKVLDNOIKKDLAD 779
QY 781 KETLENNMOHHEEFAHEKGIKILSEOKAMINAMDSKIRLEORIVELSEANKLAANSLSFT 840
DB 780 KETLENNMOHHEEFAHEKGIKILSEOKAMINAMDSKIRLEORIVELSEANKLAANSLSFT 839
QY 841 QRMNKAQOEMISELROQKFLYLETQAGLEAQNRLKEOLEKISHQDSDKXRLLELETRL 900
DB 840 QRMNKAQOEMISELROQKFLYLETQAGLEAQNRLKEOLEKISHQDSDKXRLLELETRL 899
QY 901 REVSLHEBEOKLEIKROLTELQUSLOERESQTLQAAPALBSQLEQAKTELETTAAE 960
DB 900 REVSLHEBEOKLEIKROLTELQUSLOERESQTLQAAPALBSQLEQAKTELETTAAE 959
QY 961 EEEIQAULTARDEIQREKFDALRNSCTVITDLEQNLQTEDNAELNNQNFYLSQOLDEAS 1020
DB 960 EEEIQAULTARDEIQREKFDALRNSCTVITDLEQNLQTEDNAELNNQNFYLSQOLDEAS 1019
QY 1021 GANDEIVQLRSEVDHLREITEREMOJTSQKQTEALKTTCTMLEQVMDLEALNDELE 1080
DB 1020 GANDEIVQLRSEVDHLREITEREMOJTSQKQTEALKTTCTMLEQVMDLEALNDELE 1079
QY 1081 KERQWEAMRSVLGDEKSQFEQCRVREIQRMIDTEKQSPARADORTTESROVVEALVKEHKA 1140
DB 1080 KERQWEAMRSVLGDEKSQFEQCRVREIQRMIDTEKQSPARADORTTESROVVEALVKEHKA 1139
QY 1141 EIIALQALKEOKLKESLSDKLNDEKKGAMLEMMARSLQKLETERELKORLLEEOAK 1200
DB 1140 EIIALQALKEOKLKESLSDKLNDEKKGAMLEMMARSLQKLETERELKORLLEEOAK 1199
QY 1201 LQOQMDLQKNHIFRLTQGLQBALDRADLKTRESLDEYQLENIQVLSHSEKVKMGEGTISQ 1260
DB 1200 LQOQMDLQKNHIFRLTQGLQBALDRADLKTRESLDEYQLENIQVLSHSEKVKMGEGTISQ 1259
QY 1261 QTKLIDFLQAKMDQPAKKKVPLOYNELKLALKEKARCALEBALQKTRIELRSARBEA 1320
DB 1260 QTKLIDFLQAKMDQPAKKKVPLOYNELKLALKEKARCALEBALQKTRIELRSARBEA 1319
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DB 1320 AHRKATDHPHSPATPAKQOIIAMSAIVRSPHQPSAMSLAPSPSRKESSTPEEFRRRL 1379

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QY 1381 KERNHNIPHRNVGLNMRATKCAVCLDTVHFGROASKCEQVMCHPKGSTCLPATCGL 1440
Db 1380 KERNHNIPHRNVGLNMRATKCAVCLDTVHFGROASKCEQVMCHPKGSTCLPATCGL 1439
QY 1441 PAVYATHTPAFCRDKMNSPGLQTKESPSSSLHLEGMMKVRNNKRGQGDMDRKTYLVEGS 1500
Db 1440 PAVYATHTPAFCRDKMNSPGLQTKESPSSSLHLEGMMKVRNNKRGQGDMDRKTYLVEGS 1499
QY 1501 KVLIDNEAREAGQRPVEEFELCLPDGDSVSIHGAVGASBELANTAKADVPIYLKMSHPHT 1560
Db 1500 KVLIDNEAREAGQRPVEEFELCLPDGDSVSIHGAVGASBELANTAKADVPIYLKMSHPHT 1559
QY 1561 TCMRGRLYLLASFPDKQWMTALBSVAVAGRRSRKADAKLGNLSLLKLEGGDRLD 1620
Db 1560 TCMRGRLYLLASFPDKQWMTALBSVAVAGRRSRKADAKLGNLSLLKLEGGDRLD 1619
QY 1621 MNCITLPPSDQVVLVGTREGLYALNVLNKSLLTHVGIAGVQIYIYIKOLEKLIMAGERERA 1680
Db 1620 MNCITLPPSDQVVLVGTREGLYALNVLNKSLLTHVGIAGVQIYIYIKOLEKLIMAGERERA 1679
QY 1681 LCLVDVKVKQSLAQSHLPAQPDISPNIPEAVKGCMLFGAGKLENGLCICAMPKSVYIL 1740
Db 1680 LCLVDVKVKQSLAQSHLPAQPDISPNIPEAVKGCMLFGAGKLENGLCICAMPKSVYIL 1739
QY 1741 RYNNENSKYCIKRIKIEISEFCSCIHFTNYGSLIGTKKFEYEDMKQYTLSEFLLDKNDHSLA 1800
Db 1740 RYNNENSKYCIKRIKIEISEFCSCIHFTNYGSLIGTKKFEYEDMKQYTLSEFLLDKNDHSLA 1799
QY 1801 PAVFAASSNSFPYSIVOVNAGOREEYLLCFHEFGVVDVYGRSRTDDDKMSRLPLAFA 1860
Db 1800 PAVFAASSNSFPYSIVOVNAGOREEYLLCFHEFGVVDVYGRSRTDDDKMSRLPLAFA 1859
QY 1861 YREPYLVFTHFNLSLEVLIEIQARSSAGTAPARAYLDIENPRYLGAISSGAYLASSYQDKL 1920
Db 1860 YREPYLVFTHFNLSLEVLIEIQARSSAGTAPARAYLDIENPRYLGAISSGAYLASSYQDKL 1919
QY 1921 RVICCKGNLVKESGTEHHRPSTSRSSPNKRGPTVNEHITTKVASSPAPEEGSHPREP 1980
Db 1920 RVICCKGNLVKESGTEHHRPSTSRSSPNKRGPTVNEHITTKVASSPAPEEGSHPREP 1979
QY 1981 STEHRYEGRTELRLRDKSPGRPLEREKSPGRILSTRERSPARLLFEDESSRGLPLAGAVRT 2040
Db 1980 STEHRYEGRTELRLRDKSPGRPLEREKSPGRMLSTRERSFGRLLFEDSSRGLPLAGAVRT 2039
QY 2041 PLSQVKNKWDQSSV 2054
Db 2040 PLSQVKNKWDQSSV 2053

RESULT 6
US-09-964-956-9
; Sequence 9, Application US/09964956
; Publication No. US20040043926A1
; GENERAL INFORMATION:
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Macdougall, John R
; APPLICANT: Smitheon, Glenda
; APPLICANT: Miller, Isabelle
; APPLICANT: Stone, David
; APPLICANT: Gunther, Erik
; APPLICANT: Ellerman, Karen
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine B
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Kekuda, Rameen
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Leach, Martin D
; APPLICANT: Shimkets, Richard A
; TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-124
; CURRENT APPLICATION NUMBER: US/09/964,956
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; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,631
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,633
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/235,808
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,064
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,065
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,066
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/236,135
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,434
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,321
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 60/238,399
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/238,396
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/276,667
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/294,823
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/304,868
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 2066
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-964-956-9

Query Match 99.4%; Score 10425.5; DB 11; Length 2066;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2044; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

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Db 61 ECGOPALMKIKHVSNFVRKYSDTIAELOIOPSADKFEVRSLVGCGHFAEVQVVRKATG 120
QY 121 DIYAMKVMKKKALLAEOVSFFEEERNILSRSTSPMIPOLQVAFODKXNHLVYMEYOPGG 180
Db 121 DIYAMKVMKKKALLAEOVSFFEEERNILSRSTSPMIPOLQVAFODKXNHLVYMEYOPGG 180
QY 181 DLSLNRVEDQDENILQFYLAELILAVSVHLMGVHRDIPENILVDRTHIKLVDF 240
Db 181 DLSLNRVEDQDENILQFYLAELILAVSVHLMGVHRDIPENILVDRTHIKLVDF 240
QY 241 GSAAKNNSNMVNAKLPIGTPDYMADEVLTVMNGDGKGYGLDCDWMASGVIAIYEMIYGR 300
Db 241 GSAAKNNSNMVNAKLPIGTPDYMADEVLTVMNGDGKGYGLDCDWMASGVIAIYEMIYGR 299
QY 301 SPFAEGTSARTFNININQFQFLKFPDDPKVSSPFLDLISLLCGQERLKFEGLCCHPFF 360
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QY 361 SKIDMNINRSPPEFPTLKSDDDTNSFDEPEKNSVWSSPQCLSPSGFSGEELPFVGF 420
Db 360 SKIDMNINRAPPFPVTLKSDDTNSFDEPEKNSVWSSPQCLSPSGFSGEELPFVGF 419
QY 421 YSRALGILGRSESVSGLDSPAKTSMEKKLLIKSRELQDSQDKCHMEQEMTRLHRRVS 480
Db 420 YSRALGILGRSESVSGLDSPAKTSMEKKLLIKSRELQDSQDKCHMEQEMTRLHRRVS 479
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Qy 481 EVEAVLSQKEVELKASFTQBSLLEBODLATYITTECSLSKRSLEQANMEVSOEDDKXLOLH 540
 Db 480 EVEAVLSQKEVELKASFTQBSLLEBODLATYITTECSLSKRSLEQANMEVSOEDDKXLOLH 539
 Qy 541 DIREQSRLQEIKEOEYOAQVEEMLMNNOLEEDIVSARRSDIYESLEBSRLAAEFK 600
 Db 540 DIREQSRLQEIKEOEYOAQVEEMLMNNOLEEDIVSARRSDIYESLEBSRLAAEFK 599
 Qy 601 RKATECOHKLKAKDOQKEVGEYAKLEKINAEQOLKIQELQEKLEKAVKASTATELLO 660
 Db 600 RKATECOHKLKAKDOQKEVGEYAKLEKINAEQOLKIQELQEKLEKAVKASTATELLO 659
 Qy 661 NIRAQEAARELEKLONRDESSSGIRKKLYABERRRSLKRYKLETTMERENRLKOD 720
 Db 660 NIRAQEAARELEKLONRDESSSGIRKKLYABERRRSLKRYKLETTMERENRLKOD 719
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 Db 720 IOTSQOIQMAADKILEEKGHREAOVSAOHLVYHLKQKQHYEKKIKVLNOIKODLAD 779
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 Db 780 KETLENNMQREBEAHEKGIILSEOKAMINAMDSKIRSLQRIVELSEANKLANSSLEF 839
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 Db 840 QRNKAQOEMISELRQOKFYLETQAKLEAONRKLEBOLKISHODSDKRRLLLETRL 899
 Qy 901 REVELHEBEOKLEIKROLTELQSLQEBESQTLQAARALESQLRAKTELEETTEA 960
 Db 900 REVELHEBEOKLEIKROLTELQSLQEBESQTLQAARALESQLRAKTELEETTEA 959
 Qy 961 EEEIOALTARHDEIQRKFDALRNSCTVITDLEEOINQLEEDNABLANNOFYLSKOLDEAS 1020
 Db 960 EEEIOALTARHDEIQRKFDALRNSCTVITDLEEOINQLEEDNABLANNOFYLSKOLDEAS 1019
 Qy 1021 GANDEIVOLRSEVHLRREITEREMOLTSQOKTMEALKTCTMLEEQVMDLEALNDELLE 1080
 Db 1020 GANDEIVOLRSEVHLRREITEREMOLTSQOKTMEALKTCTMLEEQVMDLEALNDELLE 1079
 Qy 1081 KERQWEMARSVLGDSEKQFECGRVRELQOMLDEKOSRRARORTTESQVVELAVKEKA 1140
 Db 1080 KERQWEMARSVLGDSEKQFECGRVRELQOMLDEKOSRRARORTTESQVVELAVKEKA 1139
 Qy 1141 EILALQOALKKEQKAKASLSKDLNDEKHAMLENNASLQOKLETERELKORLLEBOAK 1200
 Db 1140 EILALQOALKKEQKAKASLSKDLNDEKHAMLENNASLQOKLETERELKORLLEBOAK 1199
 Qy 1201 LQQQMDLQKNHIFRLTQGLQBALDRADILKTERSDBEYOLENIQVLSHEKVKMEGTISQ 1260
 Db 1200 LQQQMDLQKNHIFRLTQGLQBALDRADILKTERSDBEYOLENIQVLSHEKVKMEGTISQ 1259
 Qy 1261 QTKLIDFLQAMQDPAKKKKPILOYNELKALEKEKARCABLEALQOTRIELASABEA 1320
 Db 1260 QTKLIDFLQAMQDPAKKKKPILOYNELKALEKEKARCABLEALQOTRIELASABEA 1319
 Qy 1321 AHRKATDHPHSTPATARQOIAMSAIVSPHOPSANSLAPSSRRKESSTPEEFSRL 1380
 Db 1320 AHRKATDHPHSTPATARQOIAMSAIVSPHOPSANSLAPSSRRKESSTPEEFSRL 1379
 Qy 1381 KERMHNI PHRFNVGLNMRATKCAVCLDTVHFGROASKLECOVMCHKSTCLPATCGL 1440
 Db 1380 KERMHNI PHRFNVGLNMRATKCAVCLDTVHFGROASKLECOVMCHKSTCLPATCGL 1439
 Qy 1441 PAVATHTFEAFCDKKNSSPGLQTKPESSSLHSGMMKVPNNKRGQOGMGRKTIYVEGS 1500
 Db 1440 PAVATHTFEAFCDKKNSSPGLQTKPESSSLHSGMMKVPNNKRGQOGMGRKTIYVEGS 1499
 Qy 1501 KVLVYDNEARAGORPYEPELCLPDGDSVTHGAVGASELANTKADVPYITLKMSHPHT 1560
 Db 1500 KVLVYDNEARAGORPYEPELCLPDGDSVTHGAVGASELANTKADVPYITLKMSHPHT 1559
 Qy 1561 TCWPGRTLYLLAPSPDKQRWVTALSVVAGRVSRKAEADAKLIGNSLKLEGGDDRLD 1620

Db 1560 TCWPGRTLYLLAPSPDKQRWVTALSVVAGRVSRKAEADAKLIGNSLKLEGGDDRLD 1619
 Qy 1621 MCTLPFSQYVVLVGTSEGLYALNVLKNSLTHVVGIGAVFOIYIIXKDEKLMIMAGEERA 1680
 Db 1620 MCTLPFSQYVVLVGTSEGLYALNVLKNSLTHVVGIGAVFOIYIIXKDEKLMIMAGEERA 1679
 Qy 1681 LCLVDVKKVKOSLAOSHLPAPDISPNIPEAVKGCHEGAGKIENGCLCTCAAMPKVVIL 1740
 Db 1680 LCLVDVKKVKOSLAOSHLPAPDISPNIPEAVKGCHEGAGKIENGCLCTCAAMPKVVIL 1739
 Qy 1741 RYNNLSKYCTIRKIEITSEBSCCHFTMYSTLIGNKRYEIDMQYTLIEEFLDKNDHSLA 1800
 Db 1740 RYNNLSKYCTIRKIEITSEBSCCHFTMYSTLIGNKRYEIDMQYTLIEEFLDKNDHSLA 1799
 Qy 1801 PAVFAASNSFPVSVIVQVNSAGOREBYLLCHEFGVFPVDSIGRSRTDLDKMSRLPLAFA 1860
 Db 1800 PAVFAASNSFPVSVIVQVNSAGOREBYLLCHEFGVFPVDSIGRSRTDLDKMSRLPLAFA 1859
 Qy 1861 YREPYLPVTHNSLEVIEIQARSSAGTPARAVIDIPNRYLGPALISSGAIYLAASYODXL 1920
 Db 1860 YREPYLPVTHNSLEVIEIQARSSAGTPARAVIDIPNRYLGPALISSGAIYLAASYODXL 1919
 Qy 1921 RVICCKGNLVKESGTEHHRGSTRSSPNKRGPTTYNEHTKRVASSAPPEGSHPREP 1980
 Db 1920 RVICCKGNLVKESGTEHHRGSTRSSPNKRGPTTYNEHTKRVASSAPPEGSHPREP 1979
 Qy 1981 STPHRYEGRTLETRDSDSGRPLERKSPGRILSTRRERSPARLPEDSSRRLPLGAVRT 2040
 Db 1980 STPHRYEGRTLETRDSDSGRPLERKSPGRILSTRRERSPARLPEDSSRRLPLGAVRT 2039
 Qy 2041 PLSQVNVKWDQS 2052
 Db 2040 PLSQVNVKWDQS 2051

RESULT 7
 US-10-262-511-14
 : Sequence 14, Application US/10262511
 : Publication No. US20040038223A1
 : GENERAL INFORMATION:
 : APPLICANT: Smithson, Glenda
 : APPLICANT: Miller, Isabelle
 : APPLICANT: Peyman, John A.
 : APPLICANT: Kekuda, Rameesh
 : APPLICANT: Ju, Jingfang
 : APPLICANT: Li, Li
 : APPLICANT: Guo, Xiaojia (Sasha)
 : APPLICANT: Paturajan, Meera
 : APPLICANT: Spytek, Kimberly A.
 : APPLICANT: Edinger, Shlomit R.
 : APPLICANT: Elleman, Karen
 : APPLICANT: Maljanar, Uriel M.
 : APPLICANT: Ort, Tatiana
 : APPLICANT: Zernusen, Bryan D.
 : APPLICANT: Anderson, David W.
 : APPLICANT: Zhong, Mei
 : APPLICANT: Catterton, Elin
 : APPLICANT: Ji, Weizhen
 : APPLICANT: Miller, Charles E.
 : APPLICANT: Raetelli, Luca
 : APPLICANT: Stone, David J.
 : APPLICANT: Pena, Carol E. A.
 : APPLICANT: Shenoy, Suresh G.
 : APPLICANT: Shimkets, Richard A.
 : APPLICANT: Rothenberg, Mark E.
 : APPLICANT: Leach, Martin D.
 : APPLICANT: Agee, Michele L.
 : APPLICANT: Berghs, Constance
 : TITLE OR INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 : FILE REFERENCE: 21402-462C
 : CURRENT APPLICATION NUMBER: US/10/262,511

CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,826
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Cuiaseqdist version 0.1
SEQ ID NO 14
LENGTH: 2066
TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-14

Query Match 99.4%; Score 10425.5; DB 15; Length 2066;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2044; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

1 MUKFKYARBPDLGAGAEPIASRASRLNPFQKPEPTMOQMSPLSREGIILAFVLFE 60
1 MLKFKGARRPLDGAEPISASRASRLNLFQKPEPTMOQMSPLSREGIILAFVLFE 60
61 ECSOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVSILVCGHFAEYOVRKATG 120
61 ECQOPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVSILVCGHFAEYOVRKATG 120
121 DIYAMKWKKKKALLAQOVSPFEERNILSRSTSPWIPOLQYAFQDNHLYLMEYOPGG 180
121 DIYAMKWKKKKALLAQOVSPFEERNILSRSTSPWIPOLQYAFQDNHLYLMEYOPGG 180
121 DIYAMKWKKKKALLAQOVSPFEERNILSRSTSPWIPOLQYAFQDNHLYLMEYOPGG 180
181 DLISLNRVEDQIDENLIQFYLAELILAVHSVHMGVHRDIKRENTLVDRGTGIKLVDF 240
181 DLISLNRVEDQIDENLIQFYLAELILAVHSVHMGVHRDIKRENTLVDRGTGIKLVDF 240
181 DLISLNRVEDQIDENLIQFYLAELILAVHSVHMGVHRDIKRENTLVDRGTGIKLVDF 240
241 GSAKONNSNMVNAKLPIGTIDYVAPRVLTVMNGDGKTYGLDCDWMSSGVIAEMTYGR 300
241 GSAKONNSNMVNAKLPIGTIDYVAPRVLTVMNGDGKTYGLDCDWMSSGVIAEMTYGR 300
241 GSAKONNSNMVNAKLPIGTIDYVAPRVLTVMNGDGKTYGLDCDWMSSGVIAEMTYGR 300
301 SPFAEGTSATFNINMFORPLKFPDDPKVSSDFLDLIQSILCGOKERLKFEGICHPFF 360
301 SPFAEGTSATFNINMFORPLKFPDDPKVSSDFLDLIQSILCGOKERLKFEGICHPFF 360
300 SPFAEGTSATFNINMFORPLKFPDDPKVSSDFLDLIQSILCGOKERLKFEGICHPFF 359
361 SKIDMNNIRNSPPFVTLKSDDDTSNFDPEKKSWSVSSPCOLSPSGFSGEELPFVGF 420
361 SKIDMNNIRNSPPFVTLKSDDDTSNFDPEKKSWSVSSPCOLSPSGFSGEELPFVGF 420
360 SKIDMNNIRNSPPFVTLKSDDDTSNFDPEKKSWSVSSPCOLSPSGFSGEELPFVGF 419
421 YSRKALGILGRSESVGLDSPAKTSMKKLLIKSKELQDSODKCHMEQEMTRLHRRVS 480
421 YSRKALGILGRSESVGLDSPAKTSMKKLLIKSKELQDSODKCHMEQEMTRLHRRVS 480
420 YSRKALGILGRSESVGLDSPAKTSMKKLLIKSKELQDSODKCHMEQEMTRLHRRVS 479
481 EYEAVALISQKEVELKASTQSLLEQDIATYITTECSSIKRSLEQARMEVSOEDDKALQLH 540
481 EYEAVALISQKEVELKASTQSLLEQDIATYITTECSSIKRSLEQARMEVSOEDDKALQLH 540
480 EYEAVALISQKEVELKASTQSLLEQDIATYITTECSSIKRSLEQARMEVSOEDDKALQLH 539
541 DIBBQSKLOEIKQEOYQAOVEEMRLMMNQLBEPLVARRRSDLYESEELAESRLAAEFK 600
541 DIBBQSKLOEIKQEOYQAOVEEMRLMMNQLBEPLVARRRSDLYESEELAESRLAAEFK 600
540 DIBBQSKLOEIKQEOYQAOVEEMRLMMNQLBEPLVARRRSDLYESEELAESRLAAEFK 599

601 RKATECOHKLKAKDOGKPEVGEYALCEKINAEOQLKIOELQELKEKAVASTEATIELLO 660
600 RKATECOHKLKAKDOGKPEVGEYALCEKINAEOQLKIOELQELKEKAVASTEATIELLO 659
661 NIFQAKERARELEKIKONREDSSEGIKKLYVEEERHSHENLVKSELETTERENRLKDD 720
660 NIFQAKERARELEKIKONREDSSEGIKKLYVEEERHSHENLVKSELETTERENRLKDD 719
721 IOTKSQOIQOMADKILIELEKHEAQAQVSAQHLEVLHKKQKHAEKIKVLDNDIQKDLAD 780
720 IOTKSQOIQOMADKILIELEKHEAQAQVSAQHLEVLHKKQKHAEKIKVLDNDIQKDLAD 779
781 KETLENNMOHREBEAHEKGIKISEQAMINAMDSKIRSLFORIVELSEANKLAANSLSFT 840
780 KETLENNMOHREBEAHEKGIKISEQAMINAMDSKIRSLFORIVELSEANKLAANSLSFT 839
841 QRMMKAOEEMISELRQOKFLYEQAKLEAONKLEBOLEKISHOHSQDNRLLEETRL 900
840 QRMMKAOEEMISELRQOKFLYEQAKLEAONKLEBOLEKISHOHSQDNRLLEETRL 899
901 REVSLEHEBQKLEKQLTLEQSLQERESQLTALQAAALAESQLOAKTELEETTAEA 960
900 REVSLEHEBQKLEKQLTLEQSLQERESQLTALQAAALAESQLOAKTELEETTAEA 959
961 EEEIOALTARDEIQKFPALRNSCTVITDLSEQLNQLTEDNAELNNQNFYLSKQIDEAS 1020
960 EEEIOALTARDEIQKFPALRNSCTVITDLSEQLNQLTEDNAELNNQNFYLSKQIDEAS 1019
1021 GANDEIVOLRSEVDHRRREITREEMQTSOKQMEALKTCTMLEFQVMDLEMLNLELLE 1080
1020 GANDEIVOLRSEVDHRRREITREEMQTSOKQMEALKTCTMLEFQVMDLEMLNLELLE 1079
1081 KERQWEAMBSVLGDEKSOFECEVRRELORMIDTEKQSRABADQRTESRQVVELAVENKHA 1140
1080 KERQWEAMBSVLGDEKSOFECEVRRELORMIDTEKQSRABADQRTESRQVVELAVENKHA 1139
1141 EIALAQALKEQKAKESLSDKINDLEKKHAMENNARSIQKLETERELKORLLEBOAK 1200
1140 EIALAQALKEQKAKESLSDKINDLEKKHAMENNARSIQKLETERELKORLLEBOAK 1199
1201 LQOQOMLOKKNHIFRLQGLQEALDRADLKTESBDEYQLENTQVLSHEKVMWEGTISQ 1260
1200 LQOQOMLOKKNHIFRLQGLQEALDRADLKTESBDEYQLENTQVLSHEKVMWEGTISQ 1259
1261 OTKLIDFLQAKMDQPAKKKKVPLQVNEMLKLALEKAKACALEBEALQKTRIELBSARBEA 1320
1260 OTKLIDFLQAKMDQPAKKKKVPLQVNEMLKLALEKAKACALEBEALQKTRIELBSARBEA 1319
1321 AHRKATDHPHPTPATARQOIAMSAIVRSPEHOPASMSLAPSSRRKSSSTPEEFSRRL 1380
1320 AHRKATDHPHPTPATARQOIAMSAIVRSPEHOPASMSLAPSSRRKSSSTPEEFSRRL 1379
1381 KERMMHNIPIRRFVNGVNMARATKCAVCLDVHFRQASKCLBQVWCHPCKSTCLPATCG 1440
1380 KERMMHNIPIRRFVNGVNMARATKCAVCLDVHFRQASKCLBQVWCHPCKSTCLPATCG 1439
1441 PAEYATHTFAFCRDQKNSPGLQTKPESSSLHLEGMMKVPNNKRQOQGDRTKYIVLEGS 1500
1440 PAEYATHTFAFCRDQKNSPGLQTKPESSSLHLEGMMKVPNNKRQOQGDRTKYIVLEGS 1499
1501 KVLIVNEAREAGQRPVEEBELCLPDGVSIGHAVASBLANTAKADVPIYILMESHPHT 1560
1500 KVLIVNEAREAGQRPVEEBELCLPDGVSIGHAVASBLANTAKADVPIYILMESHPHT 1559
1561 TCMRGRTYILIASFPDQKRWJTALAESVYAGGVSEKKAADKLLGNSLLKLEGGDRDL 1620
1560 TCMRGRTYILIASFPDQKRWJTALAESVYAGGVSEKKAADKLLGNSLLKLEGGDRDL 1619
1621 MNCITLPPSDQVVLVGBEGLYALNVLKNSLTHVPGIGAVFOYIYIKOLEKGLMIAEGERA 1680
1620 MNCITLPPSDQVVLVGBEGLYALNVLKNSLTHVPGIGAVFOYIYIKOLEKGLMIAEGERA 1679

QY 1661 LCLVDVKKVKSLOSLAOSHLPADODISPNIFEAVKGCHEFGAGKINGELCTICAMPSKVITL 1740
Db 1680 LCLVDVKKVKSLOSLAOSHLPADODISPNIFEAVKGCHEFGAGKINGELCTICAMPSKVITL 1739
QY 1741 RYNNENLSKYCIKRIELETSEPCSHFTNYSLIGTNKFEYIDMKOYLTEELDKNDHSLA 1800
Db 1740 RYNNENLSKYCIKRIELETSEPCSHFTNYSLIGTNKFEYIDMKOYLTEELDKNDHSLA 1799
QY 1801 PAVFAASNSFPVSIYOVNAGOREEYLLCFHEFGVPVDSYGRSRTDCLKMSRLPLAFA 1860
Db 1800 PAVFAASNSFPVSIYOVNAGOREEYLLCFHEFGVPVDSYGRSRTDCLKMSRLPLAFA 1859
QY 1861 YREBYLFTVTHNSLEVEIEIOARSSAGTPARAAYLDIPNRYLGPALISSAYTLASSYODKL 1920
Db 1860 YREBYLFTVTHNSLEVEIEIOARSSAGTPARAAYLDIPNRYLGPALISSAYTLASSYODKL 1919
QY 1921 RVICCKGNLVKESGTEHHRGPGSTSRSPNKGPPTYNEHTTKRAVASSPAPEGSHPREP 1980
Db 1920 RVICCKGNLVKESGTEHHRGPGSTSRSPNKGPPTYNEHTTKRAVASSPAPEGSHPREP 1979
QY 1981 STPHRYEGRTELRDKSPGRPLERKSPGRILSTRERRSPARLFEDSSRGRLPAGAVRT 2040
Db 1980 STPHRYEGRTELRDKSPGRPLERKSPGRILSTRERRSPARLFEDSSRGRLPAGAVRT 2039
QY 2041 PLSGVNKKVWDOS 2052
Db 2040 PLSGVNKKVWDOS 2051

RESULT 8
US-10-017-216-4
; Sequence 4, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KAPLEBER-LIBERMAN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1 Human Myotonic Dystrophy Type Proc
; TITLE OF INVENTION: Kinase and Uses Therefor
; FILE REFERENCE: 10147-5701
; CURRENT APPLICATION NUMBER: US/10/017, 216
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 4
; LENGTH: 2055
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-017-216-4

Query Match 96.3%; Score 10109.5; DB 13; Length 2055;
Best Local Similarity 96.0%; Pred. No. 0;
Matches 1974; Conservative 40; Mismatches 39; Indels 3; Gaps 2;
QY 1 MLKFTYCARNPDLGAAPLASRASRLNLFQGRPPTTQOQMSPLSREGILDLFVLFPE 60
Db 1 MLKFTYCARNPDLGAAPLASRASRLNLFQGRPPTTQOQMSPLSREGILDLFVLFPE 60
QY 61 ECSSOPALMKTKHVNPNFRKXSDTIAELQELOPSADKDEYVNSVCCGCHFAEVQVVRKATG 120
Db 61 ECSSOPALMKTKHVNPNFRKXSDTIAELQELOPSADKDEYVNSVCCGCHFAEVQVVRKATG 120
QY 121 DIYAMKVMKKKALLAQBQVSEFEERNTLSRSTSPMTIPLQYAFQDKNHLYLVMEYOPGG 180
Db 121 DIYAMKVMKKKALLAQBQVSEFEERNTLSRSTSPMTIPLQYAFQDKNHLYLVMEYOPGG 180
QY 181 DLISLNRREYDQDENTLIQFYLAELILAVSHVLMGVVHRDICKENILVDRTHGIKLVDF 240
Db 181 DLISLNRREYDQDENTLIQFYLAELILAVSHVLMGVVHRDICKENILVDRTHGIKLVDF 240
QY 241 GSAAKNSNKKVNAKLTIGTPDYMAPEVLTVMNMGDGKTYGLDDCDWMSVGVIAIEMTYGR 300
Db 241 GSAAKNSNKKVNAKLTIGTPDYMAPEVLTVMNMGDGKTYGLDDCDWMSVGVIAIEMTYGR 299

QY 301 SPPEAGTSARTENNINMNFQRFLEKFPDDPKVSSDFLDLIQSILCCQKERLKEEGLCCHPEF 360
Db 300 TPPEAGTSARTENNINMNFQRFLEKFPDDPKVSSDFLDLIQSILCCQKERLKEEGLCCHPEF 359
QY 361 SKIDMNNIRNSPPFVFTLSDDDTSNPFDEKNSWVSSPCQSPSPGSEBELPFVGF 420
Db 360 ARTDMNNIRNSPPFVFTLSDDDTSNPFDEKNSWVSSPCQSPSPGSEBELPFVGF 419
QY 421 YSKALGILGSESVSGSDSPAKTSMEKLLISKELODSQDCHKMEQETRLHRYVS 480
Db 420 YSKALGILGSESVSGSDSPAKTSMEKLLISKELODSQDCHKMEQETRLHRYVS 479
QY 481 EYEAVALSQEVELKASSETQSLBODLATYITTECSSLSKRSLEQAPMEVSQEDDKALQLH 540
Db 480 EYEAVALSQEVELKASSETQSLBODLATYITTECSSLSKRSLEQAPMEVSQEDDKALQLH 539
QY 541 DIREOSRLOEIKQOEYQAOVEEMRLMNOLEEDLVASARRSDLYESELRESRLAAEFK 600
Db 540 DIREOSRLOEIKQOEYQAOVEEMRLMNOLEEDLVASARRSDLYESELRESRLAAEFK 599
QY 601 RKATECOHKLKAKDQCKPEVGEYAKLEKINAEOQLKIOELQELKRAVASTATELLQ 660
Db 600 RKANECHKLKAKDQCKPEVGEYAKLEKINAEOQLKIOELQELKRAVASTATELLQ 659
QY 661 NIROAKERAERLEKLNREDSSBGRKCLVEABERHSHLENKYRLTETMERENRLKD 720
Db 660 NIROAKERAERLEKLNREDSSBGRKCLVEABERHSHLENKYRLTETMERENRLKD 719
QY 721 IOTSQOIQOQADKILLEBKHRAVOYSAQHLVHLKQKQHYEKKIYVLNQIKCLAD 780
Db 720 IOTSQOIQOQADKILLEBKHRAVOYSAQHLVHLKQKQHYEKKIYVLNQIKCLAD 779
QY 781 KETLENNMOHREBEAHEKGLISBOKAMINAMDSKISLBORIYELSEBANKLAANSLSFT 840
Db 780 KESLENNMOHREBEAHEKGLISBOKAMINAMDSKISLBORIYELSEBANKLAANSLSFT 839
QY 841 QNNKAQEMISSELROQKFLYLETQAGKLEAQNRLKEBQLEKISHQDSDKNRLLELETRL 900
Db 840 QNNKAQEMISSELROQKFLYLETQAGKLEAQNRLKEBQLEKISHQDSDKNRLLELETRL 899
QY 901 REVSLHEBQLEKROULTELOLSQERESQTLQAAPALBESQLQAKTELEETTAA 960
Db 900 REVSLHEBQLEKROULTELOLSQERESQTLQAAPALBESQLQAKTELEETTAA 959
QY 961 BEELQALTAHREDEORFADLRNSCTVITDLEBQNLQTDMAENNONPFLSQOLBAS 1020
Db 960 BEELQALTAHREDEORFADLRNSCTVITDLEBQNLQTDMAENNONPFLSQOLBAS 1019
QY 1021 GANDEIVQLRSEVDHLREITEREMOQLTSQKQTEALKTCTMLEBQVMDLEALNDELLE 1080
Db 1020 GANDEIVQLRSEVDHLREITEREMOQLTSQKQTEALKTCTMLEBQVMDLEALNDELLE 1079
QY 1081 KEROMEAMRSVLDGDEKSQFECRAVELQRMLDTEKQSPARADQRTTESROVVELAVKCHKA 1140
Db 1080 KEROMEAMRSVLDGDEKSQFECRAVELQRMLDTEKQSPARADQRTTESROVVELAVKCHKA 1139
QY 1141 EILALQALKEOKUKASLSDKLNDLEKKHAMLENNARSLOQKLETERBELKORLLEQAK 1200
Db 1140 EILALQALKEOKUKASLSDKLNDLEKKHAMLENNARSLOQKLETERBELKORLLEQAK 1199
QY 1201 LQOQMDLQKNHIFALTOGLOEALDRADLKTESDLEYQLENTIOVLSHSEKVKMEGTSIQ 1260
Db 1200 LQOQMDLQKNHIFALTOGLOEALDRADLKTESDLEYQLENTIOVLSHSEKVKMEGTSIQ 1259
QY 1261 QTKLIDFLQAKMDQPAKKKVPLOYNELKALKEKAPCABLEBALOKTRIELRSARBEA 1320
Db 1260 QTKLIDFLQAKMDQPAKKKVPLOYNELKALKEKAPCABLEBALOKTRIELRSARBEA 1319
QY 1321 AHRKATDHPSPATARQOILAMSAIVRSPHOQSAWSLAPPSRKESSTPEEFSRL 1380
Db 1320 AHRKATDHPSPATARQOILAMSAIVRSPHOQSAWSLAPPSRKESSTPEEFSRL 1379

QY 1381 KERMHNIPHRFNVGLMRAATKCAVCLDTHFGRQASKCLBEOVMCHPCKSTCLPATCGL 1440
Db 1380 KERMHNIPHRFNVGLMRAATKCAVCLDTHFGRQASKCLBEOVMCHPCKSTCLPATCGL 1439
QY 1441 PARYATHFPAFORDKNNSPGLQTKPSSSLHLEGMMKVPRNNRGGQGDNRKXIVLEGS 1500
Db 1440 PARYATHFPAFORDKNNSPGLQTKPSSSLHLEGMMKVPRNNRGGQGDNRKXIVLEGS 1499
QY 1501 KVL1YDNEAREAGORPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIYLKXNESHPT 1560
Db 1500 KVL1YDNEAREAGORPVEEFELCLPDGDVSIHGAVGASELANTAKADVPIYLKXNESHPT 1559
QY 1561 TCMPEGLTYLLASFPPOKXWVTALBSVAVAGGRVSRKADAKLGNLSLKLEGGDRLD 1620
Db 1560 TCMPEGLTYLLASFPPOKXWVTALBSVAVAGGRVSRKADAKLGNLSLKLEGGDRLD 1619
QY 1621 MNC1LPSDDOVLVGTGEGYALNVNLKNSLTHVPDGAVFQIYIIXOLEKULMAGBERA 1680
Db 1620 MNC1LPSDDOVLVGTGEGYALNVNLKNSLTHVPDGAVFQIYIIXOLEKULMAGBERA 1679
QY 1681 LCLVDYKVKQSLAQSHLPAQDISPNIPEAVKGCGLFGAGKLENGLCICAMPSKVYL 1740
Db 1680 LCLVDYKVKQSLAQSHLPAQDISPNIPEAVKGCGLFGAGKLENGLCICAMPSKVYL 1739
QY 1741 RYNNENSKYCIKKEIETSPSCSIHFTNYSILIGTNKPYEIDMKQYTLBEPFLDKNDHSLA 1800
Db 1740 RYNNENSKYCIKKEIETSPSCSIHFTNYSILIGTNKPYEIDMKQYTLBEPFLDKNDHSLA 1799
QY 1801 PAVPAASNSPPVSIYOVNAGOREEYLLCFHGVGVVDSYGRSRPDDLKMSRLPLAFA 1860
Db 1800 PAVPAASNSPPVSIYOVNAGOREEYLLCFHGVGVVDSYGRSRPDDLKMSRLPLAFA 1859
QY 1861 YREBYLVTFHFNLSLEVIEIOARSSAGTPARAYLDIPNRYLGPALSSGAYLASSYODKL 1920
Db 1860 YREBYLVTFHFNLSLEVIEIOARSSAGTPARAYLDIPNRYLGPALSSGAYLASSYODKL 1919
QY 1921 RYVICKGNLVKESGTEHHRGDPSTSRSSPNKRGPTTNEHTTKRVASSPAPPEGSHPREP 1980
Db 1920 RYVICKGNLVKESGTEHHRGDPSTSRSSPNKRGPTTNEHTTKRVASSPAPPEGSHPREP 1979
QY 1981 STPHRY--RGRMTLRDRKSPGRPLERKSPGRILSTRRRSPARLPEDSRGLPLGAV 2038
Db 1980 STPHRY--RGRMTLRDRKSPGRPLERKSPGRILSTRRRSPARLPEDSRGLPLGAV 2039
QY 2039 RTPLSQVNAKYWDOSV 2054
Db 2040 RTPLSQVNAKYWDOSV 2055

RESULT 9
US-10-017-216-2
; Sequence 2, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KABELLER-LIEBERMAN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1el Human Myoclonic Dystrophy Type Prot
; TITLE OF INVENTION: Kinase and Uses Therefor
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017, 216
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-216-2

Query Match 95.5%; Score 10022.5; DB 13; Length 2053;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 5; Indels 81; Gaps 3;

QY 1 MKFKYGAENPLDAGAEPIASPASLNLFPQCKPPMTQOQMSPLSRBSLIDALFVLE 60
Db 1 MKFKYGAENPLDAGAEPIASPASLNLFPQCKPPMTQOQMSPLSRBSLIDALFVLE 60
QY 61 EGSOPALMKIKHNSNVKRYSDTIAELOEPASXDPFVRSILVGCCHFAFVQVVRKATG 120
Db 61 EGSOPALMKIKHNSNVKRYSDTIAELOEPASXDPFVRSILVGCCHFAFVQVVRKATG 120
QY 121 DIYAMVKKKALLAEOVSFPFEEERNILSRSTSPMIPOLQVAFODKNHLYLVMEYQPGG 180
Db 121 DIYAMVKKKALLAEOVSFPFEEERNILSRSTSPMIPOLQVAFODKNHLYLVMEYQPGG 180
QY 181 DLISLNRVEDQIDENLQFYLAELILAVSHVMGYVRDIPENILVDRTHIKLVDF 240
Db 181 DLISLNRVEDQIDENLQFYLAELILAVSHVMGYVRDIPENILVDRTHIKLVDF 240
QY 241 GSAKXNSNMVNAKPIGTPDYMABEVLTVNMGDGKGTGLCDMMSVGVIAYEM1YGR 300
Db 241 GSAKXNSNMVNAKPIGTPDYMABEVLTVNMGDGKGTGLCDMMSVGVIAYEM1YGR 300
QY 301 SPFAEGTSARTFNNINMFORFLKFPDDPKVSDPFLDLOSILCGOKERLKEGLCCHPFF 360
Db 301 SPFAEGTSARTFNNINMFORFLKFPDDPKVSDPFLDLOSILCGOKERLKEGLCCHPFF 360
QY 361 SKIDMNNIRNSPPPVPTLKSDDDTSNFDEPEKNSVSSPCQLSPSGSGEELPVYGF 420
Db 361 SKIDMNNIRNSPPPVPTLKSDDDTSNFDEPEKNSVSSPCQLSPSGSGEELPVYGF 420
QY 421 YSKALGILGRSEVSGGLSPATSSMEKKL1KSKELDOSQKCHMEDEMR1LHRVS 480
Db 421 YSKALGILGRSEVSGGLSPATSSMEKKL1KSKELDOSQKCHMEDEMR1LHRVS 480
QY 481 EYAVAVLSQKEVELKASETORSLLEODLATYITECSSLKSLEBOARNEVSGEDKALQLH 540
Db 481 EYAVAVLSQKEVELKASETORSLLEODLATYITECSSLKSLEBOARNEVSGEDKALQLH 540
QY 541 DIREQSRKLOEIKOEYQAOVEEMRLMNOLEEDLYSARRRSLYSELRBSLAAEFK 600
Db 541 DIREQSRKLOEIKOEYQAOVEEMRLMNOLEEDLYSARRRSLYSELRBSLAAEFK 600
QY 601 RKAETCOHKLKAKDOGKPEVGYALKEK1MAQOLKIOELORKEKAVASTEATQLQ 660
Db 601 RKAETCOHKLKAKDOGKPEVGYALKEK1MAQOLKIOELORKEKAVASTEATQLQ 660
QY 661 N1ROAKERAERLELEKONREDSSEGIKKLVLEAEBRRHSLENNKYLETERRERENLKOD 720
Db 661 N1ROAKERAERLELEKONREDSSEGIKKLVLEAEBRRHSLENNKYLETERRERENLKOD 720
QY 721 IQTKSQOIQOMADKILLEBKREAOVSAQHLEVHLKQKQHYEYKIKVLNDQIKODLAD 780
Db 721 IQTKSQOIQOMADKILLEBKREAOVSAQHLEVHLKQKQHYEYKIKVLNDQIKODLAD 780
QY 781 KETLENNMQHHEEAHEKGLLSEOKAMTANAMSKIRSEORIVELSEANKLAANS1LFT 840
Db 781 KETLENNMQHHEEAHEKGLLSEOKAMTANAMSKIRSEORIVELSEANKLAANS1LFT 840
QY 841 QRMKAQOEMISELROOKFYLFTQAGKLEAONKLEBOLEKISHODSDKNRLLLEETRL 900
Db 841 QRMKAQOEMISELROOKFYLFTQAGKLEAONKLEBOLEKISHODSDKNRLLLEETRL 900
QY 901 REVSLEHEBQKELKQUTELQSLQERBSQUTALOAPRAALBSQURQAKTELEETTAEA 960
Db 901 REVSLEHEBQKELKQUTELQSLQERBSQUTALOAPRAALBSQURQAKTELEETTAEA 960
QY 961 EEEIOALTARBDIQKRFALRNSCTVITDLEEQNLQUTEDNAELNNQNFYLSKQDEAS 1020
Db 961 EEEIOALTARBDIQKRFALRNSCTVITDLEEQNLQUTEDNAELNNQNFYLSKQDEAS 1004
QY 1021 GANDEIVOLRSEVDHLRREITEREMQUTSQKOTMEALKTTCTMLEEQVMDLEALNDELLE 1080
Db 1005 GANDEIVOLRSEVDHLRREITEREMQUTSQKOTMEALKTTCTMLEEQVMDLEALNDELLE 1064

1081 KERQEWARSVLGDEKSOFEGRVRELOMILDTKOSRARADORTTESNOVELAKKEKA 1140
1065 KERQEWARSVLGDEKSOFEGRVRELOMILDTKOSRARADORTTESNOVELAKKEKA 1124
1141 EIALAQAALKEQKLAESLSDKNDLEKHAMLENNASLOOKETERELKORLLEBOAK 1200
1125 EIALAQAALKEQKLAESLSDKNDLEKHAMLENNASLOOKETERELKORLLEBOAK 1184
1201 LQQQMDLOKNIHIFRITGLOALRADILKTERSDLEYOLENIQVLYSHEKVKMEGTISQ 1260
1185 LQQQMDLOKNIHIFRITGLOALRADILKTERSDLEYOLENIQVLYSHEKVKMEGTISQ 1244
1261 QTKLIDLOAKMDQPAKKKK-----VPLQVNEKLALKEKARCALEEA 1305
1245 QTKLIDLOAKMDQPAKKKKGLFSRRKEDPALPTQVPLQVNEKLALKEKARCALEEA 1304
1306 LOKTRIELRSAREBAARHAKATDHPHSTPATAROOIAMSALVRSPEHOPMSMLIAPSS 1365
1305 LOKTRIELRSAREBAARHAKATDHPHSTPATAROOIAMSALVRSPEHOPMSMLIAPSS 1364
1366 RRKESSTPEEFSRRLKERMHNIIPHRFVNGINMRATKCAVCLDTVHFGROASKLECOVM 1425
1365 RRKESSTPEEFSRRLKERMHNIIPHRFVNGINMRATKCAVCLDTVHFGROASKLECOVM 1424
1426 CHPKCSTCLPATCGIPAYATHFTBAFCRDKNSSBGLQTKEPSSSLHEGMKQPRNNKR 1485
1425 CHPKCSTCLPATCGIPAYATHFTBAFCRDKNSSBGLQTKEPSSSLHEGMKQPRNNKR 1484
1486 GQOQMDRKTYLVEGSKVLIYNEAREAGORVPEEBELCLPDGVS IHGAVASASELANAK 1545
1485 GQOQMDRKTYLVEGSKVLIYNEAREAGORVPEEBELCLPDGVS IHGAVASASELANAK 1544
1546 ADVBYILKMHESHPTTCMGRFTLYLLAFSPFDKORWYTALESVVAAGVSRSEKADAKL 1605
1545 A-----EKABAKL 1554
1606 LGNSLLKLEBDDRLDNNCTLPFSQVYLVGTEBGLYALNVLKNSLTHVPGI GAVFOIYI 1665
1555 LGNSLLKLEBDDRLDNNCTLPFSQVYLVGTEBGLYALNVLKNSLTHVPGI GAVFOIYI 1614
1666 KDLEKLMIGEERLALCLVDKVKYKOSLAOSHLPADPISNIEAVKGCILFGAGKIEN 1725
1615 KDLEKLMIGEERLALCLVDKVKYKOSLAOSHLPADPISNIEAVKGCILFGAGKIEN 1674
1726 GLCICAMPKSVLLIARVNEMLSKYCIKKEIETSEPCSIHFTNTSIIIGTKFYEIMQ 1785
1675 GLCICAMPKSVLLIARVNEMLSKYCIKKEIETSEPCSIHFTNTSIIIGTKFYEIMQ 1734
1786 YTLBEFLDKNDHSLAPVPAASSNSPVSIIVONSAGQREBYLLCFHEFGVFDVSGRS 1845
1735 YTLBEFLDKNDHSLAPVPAASSNSPVSIIVONSAGQREBYLLCFHEFGVFDVSGRS 1794
1846 RTDLDKRSRLPLAFAYREPLYFVTHENSLEYIEIOASSSACTPARAYLIDIPNPLYLPAI 1905
1795 RTDLDKRSRLPLAFAYREPLYFVTHENSLEYIEIOASSSACTPARAYLIDIPNPLYLPAI 1854
1906 SSGAIYLAASSYQDKLAVICCKGNLVKSGTEHHRGPTSSRSPKRGPPPTNEITRVA 1965
1855 SSGAIYLAASSYQDKLAVICCKGNLVKSGTEHHRGPTSSRSPKRGPPPTNEITRVA 1914
1966 SSPAPPEGSHPREPTPHRYREGRTLRDCKSPGRLEKRSBGRIILSTRERSPARLP 2025
1915 SSPAPPEGSHPREPTPHRYREGRTLRDCKSPGRLEKRSBGRIILSTRERSPARLP 1974
2026 EDSRRGLPAGAVRTPLSQVNVKWDQS 2053
1975 EDSRRGLPAGAVRTPLSQVNVKWDQS 2002

GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
; FILE REFERENCE: Mpl01-294P1RNM
; CURRENT APPLICATION NUMBER: US/10/325,430
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/341,953
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-325-430-12
Query Match 95.5%; Score 10022.5; DB 14; Length 2053;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 5; Indels 81; Gaps 3;
QY 1 MLKRYGARNPLDGAAPLPIASRASRLNLFQKRPPTQOQMSPLSREGILDALFVLFE 60
DB 1 MLKRYGARNPLDGAAPLPIASRASRLNLFQKRPPTQOQMSPLSREGILDALFVLFE 60
QY 61 ECGSPALMKIKHVNFPFRKYSDDTIAELOOPSADKDFEVRSLVCGHFAEVOVVRKATG 120
DB 61 ECGSPALMKIKHVNFPFRKYSDDTIAELOOPSADKDFEVRSLVCGHFAEVOVVRKATG 120
QY 121 DIYMKYMKKKALLAQQVSPFEERNILSRSTSPMIPOLOYARODKHLVLYMEYOPGG 180
DB 121 DIYMKYMKKKALLAQQVSPFEERNILSRSTSPMIPOLOYARODKHLVLYMEYOPGG 180
QY 121 DIYMKYMKKKALLAQQVSPFEERNILSRSTSPMIPOLOYARODKHLVLYMEYOPGG 180
DB 121 DIYMKYMKKKALLAQQVSPFEERNILSRSTSPMIPOLOYARODKHLVLYMEYOPGG 180
QY 181 DLISLNRVEDQDENTLIFOYLAELILAVHSVHLMGVHRDIKRENILVDRTHI KLVD 240
DB 181 DLISLNRVEDQDENTLIFOYLAELILAVHSVHLMGVHRDIKRENILVDRTHI KLVD 240
QY 241 GSAKKNMSNKNVAKLPIGTPDYAPVLYTMMNDGKTYGLDDCDMWSVGVIAYEMTYGR 300
DB 241 GSAKKNMSNKNVAKLPIGTPDYAPVLYTMMNDGKTYGLDDCDMWSVGVIAYEMTYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKPPDPKYSDPLDIQSLLCGQKELKPEGKCHPFF 360
DB 301 SPFAEGTSARTFNINMFORFLKPPDPKYSDPLDIQSLLCGQKELKPEGKCHPFF 360
QY 361 SKIDMNNIRNSPPFVPTLKSDDDTSNFDEBKNSWVSSPCQLSPSGFSGEELPFGFS 420
DB 361 SKIDMNNIRNSPPFVPTLKSDDDTSNFDEBKNSWVSSPCQLSPSGFSGEELPFGFS 420
QY 421 YSKALGILGSESVSGLDSPAKTSMEKULLYSKELQDSQDKHMQEOMTLLHRRVS 480
DB 421 YSKALGILGSESVSGLDSPAKTSMEKULLYSKELQDSQDKHMQEOMTLLHRRVS 480
QY 481 EVEAVLSQKVELKASSTORSILBODLATYITTECSSLKRSLQORMEVSOEDKALOLH 540
DB 481 EVEAVLSQKVELKASSTORSILBODLATYITTECSSLKRSLQORMEVSOEDKALOLH 540
QY 541 DIBQSRKLOIEKEOEYQAOVVEKRLMNNQLEBDIVSARRSDLYESELRESRLAAEFK 600
DB 541 DIBQSRKLOIEKEOEYQAOVVEKRLMNNQLEBDIVSARRSDLYESELRESRLAAEFK 600
QY 601 RKATECOHKLKAKDOQKPEVGEYAKLEKINABOQLKIOELOELKAVASTATELLO 660
DB 601 RKATECOHKLKAKDOQKPEVGEYAKLEKINABOQLKIOELOELKAVASTATELLO 660
QY 661 NIKOAKERARELEKONREDSSEGIKRLVBAEERHSLENKYKRLJETMERRENRLKDD 720
DB 661 NIKOAKERARELEKONREDSSEGIKRLVBAEERHSLENKYKRLJETMERRENRLKDD 720
QY 721 IOTKSQOIQOMADKILEKREHBAVSAOHLBVLHKKOBYEKEIKVLDNQIKDOLAD 780
DB 721 IOTKSQOIQOMADKILEKREHBAVSAOHLBVLHKKOBYEKEIKVLDNQIKDOLAD 780

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Db      705  IQRKSOQIQQMADKILLEEKHREAOVSAOHLFEVHLQKQEHYBEKKIYVLDNQKXLDAD.764
Qy      781  KELLNNMOHSEBAHKEKGLISROKAMINAMOSKINSLEORIYELSEANKLIANSLSFT 840
Db      765  KELLNNMOHSEBAHKEKGLISROKAMINAMDSKINSLEORIVELSEANKLIANSLSFT 824
Qy      841  QRNNKAQENISSELROQKFYLETOAGKLEAQNRLKEQLEKISHQHSDKXRLLEETRL 900
Db      825  QRNNKAQENISSELROQKFYLETOAGKLEAQNRLKEQLEKISHQHSDKXRLLEETRL 884
Qy      901  REVSLEHEBOKLEIKROLTELQSLQREBSQTLQAARALBSQLEPAKTELEETTAEA 960
Db      885  REVSLEHEBOKLEIKROLTELQSLQREBSQTLQAARALBSQLEPAKTELEETTAEA 944
Qy      961  EEEIQAULTARHDEIQRKFADLRNSCTVITDLEBQNLQTEDNAELNNQNFYLSQLEBAS 1020
Db      945  EEEIQAULTARHDEIQRKFADLRNSCTVITDLEBQNLQTEDNAELNNQNFYLSQLEBAS 1004
Qy      1021  GANDEIVQLRSEVDHLRREITEREMOLTSOKQWEALKTCTMLEBQVMDLEALNDELLE 1080
Db      1005  GANDEIVQLRSEVDHLRREITEREMOLTSOKQWEALKTCTMLEBQVMDLEALNDELLE 1064
Qy      1081  KERQWEAMRSVLDGEKSQFECRVLELOPMLDTEKQSPARADQRTTESRQVVELAVKEHKA 1140
Db      1065  KERQWEAMRSVLDGEKSQFECRVLELOPMLDTEKQSPARADQRTTESRQVVELAVKEHKA 1124
Qy      1141  EITLALQALKEQKKAESLSQKNDLEKKHMLMNNRSLQOKLETREIKORLLEBOAK 1200
Db      1125  EITLALQALKEQKKAESLSQKNDLEKKHMLMNNRSLQOKLETREIKORLLEBOAK 1184
Qy      1201  LQOQMDLOKNHIFELTQLOEALDRADLKTESDLEVOLENIQVLYSHEKVKMEGTISQ 1260
Db      1185  LQOQMDLOKNHIFELTQLOEALDRADLKTESDLEVOLENIQVLYSHEKVKMEGTISQ 1244
Qy      1261  QTKLIDFLQAKMDQPAKKKK-----VPLQVNEKLALKEKARCAELIEEA 1305
Db      1245  QTKLIDFLQAKMDQPAKKKKGLFSRRKEDPALPTQVPLQVNEKLALKEKARCAELIEEA 1304
Qy      1306  LQKTRILRSAREEAARPKATDHPSTPARARQOIMSALVRSPELOPMSLSLAPSS 1365
Db      1305  LQKTRILRSAREEAARPKATDHPSTPARARQOIMSALVRSPELOPMSLSLAPSS 1364
Qy      1366  RRKESSTPEEFSRLKERMHNIPIHRENVGLMNRATCAVCLDTPVHFGROASKLEQCV 1425
Db      1365  RRKESSTPEEFSRLKERMHNIPIHRENVGLMNRATCAVCLDTPVHFGROASKLEQCV 1424
Qy      1426  CHERCSTCLPATCGLPAYATHTFEAFCRDKMNSPGLQTKEPSSSLHLEGMMKVPNNKR 1485
Db      1425  CHERCSTCLPATCGLPAYATHTFEAFCRDKMNSPGLQTKEPSSSLHLEGMMKVPNNKR 1484
Qy      1486  GQOQMDKRYIVLESSKVIYVNEAREAGQRVESFELCLPGDVSIHGAVASLANTAK 1545
Db      1485  GQOQMDKRYIVLESSKVIYVNEAREAGQRVESFELCLPGDVSIHGAVASLANTAK 1544
Qy      1546  ADVPYILKMHESHPTTCWPGRTLYILAFSPDQQRWYATLESVVAAGVSEKKAADAKL 1605
Db      1545  A-----EKKEADAKL 1554
Qy      1606  LGNSLKLKLEGGDRLLDMNCTLPFSDQVVLVTEBGLYALNVKLNSLTHVPGIGAUFQYII 1665
Db      1555  LGNSLKLKLEGGDRLLDMNCTLPFSDQVVLVTEBGLYALNVKLNSLTHVPGIGAUFQYII 1614
Qy      1666  KDLKELMLIAGEBRLCLVDYKVKYQSLAQSHLPAQPIISNITPAVWGCHLFGAKIKEN 1725
Db      1615  KDLKELMLIAGEBRLCLVDYKVKYQSLAQSHLPAQPIISNITPAVWGCHLFGAKIKEN 1674
Qy      1726  GLCTCAMPKSVVILIRYNNENSKYCIRKEITSEPCSCITHNTNSILIGTKFYEIDMKQ 1785
Db      1675  GLCTCAMPKSVVILIRYNNENSKYCIRKEITSEPCSCITHNTNSILIGTKFYEIDMKQ 1734
Qy      1786  YTLKEFLDKNDHSLAPAVFAASNSFPVSIQVNSAGQREBYLLCFHEFGVFDVSYGRS 1845

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Db      1735  YTLKEFLDKNDHSLAPAVFAASNSFPVSIQVNSAGQREBYLLCFHEFGVFDVSYGRS 1794
Qy      1846  RTDDLKMSRLPLAFAYREPYLFTVTHNSLEVIEIQARSSAGTAPARAYLDIPNRYLGPAT 1905
Db      1795  RTDDLKMSRLPLAFAYREPYLFTVTHNSLEVIEIQARSSAGTAPARAYLDIPNRYLGPAT 1854
Qy      1906  SSGAIIYASSYQDKLRYTCCKGMUYKESGTEHHRGSGTSSSNPKGPPTYNHEITRVA 1965
Db      1855  SSGAIIYASSYQDKLRYTCCKGMUYKESGTEHHRGSGTSSSNPKGPPTYNHEITRVA 1914
Qy      1966  SSPAPPEGSPHPEPSTPHRYREGRTELRDKSPGPRLEKSPGRILSTRERSPARLF 2025
Db      1915  SSPAPPEGSPHPEPSTPHRYREGRTELRDKSPGPRLEKSPGRILSTRERSPARLF 1974
Qy      2026  EDSRGRPLPAGAVRTPLSQVNVWDQSS 2053
Db      1975  EDSRGRPLPAGAVRTPLSQVNVKRGQSA 2002

RESULT 11
US-10-757-262-52
; Sequence 52, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicneci, Venkateswarlu
; APPLICANT: Eliasof, Scott D.
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43232, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 185447, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007P1RNNONMIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; PRIOR FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 2053
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-52

Query Match 95.5%; Score 10022.5; DB 16; Length 2053;
Beet Local Similarity 95.7%; Pred. No. 0;
Matches 1979; Conservative 3; Mismatches 5; Indels 81; Gaps 3;

Qy      1  MLKFKYARNPLDGAAPIASRASRLNLFQKGPPTMQQMSPLSRREGILDLFLVLF 60

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Db      1 MLKRYGARNPLDGAEPISASRLNLFPGKAPFPWTQOQMBLSREGILDLFVLE 60
Qy      61 ECGPALMKIKHVSFVRKYSDDTIAELOLPASADFEVRSIVGCGHFAVOVREKATG 120
Db      61 ECGPALMKIKHVSFVRKYSDDTIAELOLPASADFEVRSIVGCGHFAVOVREKATG 120
Qy      121 DIYAMKMKKALLAOQVSPFEERINLSRSTSPWIPOLQYAFODKXHLVYVMEYORG 180
Db      121 DIYAMKMKKALLAOQVSPFEERINLSRSTSPWIPOLQYAFODKXHLVYVMEYORG 180
Qy      181 DLASLARVEDQDENLIFOYLAELILAVHSVHLMGVYHRDIKENTILVDTGHIKLVDF 240
Db      181 DLASLARVEDQDENLIFOYLAELILAVHSVHLMGVYHRDIKENTILVDTGHIKLVDF 240
Qy      241 GSAAKNSNKNVNAKPIGTEDYMAPEVLTVMNGDGKTYGLDGDWMSVGVIAVEMTYGR 300
Db      241 GSAAKNSNKNVNAKPIGTEDYMAPEVLTVMNGDGKTYGLDGDWMSVGVIAVEMTYGR 300
Qy      301 SPFAEGTSATENNINMFORFLKFPDPKYSDDLIOQLCGQKERLKEGICHPFF 360
Db      301 SPFAEGTSATENNINMFORFLKFPDPKYSDDLIOQLCGQKERLKEGICHPFF 360
Qy      361 SKIDMNNIRNSPPFVPTLKSDDTNSPDEBEKNSWSSPCOLSPSGFSGEELPFGFS 420
Db      361 SKIDMNNIRNSPPFVPTLKSDDTNSPDEBEKNSWSSPCOLSPSGFSGEELPFGFS 420
Qy      421 YSKALGILGRSESVVSGIDSPAKTSMEKLLIKSKELQDSQDCHMEQMTLHRVS 480
Db      421 YSKALGILGRSESVVSGIDSPAKTSMEKLLIKSKELQDSQDCHMEQMTLHRVS 480
Qy      481 EYEAVALSOKVEVLEKASFTQSLBODLATYITTECSSLKSLEQARMEVSEDKALQLH 540
Db      481 EYEAVALSOKVEVLEKASFTQSLBODLATYITTECSSLKSLEQARMEVSEDKALQLH 540
Qy      541 DIREOSRKLQIKOEYOAOVEEMRLMNOLEBDLVARRSDIYSELSERSLAAEFK 600
Db      541 DIREOSRKLQIKOEYOAOVEEMRLMNOLEBDLVARRSDIYSELSERSLAAEFK 600
Qy      601 RKAETECOHKLKAKDOQKPEVGEYAKLEKINAEQOLKIOELOELJFAVASTATEBLQ 660
Db      601 RKAETECOHKLKAKDOQKPEVGEYAKLEKINAEQOLKIOELOELJFAVASTATEBLQ 660
Qy      661 NROAKERAERLELEKONREDSSEGIIRKULVEABERHSLBNKYKLETERRENRKLD 720
Db      661 NROAKERAERLELEKONREDSSEGIIRKULVEABERHSLBNKYKLETERRENRKLD 720
Qy      721 IOTKSQOIQOMADKILEBEKHPAOSAOHLEBVLKQKQOHTBEKIKVLDNOIKKDLAD 780
Db      721 IOTKSQOIQOMADKILEBEKHPAOSAOHLEBVLKQKQOHTBEKIKVLDNOIKKDLAD 780
Qy      781 KETLENNMORHEBEAHEKGLISEOKAMINAMDSKIRLEBORIYELSEANKLANSLFT 840
Db      781 KETLENNMORHEBEAHEKGLISEOKAMINAMDSKIRLEBORIYELSEANKLANSLFT 840
Qy      841 ORNMKAQOEEMISELROQKYLETOAGKLEAONRKLBEQLEKISHODSDKNRLELETRL 900
Db      841 ORNMKAQOEEMISELROQKYLETOAGKLEAONRKLBEQLEKISHODSDKNRLELETRL 900
Qy      901 RUTSLEHEBKLEKQLTLOLSLORESQOLNLOAAABAALSQOLROATTELEETTAA 960
Db      901 RUTSLEHEBKLEKQLTLOLSLORESQOLNLOAAABAALSQOLROATTELEETTAA 960
Qy      961 EEBIOLATARDEIORKFDAIRNSCTVITLBEOLNOLTEDNAELNNQNFYLSKOLDEAS 1020
Db      961 EEBIOLATARDEIORKFDAIRNSCTVITLBEOLNOLTEDNAELNNQNFYLSKOLDEAS 1020
Qy      1021 GANDEIVOLRSVVDHLRREITEREMOJTSQKQTEALKTCTMLEBQVMDLEALNDELLE 1080
Db      1021 GANDEIVOLRSVVDHLRREITEREMOJTSQKQTEALKTCTMLEBQVMDLEALNDELLE 1080
Qy      1081 KEROWEAMRSVLDDEKSOFCRCRVELQRMJLDEKQSAARDQRTTESQVVELAVXENKA 1140

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Db      1065 KEROWEAMRSVLDDEKSOFCRCRVELQRMJLDEKQSAARDQRTTESQVVELAVXENKA 1124
Qy      1141 EILALOQALKEQKLAASISDKLNDLEKHAMLENNASLOOKLETTERELKORLLEBOAK 1200
Db      1125 EILALOQALKEQKLAASISDKLNDLEKHAMLENNASLOOKLETTERELKORLLEBOAK 1184
Qy      1201 LOQOMDIQKXHIPLUTGLOEALDRADLLKTERSDELEYOLENIOVLYSHEKVRKEGTSQ 1260
Db      1185 LOQOMDIQKXHIPLUTGLOEALDRADLLKTERSDELEYOLENIOVLYSHEKVRKEGTSQ 1244
Qy      1261 OTKLIDELQAKMDOPAKKKK-----VPLQVNELKUALKEKARCALEBEA 1305
Db      1245 OTKLIDELQAKMDOPAKKKKGLFSRRKEDPALPTQVPLQVNELKUALKEKARCALEBEA 1304
Qy      1306 LQKTRIELRSAREBAARAKATDHPHSTPATARQOIMSAIVRSPEHQPMSMLAPSS 1365
Db      1305 LQKTRIELRSAREBAARAKATDHPHSTPATARQOIMSAIVRSPEHQPMSMLAPSS 1364
Qy      1366 RRKESSTPEEFSSRLKERMHNIIPHRNVGILNRATCAVCLDTVHFGROASKLECOVM 1425
Db      1365 RRKESSTPEEFSSRLKERMHNIIPHRNVGILNRATCAVCLDTVHFGROASKLECOVM 1424
Qy      1426 CHPKCSTCLPATGCLPAEYATHFTEARCRDKMSPGIOTKEPSSSLHEGMMKVPNNKR 1485
Db      1425 CHPKCSTCLPATGCLPAEYATHFTEARCRDKMSPGIOTKEPSSSLHEGMMKVPNNKR 1484
Qy      1486 GQOGMDRKYIVLESGSKYLIYDNEAREAGORPVEFECLCPDGDVSIHGAVASELANTAK 1545
Db      1485 GQOGMDRKYIVLESGSKYLIYDNEAREAGORPVEFECLCPDGDVSIHGAVASELANTAK 1544
Qy      1546 ADVPEYILKMHSHPTTCWPGRTIYLLAPSPFDKQWVTALESVAVAGRVSRKADAKL 1605
Db      1545 A-----EKAEDAKL 1554
Qy      1606 LGNSILKLBGDDRLDMNCTLPFSDQVVLNGBTEBGLYALNKLKSLTHVPGAGFQIYI 1665
Db      1555 LGNSILKLBGDDRLDMNCTLPFSDQVVLNGBTEBGLYALNKLKSLTHVPGAGFQIYI 1614
Qy      1666 KDLKELMIMAGEBALCLVIVKVKVQSLAOSHLPAOPDISPNIPEAVKGCILPAGAKTEN 1725
Db      1615 KDLKELMIMAGEBALCLVIVKVKVQSLAOSHLPAOPDISPNIPEAVKGCILPAGAKTEN 1674
Qy      1726 GLCICAMPKSKVILARNENLSKVCIRKEIETSEPCSCIHFTNYSILIGNKFEYIDMKQ 1785
Db      1675 GLCICAMPKSKVILARNENLSKVCIRKEIETSEPCSCIHFTNYSILIGNKFEYIDMKQ 1734
Qy      1786 YTLBEFLDKNDHSLAPVFAASSNSFPVSIYOVNSAQOREBYLLCFHEFGVFDVSYGRS 1845
Db      1735 YTLBEFLDKNDHSLAPVFAASSNSFPVSIYOVNSAQOREBYLLCFHEFGVFDVSYGRS 1794
Qy      1846 RTDOLKMSRLPLAFAYABEPLFTYHFNLSLEVIEIOARSSAGTPARAYLDIPNRYLGPAT 1905
Db      1795 RTDOLKMSRLPLAFAYABEPLFTYHFNLSLEVIEIOARSSAGTPARAYLDIPNRYLGPAT 1864
Qy      1906 SSGAITYLAASYODKLRYICCKGNLVKESGTEHHRGPSTSRSPNKRGPPTYNEHITRVA 1965
Db      1855 SSGAITYLAASYODKLRYICCKGNLVKESGTEHHRGPSTSRSPNKRGPPTYNEHITRVA 1914
Qy      1966 SSPAPPEGSPHREBPSTPHRYRGRTLELRDKSPGRPLEBKEKSPGRILSTRERSRPLF 2025
Db      1915 SSPAPPEGSPHREBPSTPHRYRGRTLELRDKSPGRPLEBKEKSPGRILSTRERSRPLF 1974
Qy      2026 EDSRGRPLPAGAVRTPLSQVNAKWDOS 2053
Db      1975 EDSRGRPLPAGAVRTPLSQVNAKWDOS 2002

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RESULT 12
US-10-028-946-4
; Sequence 4, Application US/10028946
; Publication No. US20020123622A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan

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; APPLICANT: Miranda, Maricar
; APPLICANT: Fridtjof, Carl Johan
; TITLE OF INVENTION: No. US20020123622A1 Human Kinases and Polynucleotides Encoding
; FILE REFERENCE: Lex -0289-USA
; CURRENT APPLICATION NUMBER: us/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-028-946-4

Query Match      94.5%; Score 9916; DB 13; Length 1958;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  MLKFKYGARNDLPGAAPLPIASRASRLNLFPGCKPPTQOQMSPLSREGILDALFVLFE 60
DB      1  MKFKYGARNDLPGAAPLPIASRASRLNLFPGCKPPTQOQMSPLSREGILDALFVLFE 60
QY      61  ECSQPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVSIVGCGHFAEVQVREKATG 120
DB      61  ECSQPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVSIVGCGHFAEVQVREKATG 120
QY      121  DIYAMVKKKALLAOQVSPFEERNILSRSTSPMIPOLQVAFODKNHLYLWVEYQPG 180
DB      121  DIYAMVKKKALLAOQVSPFEERNILSRSTSPMIPOLQVAFODKNHLYLWVEYQPG 180
QY      181  DLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKRENILVDRTHIKLVDF 240
DB      181  DLSLNRYEDQDENLIQFYLAELILAVSHVLMGVHRDIKRENILVDRTHIKLVDF 240
QY      241  GSAKAKNSNMVNAKLPITGPDYMAPEVLTVMNGDGKTYGLCDWMVGVIAVEMTYGR 300
DB      241  GSAKAKNSNMVNAKLPITGPDYMAPEVLTVMNGDGKTYGLCDWMVGVIAVEMTYGR 300
QY      301  SPBAEGSARTFNINMFORFLKPPDPKYSDFLDLISLGGCKRLLKFEGLCGHPF 360
DB      301  SPBAEGSARTFNINMFORFLKPPDPKYSDFLDLISLGGCKRLLKFEGLCGHPF 360
QY      361  SKIDWNINRNSPPFPYTLKSDDDTSNFDPEKNSWVSSPCQLSPSGFGEELPFVGF 420
DB      361  SKIDWNINRNSPPFPYTLKSDDDTSNFDPEKNSWVSSPCQLSPSGFGEELPFVGF 420
QY      421  YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSODKCHMEQEMTRLHRVS 480
DB      421  YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSODKCHMEQEMTRLHRVS 480
QY      481  EVAVALISQKEVELKASTQSLLEODLATYITTECSSIKRSLQEAQRMVSDQDQALH 540
DB      481  EVAVALISQKEVELKASTQSLLEODLATYITTECSSIKRSLQEAQRMVSDQDQALH 540
QY      541  DIREQSKLOEIKEOEQVAVEMKRLMMNLLEEDIVASARRSDLYESELEESRLAAEFK 600
DB      541  DIREQSKLOEIKEOEQVAVEMKRLMMNLLEEDIVASARRSDLYESELEESRLAAEFK 600
QY      601  RKATECOHKLKAKDQGPVEGYAKLEKINAEQOLKIQELQELKAVASTATETLQ 660
DB      601  RKATECOHKLKAKDQGPVEGYAKLEKINAEQOLKIQELQELKAVASTATETLQ 660
QY      661  NITQAKRARRRELKLONRDSSGRTFKKIYEAERHSLLENKYKRLTETTERENRLK 720
DB      661  NITQAKRARRRELKLONRDSSGRTFKKIYEAERHSLLENKYKRLTETTERENRLK 720
QY      721  IQRSQOIQOAMADKILEBEKREAOVSAOHLVHLKQKQHYEKKIYLDNOIKQDLAD 780
DB      721  IQRSQOIQOAMADKILEBEKREAOVSAOHLVHLKQKQHYEKKIYLDNOIKQDLAD 780
QY      781  KETLENNMQHBEBAHEKGIILSEQKAMINAMDSKIRSLQRIVELSEANKLANSSLFT 840
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DB      781  KETLENNMQHBEBAHEKGIILSEQKAMINAMDSKIRSLQRIVELSEANKLANSSLFT 840
QY      841  QRMKAQEMISLROOKFYLETOACKLEONRKLBEOLKISHODSDKNRLLEETRL 900
DB      841  QRMKAQEMISLROOKFYLETOACKLEONRKLBEOLKISHODSDKNRLLEETRL 900
QY      901  REVSLEHEBOKLEKQLTLELOLSLOERSSQLTALQAAALLESQIRQAKTELEETTA 960
DB      901  REVSLEHEBOKLEKQLTLELOLSLOERSSQLTALQAAALLESQIRQAKTELEETTA 960
QY      961  EEEIOALTARSDIOKRPALRNSCTVITDLEBOLNLTEDNAELNNQNYLSKOIDEAS 1020
DB      961  EEEIOALTARSDIOKRPALRNSCTVITDLEBOLNLTEDNAELNNQNYLSKOIDEAS 1020
QY      1021  GANDEIVOLRSEVDHNRREITEREMOLTSQKQTEALKTTCMLBEOVMDLEALNDELLE 1080
DB      1021  GANDEIVOLRSEVDHNRREITEREMOLTSQKQTEALKTTCMLBEOVMDLEALNDELLE 1080
QY      1081  KERQWEAMRSVLGDEKSOFECEVRBELQRMIDTEKQSRADQRTTESQVVELAVENKA 1140
DB      1081  KERQWEAMRSVLGDEKSOFECEVRBELQRMIDTEKQSRADQRTTESQVVELAVENKA 1140
QY      1141  EILALQOALKEQKLKAESLSDKLNDELKHAMLENNARSLQCKLETREILKORLSEQAK 1200
DB      1141  EILALQOALKEQKLKAESLSDKLNDELKHAMLENNARSLQCKLETREILKORLSEQAK 1200
QY      1201  LQQQMDLQKNHIFRLTQGLQELADRADLKTERTSDLEYOLENIQVLYSHEKVMEGTISQ 1260
DB      1201  LQQQMDLQKNHIFRLTQGLQELADRADLKTERTSDLEYOLENIQVLYSHEKVMEGTISQ 1260
QY      1261  QTKLIDFLQAKMDQPAKKKVPLOYNELKLALKEKARCALEBALQKTRIELRSAREEA 1320
DB      1261  QTKLIDFLQAKMDQPAKKKVPLOYNELKLALKEKARCALEBALQKTRIELRSAREEA 1320
QY      1321  AHRKATDHPSPAPARQOIASALVRSPEHOPASMSLAPSSRKESSTPEESRRL 1380
DB      1321  AHRKATDHPSPAPARQOIASALVRSPEHOPASMSLAPSSRKESSTPEESRRL 1380
QY      1381  KERMHNNIPIHFPVNGINMRATKCAVCLDVTYHFGROASKLEQVMCHPKCSTCLPATCGL 1440
DB      1381  KERMHNNIPIHFPVNGINMRATKCAVCLDVTYHFGROASKLEQVMCHPKCSTCLPATCGL 1440
QY      1441  PAEYATHTBAFCRDYNSPGLQTKEPSSLHLEGMKYPRNNKRGQOQDRKTYLLEGS 1500
DB      1441  PAEYATHTBAFCRDYNSPGLQTKEPSSLHLEGMKYPRNNKRGQOQDRKTYLLEGS 1500
QY      1501  KVLIVNNEAREAGORVVEBELCLPDGVSIHGAVASLANTAKADVPIYILKMEHPHT 1560
DB      1501  KVLIVNNEAREAGORVVEBELCLPDGVSIHGAVASLANTAKADVPIYILKMEHPHT 1560
QY      1561  TCMFGRTLYLAPSPFDKQRMVTALSVVAGGVSRREKADAKLGNLSILKLEGGDRLD 1620
DB      1561  TCMFGRTLYLAPSPFDKQRMVTALSVVAGGVSRREKADAKLGNLSILKLEGGDRLD 1620
QY      1621  MNCTLPFSDQVVLVGTBGLYALNLVKNLSLTHVPGIYAVFOYIYIYDLEKLMIAEBERA 1680
DB      1621  MNCTLPFSDQVVLVGTBGLYALNLVKNLSLTHVPGIYAVFOYIYIYDLEKLMIAEBERA 1680
QY      1681  LCLVYKVKYKQSLAOSHLPADPDISPNIPEAVNGCHLFGAGKLENGLCIQAAPSRVYL 1740
DB      1681  LCLVYKVKYKQSLAOSHLPADPDISPNIPEAVNGCHLFGAGKLENGLCIQAAPSRVYL 1740
QY      1741  RYVENLSKYCIRKEIETSEPCSIHFTNYSILGTNKFHEIDMKQYTLBEFLDKNDHSLA 1800
DB      1741  RYVENLSKYCIRKEIETSEPCSIHFTNYSILGTNKFHEIDMKQYTLBEFLDKNDHSLA 1800
QY      1801  PAVFAASNSFPVSIYQVNASAGREBYLLCFHFGFVDSYGRSRTDILKMSRLPLAFA 1860
DB      1801  PAVFAASNSFPVSIYQVNASAGREBYLLCFHFGFVDSYGRSRTDILKMSRLPLAFA 1860
QY      1861  YREPYLFTVHNSLEBYIELQARSSAGTPARAYLIDINPYLGAATSSGATYLAASSVODKL 1920
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Db 1861 YREPYLFVTHFNLSLEVEIEIQARSSAGTPARAYLIDIPNRYLGPALSSGATYIASSYQDKL 1920
 QY 1921 RVICCKGNLVKESGTEHHRGPSTSR 1945
 Db 1921 RVICCKGNLVKESGTEHHRGPSTSR 1945

RESULT 13
 US-09-964-956-40
 ; Sequence 40, Application US/09964956
 ; Publication No. US20040043926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerlach, Valerie L
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Miller, Isabelle
 ; APPLICANT: Stone, David
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Grose, William M
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Leach, Martin D
 ; APPLICANT: Shukets, Richard A
 ; TITLE OF INVENTION: No. US20040043926A1 Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-124
 ; CURRENT APPLICATION NUMBER: US/09/964,956
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/235,631
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235,633
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235,808
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,064
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,065
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,066
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,135
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 60/237,434
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/238,321
 ; PRIOR FILING DATE: 2000-10-05
 ; PRIOR APPLICATION NUMBER: 60/238,399
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,396
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/276,667
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/294,823
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: 60/304,868
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 40
 ; LENGTH: 1641
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-964-956-40

Query Match 77.8%; Score 8161; DB 11; Length 1641;
 Best Local Similarity 95.7%; Pred. No. 0;
 Matches 1610; Conservative 15; Mismatches 14; Indels 44; Gaps 2;
 QY 374 PVPVTLKSDDTSNFDEPKNSWVSSPCQLSPSGFSGBELPVGFSYKALGILGRSES 433

Db 1 PVPVTLKSDDTSNFDEPKNSWVSSPCQLSPSGFSGBELPVGFSYKALGILGRSES 60
 QY 434 VVSGLDSPAKTSSMEKLLIKSKELQSDQKCHMEQEMTLHRVSEVAVLQKEVEL 493
 Db 61 VVSLDSPAIVSSMEKLLIKSKELQSDQKCHMEQEMTLHRVSEVAVLQKEVEL 120
 QY 494 KASRTQSLLEQDLATYITTCSSLKRSLEQARMEVSOEDDKALQLLHDIHQSRKLQEL 553
 Db 121 KASRTQSLLEQDLATYITTCSSLKRSLEQARMEVSOEDDKALQLLHDIHQSRKLQEL 180
 QY 554 EOEYQAVEEMRLMNNQLEBDLVASARRSDLYESIELRSRLAAEFPRKATECQHKLLKA 613
 Db 181 EOEYQAVEEMRLMNNQLEBDLVASARRSDLYESIELRSRLAAEFPRKATECQHKLLKA 240
 QY 614 KDQKPEVGEYAKLEKINAEQQLKIOELQELQAVASTATELQNIQAKRAEREL 673
 Db 241 KDQKPEVGEYAKLEKINAEQQLKIOELQELQAVASTATELQNIQAKRAEREL 300
 QY 674 EKLQNRDSEGIKRLKLEAERHSHLENKYKRLTEMRERENRLKDIQTKSQOIQWAD 733
 Db 301 EKLQNRDSEGIKRLKLEAERHSHLENKYKRLTEMRERENRLKDIQTKSQOIQWAD 321
 QY 734 KILEEKHREAOVSAGHLEVHLKQEQHYBEKIKVLDNQIKQDLADKETLNNMOHRE 793
 Db 322 ---ELEKHEAOVSAGHLEVHLKQEQHYBEKIKVLDNQIKQDLADKETLNNMOHRE 378
 QY 794 EAHKKGILSEOKMIMAMDSKIRSLRQRYVELSEANKLANSSLTORNMKAQEBMISE 853
 Db 379 EAHKKGILSEOKMIMAMDSKIRSLRQRYVELSEANKLANSSLTORNMKAQEBMISE 438
 QY 854 LRQKPYLETQAGLEAONKRLBEOLBKISHODSDNRLLLETRRLREVSLEBEQKLE 913
 Db 439 LRQKPYLETQAGLEAONKRLBEOLBKISHODSDNRLLLETRRLREVSLEBEQKLE 498
 QY 914 LKQOLTELQSLQREBQTLALQAAALASQLEQATTELETTAAABEIQALTARDE 973
 Db 499 LKQOLTELQSLQREBQTLALQAAALASQLEQATTELETTAAABEIQALTARDE 558
 QY 974 IORFQDALRNSCTYITLLEOLNLTEDNAELNNQNYLSQDLQEAAGANEIQLRSEV 1033
 Db 559 IORFQDALRNSCTYITLLEOLNLTEDNAELNNQNYLSQDLQEAAGANEIQLRSEV 618
 QY 1034 DHLREITEREMQLTSGQOTMEALKTTCTMLEBQVMDLEALNDELLEKEREQMEAMRSVLG 1093
 Db 619 DHLREITEREMQLTSGQOTMEALKTTCTMLEBQVMDLEALNDELLEKEREQMEAMRSVLG 678
 QY 1094 DEKSQFECRVRELQRMIDTEKQSPARADORTTESRQVVELAVKHNKAEIILALQALKEQK 1153
 Db 679 DEKSQFECRVRELQRMIDTEKQSPARADORTTESRQVVELAVKHNKAEIILALQALKEQK 738
 QY 1154 LKAEISLSDKNDLEKRAMLEMANRSIQKLETERELKQRLLEQAKLQOQMDLQKNHIF 1213
 Db 739 LKAEISLSDKNDLEKRAMLEMANRSIQKLETERELKQRLLEQAKLQOQMDLQKNHIF 798
 QY 1214 RLTOGLQDALDRADLKTERTSDLEYOLENIQVLYSHKVKMEGTISQOTKLIDLEQAKMD 1273
 Db 799 RLTOGLQDALDRADLKTERTSDLEYOLENIQVLYSHKVKMEGTISQOTKLIDLEQAKMD 858
 QY 1274 QPAKKKKVPLQYNELKLALBEXAKARCALEBALQKTRIELRSAREBAHRKATDHPHST 1333
 Db 859 QPAKKKKVPLQYNELKLALBEXAKARCALEBALQKTRIELRSAREBAHRKATDHPHST 918
 QY 1334 PATRQOIASATVRSFHHQPSMSSLAPSSRKESSTPEEPRRLKERNNHNIPIRPN 1393
 Db 919 PATRQOIASATVRSFHHQPSMSSLAPSSRKESSTPEEPRRLKERNNHNIPIRPN 978
 QY 1394 VGLNMRATKCAVCLDYHFGROASKLEQVCMCHPKSCSTLPATCGLPAAVATHTFAFC 1453
 Db 979 VGLNMRATKCAVCLDYHFGROASKLEQVCMCHPKSCSTLPATCGLPAAVATHTFAFC 1038
 QY 1454 RDKNSFGLQTKBSSSLHLEGWKKVPRNNKRGQGWDRXYIVLBSKVLTYDNEAPDAG 1513

Db 1039 RDKNNSPGLQSKBESSLHLEGMKVPNNKRGQOQCHDRKTYLESGSKVLIYNBAREAG 1098
Qy 1514 QRPVEEFELCLPDGDSVHIGA VAGASELANAKADVPIYLKXESHPTTCMPGRTLYLLAP 1573
Db 1099 QRPVEEFELCLPDGDSVHIGA VAGASELANAKADVPIYLKXESHPTTCMPGRTLYLLAP 1158
Qy 1574 SFPKQKQWYNALBESVAVAGVRSEKAKADAKLGNLSLLKLBGDRDLDMNCTLPSPDQVYL 1633
Db 1159 SFPKQKQWYNALBESVAVAGVRSEKAKADAKLGNLSLLKLBGDRDLDMNCTLPSPDQVYL 1218
Qy 1634 VGTBEGYALNVLKNSLTHVYGAIVFOIYIILKLEKLMTAGERALLCLVDYKVKQSL 1693
Db 1219 VGTBEGYALNVLKNSLTHVYGAIVFOIYIILKLEKLMTAGERALLCLVDYKVKQSL 1278
Qy 1694 AQSHLPAPQDIPSPNIFPAVKGCHLFGAKILENGLCI CAMPSKVYIIRYENISKCYCIRK 1753
Db 1279 AQSHLPAPQDIPSPNIFPAVKGCHLFGAKILENGLCI CAMPSKVYIIRYENISKCYCIRK 1338
Qy 1754 EIEFSEPCSCIFHTNYSILIGTNKFYEIDMKQYTLDEFLDKNDHSLAPVPAASNSPVP 1813
Db 1339 EIEFSEPCSCIFHTNYSILIGTNKFYEIDMKQYTLDEFLDKNDHSLAPVPAASNSPVP 1398
Qy 1814 SIYOVNAGOREEYLLCFHEGVPVDSYGRSRRTDLMKMSRLPLAFAYREBYLFTVTHFNS 1873
Db 1399 SIYOVNAGOREEYLLCFHEGVPVDSYGRSRRTDLMKMSRLPLAFAYREBYLFTVTHFNS 1458
Qy 1874 LEVIEIGARSSAGTAPAYALDIPNRYLGAIPAISSGAIYLA SYODKLRVICCKNLVKE 1933
Db 1459 LEVIEIGARSSAGTAPAYALDIPNRYLGAIPAISSGAIYLA SYODKLRVICCKNLVKE 1518
Qy 1934 GTEHHRPSTSRSSPNKRGPTTYNEHTTKRVASPAPEGSHRREBTPRY--REGRT 1991
Db 1519 GTEHHRPSTSRSSPNKRGPTTYNEHTTKRVASPAPEGSHRREBTPRY--REGRT 1578
Qy 1992 ELRRDKPPGRLPESEKSPGRILSTRERSPARLFEDESRGRLLPAGAVRTPLSQVNXWMDQ 2051
Db 1579 ELRRDKPPGRLPESEKSPGRILSTRERSPARLFEDESRGRLLPAGAVRTPLSQVNXWMDQ 1638
Qy 2052 SSV 2054
Db 1639 SSV 1641

RESULT 14
US-10-017-216-5
; Sequence 5, Application US/10017216
; Publication No. US20020160483A1
; GENERAL INFORMATION:
; APPLICANT: KABELLER-LIBERMANN, Rosana
; TITLE OF INVENTION: 13245, A No. US20020160483A1e1 Human Myotonic Dystrophy Type Prot
; FILE REFERENCE: 10147-57U1
; CURRENT APPLICATION NUMBER: US/10/017, 216
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/242,429
; PRIOR FILING DATE: 2000-10-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1641
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-017-216-5

Query Match 77.8%; Score 8161; DB 13; Length 1641;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1610; Conservative 15; Mismatches 14; Indels 44; Gaps 2;

Qy 374 PFVPTLKSDDDTSNFDPERKNSWVSSPCQLSPGSGEELPFVGFYSKALGILGRSES 433
Db 1 PFVPTLKSDDDTSNFDPERKNSWVSSPCQLSPGSGEELPFVGFYSKALGILGRSES 60
Qy 434 VVSGLDSPATTSMEKKLLIKSKELQDSQDKCHMEQEMTRLHRRVSEVAVALSQKEVEL 493

Db 61 VVSSLSBPAYVSSMEKKLLIKSKELQDSQDKCHMEQEMTRLHRRVSEVAVALSQKEVEL 120
Qy 494 KASETORSLLEODLATYITECSSLKRSLLEQARNEVSOEDDKALQLHDIREQSRKLOEIK 553
Db 121 KASETORSLLEODLATYITECSSLKRSLLEQARNEVSOEDDKALQLHDIREQSRKLOEIK 180
Qy 554 EOETQAOVEEMRLMNOLEBDLYSARRSDLYSELSRESHLAEBFRKATTECOHKLKA 613
Db 181 EOETQAOVEEMRLMNOLEBDLYSARRSDLYSELSRESHLAEBFRKATTECOHKLKA 240
Qy 614 KDOGKPEVGEYAKLEKINAEOQLKIOELQKLEKAVASTATEATLELONIKQAKERAREL 673
Db 241 KDOGKPEVGEYAKLEKINAEOQLKIOELQKLEKAVASTATEATLELONIKQAKERAREL 300
Qy 674 EKLQNRDSSSEGIKKCLVEABERRHSLNKKRLFTMERRENNLKODIQTKSQOIQOMAD 733
Db 301 EKLQNRDSSSEGIKKCLVEABERRHSLNKKRLFTMERRENNLKODIQTKSQOIQOMAD 321
Qy 734 KIIELEKREAOVSAQHLEVHLKQKQHYEKKIYVLNQIKKDLADKETLBNMQRHEE 793
Db 322 ---ELEKREAOVSAQHLEVHLKQKQHYEKKIYVLNQIKKDLADKETLBNMQRHEE 378
Qy 794 EAEHKGKILSEOKAMINAMDSKIRSLFORIVELSEANKLAANSLFTORNMKAQOEIMISE 853
Db 379 EAEHKGKILSEOKAMINAMDSKIRSLFORIVELSEANKLAANSLFTORNMKAQOEIMISE 438
Qy 854 LRQOKFYLETOAQKLEAONKRLBEOLKISHODSDKNRLLEETRLREVSLEHEQKLE 913
Db 439 LRQOKFYLETOAQKLEAONKRLBEOLKISHODSDKNRLLEETRLREVSLEHEQKLE 498
Qy 914 LKQTLTQLSLOBRSQTLALQAPALLESQURQAKTELEFTTAEBEETIOALTARDE 973
Db 499 LKQTLTQLSLOBRSQTLALQAPALLESQURQAKTELEFTTAEBEETIOALTARDE 558
Qy 974 IORRFPALRNSCTVITDLEBQLNQLTEDNAELNNOFPYLSKQDEASGANDEIVOLRSEV 1033
Db 559 IORRFPALRNSCTVITDLEBQLNQLTEDNAELNNOFPYLSKQDEASGANDEIVOLRSEV 618
Qy 1034 DHLRREITEREMQLTQSOKQTMALKTTCTMLBEQVMDLEALNDELLEKEROEAMRSVLG 1093
Db 619 DHLRREITEREMQLTQSOKQTMALKTTCTMLBEQVMDLEALNDELLEKEROEAMRSVLG 678
Qy 1094 DEKSOFEQCVREIQRMLDTEKOSARADQRTSSRQVVELAVENHAEITLALOALKEOK 1153
Db 679 DEKSOFEQCVREIQRMLDTEKOSARADQRTSSRQVVELAVENHAEITLALOALKEOK 728
Qy 1154 LKAEISLQKLNDELKNGHMLNMMARSLOQLETERELKORLLEEOAKLQOQMDLOKXHF 1213
Db 739 LKAEISLQKLNDELKNGHMLNMMARSLOQLETERELKORLLEEOAKLQOQMDLOKXHF 798
Qy 1214 RLTOGLQEALDRADLKTERTSDLEYOLENIQVLYSHKVMMEGTISQOTGLIDFLQAKMD 1273
Db 799 RLTOGLQEALDRADLKTERTSDLEYOLENIQVLYSHKVMMEGTISQOTGLIDFLQAKMD 858
Qy 1274 QPAAKKKKVPLQVNEKLALKEKARCALEBEALQKTRIELRSAREEAAHKAADHHPST 1333
Db 859 QPAAKKKKVPLQVNEKLALKEKARCALEBEALQKTRIELRSAREEAAHKAADHHPST 918
Qy 1334 PATARQOIAMSAIVRSEPHOPSAMSLAPPSRRKESSTPEERSRKLKERMHNNIPHRFN 1393
Db 919 PATARQOIAMSAIVRSEPHOPSAMSLAPPSRRKESSTPEERSRKLKERMHNNIPHRFN 978
Qy 1394 VGLNMBATKCAVCLDVHFGROASKLECOVMCHPKCSTCLPATCGLPAYATHFTEAFC 1453
Db 979 VGLNMBATKCAVCLDVHFGROASKLECOVMCHPKCSTCLPATCGLPAYATHFTEAFC 1038
Qy 1454 RDKNNSPGLQTKPSSSLHLEGMKVPNNKRGQOQCHDRKTYLESGSKVLIYNBAREAG 1513
Db 1039 RDKNNSPGLQTKPSSSLHLEGMKVPNNKRGQOQCHDRKTYLESGSKVLIYNBAREAG 1098
Qy 1514 QRPVEEFELCLPDGDSVHIGA VAGASELANAKADVPIYLKXESHPTTCMPGRTLYLLAP 1573

Db 1099 QRPVEEPELCPDDDSIHGAVGASELANTAKADVPIILKMHSHPTTCMPGRILYLLAP 1158
 QY 1574 SPFDKQWMTALLESVAVGAVRSREKAEADAKLGNLSLKJEGDDRLDMNCTLPSPDQVYL 1633
 Db 1159 SFPDKQWMTALLESVAVGAVRSREKAEADAKLGNLSLKJEGDDRLDMNCTLPSPDQVYL 1218
 QY 1634 VGTGEGYALNVLKNSLTHVPGICAVPOIYIILKLEKMLMAGEBRALCLVDYKKVQSL 1633
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 Db 1279 AQSHLPAPDISPNIFFAVKGCGLFGAGKIENGCLCIAMPSKVYILRYNENLSKYCIRK 1338
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 QY 1814 SIYQVNSAGQREBYLLCFHEGCVFVDSYGRSRITDDLKWSHPLAFAYREYILFVTHFNS 1873
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 QY 2052 SSV 2054
 Db 1639 SSV 1641

RESULT 15

US-09-964-956-41
 ; Sequence 41, Application US/09964956
 ; Publication No. US20040043926A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gerlach, Valerie L
 ; APPLICANT: MacDougall, John R
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Miller, Isabelle
 ; APPLICANT: Stone, David
 ; APPLICANT: Gunther, Erik
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Groesse, William M
 ; APPLICANT: Alsobrook II, John P
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Leach, Martin D
 ; APPLICANT: Shimkets, Richard A
 ; TITLE OF INVENTION: No. US20040043926A1el Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-124
 ; CURRENT APPLICATION NUMBER: US/09/964,956
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/235,631
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235,633
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/235,808
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,064
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 ; PRIOR APPLICATION NUMBER: 60/236,065

; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,066
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,135
 ; PRIOR FILING DATE: 2000-09-28
 ; PRIOR APPLICATION NUMBER: 60/237,434
 ; PRIOR FILING DATE: 2000-10-03
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 ; PRIOR APPLICATION NUMBER: 60/238,399
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/238,396
 ; PRIOR FILING DATE: 2000-10-06
 ; PRIOR APPLICATION NUMBER: 60/276,667
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/294,823
 ; PRIOR FILING DATE: 2001-05-31
 ; PRIOR APPLICATION NUMBER: 60/304,868
 ; PRIOR FILING DATE: 2001-07-12
 ; NUMBER OF SEQ ID NOS: 127
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 41
 ; LENGTH: 1597
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-964-956-41

Query Match 75.6%; Score 7935; DB 11; Length 1597;

Best Local Similarity 98.2%; Pred. No. 0; Matches 1561; Conservative 16; Mismatches 10; Indels 2; Gaps 1;

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 QY 528 VSQEDDYALQLHDIREQSRKLOEIKQOYQAOVEERLMMNQLBEDLVARRRSDLYES 587
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Qy 1128 RQVELLAVKEHKAIIIALQALKEQKLKASLSKDLNDEKHAMLENNARSLOQKLETE 1187

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Db 909 KESTPEEFSSRLKERHNNIPIHFNVLNMRATKCAVCLDTVHFGROASKLECOVMCH 968

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Qy 1488 QGMDRKTYIVLEGSFVLYDNEAREAGORPVEFELCLPDGVSIHGAVGASELANTAKAD 1547

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Qy 1668 LEKLMITAGEERALCLVDVKKVKOSLAQSHLPAQPDISPNIIEAVKGCCHLFGAGKIENGL 1727

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Qy 1848 DDLKMSRLPLAFAYREPYLPVTHFNSLLEVIIEIQARSSAGTPARAYLDIPNRYLGAIISS 1907

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Qy 1908 GATYLAASYQDKLAVITCKGKLVKESGTEHHRGSTSRSSPNKRGPTNYNEHTKRYASS 1967

Db 1449 GATYLAASYQDKLAVITCKGKLVKESGTEHHRGSTSRSSPNKRGPTNYNEHTKRYASS 1508

Qy 1968 PAPPEGSHPREPSTPHRY--REGRETLRDKSPGRPLEREKSPGRILISTRERSPARLF 2025

Db 1509 PAPPEGSHPREPSTPHRYRDRERTELRDKSPGRPLEREKSPGRILISTRERSPARLF 1568

Qy 2026 EDSGRGLPAGAVRTPLSQVNVKWDQSSV 2054

Db 1569 EDSGRGLPAGAVRTPLSQVNVKWDQSSV 1597

Search completed: May 11, 2005, 17:00:24
Job time : 215 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2005, 16:33:19 ; Search time 56 Seconds
(Without Alignments)
2738.021 Million cell updates/sec

Title: US-10-791-666-2
Perfect score: 10493
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCUTS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	10493	100.0	2054	US-10-028-946-2	Sequence 2, Appli
2	9916	94.5	1958	US-10-028-946-4	Sequence 4, Appli
3	2440	23.3	497	US-09-804-471A-2	Sequence 2, Appli
4	2440	20.7	497	US-10-238-709-2	Sequence 2, Appli
5	2175.5	20.7	494	US-09-804-471A-4	Sequence 4, Appli
6	2175.5	20.7	494	US-10-238-709-4	Sequence 4, Appli
7	1287	12.3	257	US-09-916-204-2	Sequence 2, Appli
8	1287	12.3	257	US-10-282-048-2	Sequence 2, Appli
9	1263.5	12.0	1384	US-08-685-576-1	Sequence 1, Appli
10	1260	12.0	1354	US-08-685-576-2	Sequence 1, Appli
11	1257	12.0	1388	US-08-685-576-4	Sequence 4, Appli
12	1257	12.0	1388	US-09-976-594-296	Sequence 286, App
13	1183	11.3	251	US-09-916-204-4	Sequence 4, Appli
14	1183	11.3	251	US-10-282-048-4	Sequence 4, Appli
15	1180	11.2	251	US-09-916-204-5	Sequence 5, Appli
16	1180	11.2	251	US-09-916-204-6	Sequence 6, Appli
17	1180	11.2	251	US-10-282-048-5	Sequence 5, Appli
18	1180	11.2	251	US-10-282-048-6	Sequence 6, Appli
19	1048.5	10.0	900	US-08-630-822A-62	Sequence 62, Appli
20	1048.5	10.0	900	US-09-005-069-62	Sequence 62, Appli
21	1048.5	10.0	900	US-09-171-156A-21	Sequence 21, Appli
22	1048.5	10.0	900	US-09-004-730A-21	Sequence 21, Appli
23	1048.5	10.0	900	US-08-981-799A-21	Sequence 21, Appli
24	906.5	8.6	509	US-09-949-016-8511	Sequence 8511, Ap
25	857.5	8.2	420	US-08-685-871-58	Sequence 58, Appli
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28	840.5	8.0	420	3	US-08-685-871-59	Sequence 59, Appli
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35	701	6.7	526	3	US-09-442-100-12	Sequence 12, Appli
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39	683	6.5	404	2	US-08-860-150-3	Sequence 3, Appli
40	683	6.5	404	3	US-09-338-132-3	Sequence 3, Appli
41	677	6.5	464	2	US-08-878-989-4	Sequence 4, Appli
42	674.5	6.4	464	3	US-09-272-796-4	Sequence 4, Appli
43	674.5	6.4	465	2	US-08-878-989-18	Sequence 18, Appli
44	674.5	6.4	465	2	US-08-860-150-7	Sequence 7, Appli
45	674.5	6.4	465	3	US-09-338-132-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-10-028-946-2
; Sequence 2, Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Carl Ushan
; TITLE OF INVENTION: No. 6734009e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 2054
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-2

Query Match	100.0%;	Score 10493;	DB 4;	Length 2054;
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DB	1	MLKFKYGARNPIDGAAEPIASRASRLNLFQCKPPTMOQMSPLSREGILDALFVLF60		
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DB	61	ECSPALMKIKHSNFFVKYSDTIAEQELQPSAKDFEVSIVGCGHFAEYVVRKATG120		
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DB	241	GSAAKNSNKNVNAKLPITGPDYVAPFVLTVNMGDKGTGGLDCDMSVGVIAYEMTYGR300		
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D 421 YSKRALGILGSEBSVSLDSPAKTSSMEKLLIISKRLQDSQDCHMEQEMTLHRVS 480
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QY 1741 RYNNENISKYICIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLBEFLDKNDHSLA 1800
D 1741 RYNNENISKYICIRKEIETSEPCSCIHFTNYSILIGTNKFYEIDMKQYTLBEFLDKNDHSLA 1800
QY 1801 PAYPAASNSFPVSIYOVNAGQREBYLCEHBFQVVDYGRSRRTDLKMSRLPLAFA 1860
D 1801 PAYPAASNSFPVSIYOVNAGQREBYLCEHBFQVVDYGRSRRTDLKMSRLPLAFA 1860
QY 1861 YREBYLFTVHPNSLEVEIQARSSAGTPARAYLDIPRRLGLRALSGLAYLASSYQDK 1920
D 1861 YREBYLFTVHPNSLEVEIQARSSAGTPARAYLDIPRRLGLRALSGLAYLASSYQDK 1920
QY 1921 RVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPTTYNEHITKRVASSAPDEGSHPREP 1980
D 1921 RVICCKGNLVKESGTEHHRGPSTSRSSPNKRGPTTYNEHITKRVASSAPDEGSHPREP 1980
QY 1981 STPHRYAEGRTLRDQSPRPLERKSPGRILSTRERSPARLFEBSRGRPLAGAVRT 2040
D 1981 STPHRYAEGRTLRDQSPRPLERKSPGRILSTRERSPARLFEBSRGRPLAGAVRT 2040
QY 2041 PLSQVNMVMOSSV 2054
D 2041 PLSQVNMVMOSSV 2054

RESULT 2
US-10-028-946-4
; Sequence 4, Application US/10028946
; Patent No. 6734009
; GENERAL INFORMATION:
; APPLICANT: Yu, Xuanchuan
; APPLICANT: Miranda, Mariacar
; APPLICANT: Fridde, Carl Johan
; TITLE OF INVENTION: No. 6734009e1 Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0289-USA
; CURRENT APPLICATION NUMBER: US/10/028,946
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/258,335
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1958
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-028-946-4

Query Match 94.5%; Score 9916; DB 4; Length 1958;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNDLDAAGAEPIASRASRLNLFQGKPPMTQOQNSPLSRBGILDLALFVLFE 60
D 1 MLKFKYGARNDLDAAGAEPIASRASRLNLFQGKPPMTQOQNSPLSRBGILDLALFVLFE 60

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QY	61	EC	SOPALMKITKIVSVNFVKY	SOTTAELQELQSPAKD	FEVRSIVGCGHFAEVOVREKATG	120		
Db	61	EC	SOPALMKIKIVSVNFVKY	SDTIAELQELQSPAKD	FEVRSIVGCGHFAEVOVREKATG	120		
QY	121	DI	YAKWMMKKLLAQEOVS	FFEEBENITLSRSTSPMI	POLOQAFOQKHLIYLMEQPOG	180		
Db	121	DI	YAKWMMKKLLAQEOVS	FFEEBENITLSRSTSPMI	POLOQAFOQKHLIYLMEQPOG	180		
QY	181	DL	SLSTRNREYDQDENL	IQFYLAELIAVSHVLMQYVRDI	KPEVILVDRGHTGLVDF	240		
Db	181	DL	SLSTRNREYDQDENL	IQFYLAELIAVSHVLMQYVRDI	KPEVILVDRGHTGLVDF	240		
QY	241	GSA	AKNSNKNVNAKLP	IGTDPYMAEVLTVNMGDKGTGY	GLDCDMSVGVIAYEMTYGR	300		
Db	241	GSA	AKNSNKNVNAKLP	IGTDPYMAEVLTVNMGDKGTGY	GLDCDMSVGVIAYEMTYGR	300		
QY	301	SP	FACTSARTTNNTMNF	ORFLKFPDDPKVSSDFLDL	IOSLLCGQERUKFPGLCCHPF	360		
Db	301	SP	FACTSARTTNNTMNF	ORFLKFPDDPKVSSDFLDL	IOSLLCGQERUKFPGLCCHPF	360		
QY	361	SK	IDNNNRNSPPVP	PTLKSDDDTSNPEBKNMSVSS	PCOLSPSGSGEELPPVGS	420		
Db	361	SK	IDNNNRNSPPVP	PTLKSDDDTSNPEBKNMSVSS	PCOLSPSGSGEELPPVGS	420		
QY	421	YS	KALGILGRSBSV	SGLDSPAKTSMEKKLI	IKSKEILOSDQDKCHMQEWTPLHRRVS	480		
Db	421	YS	KALGILGRSBSV	SGLDSPAKTSMEKKLI	IKSKEILOSDQDKCHMQEWTPLHRRVS	480		
QY	481	EVE	AVLSQKEVELKAS	SETORSILLEODLATYIT	TECSSLRKSLQAEWVSQEDKALQLLH	540		
Db	481	EVE	AVLSQKEVELKAS	SETORSILLEODLATYIT	TECSSLRKSLQAEWVSQEDKALQLLH	540		
QY	541	DI	RESRKLOETKEBOYA	QVEEMLMNQLEEDV	VSARRSDLYESERRESLAAEERK	600		
Db	541	DI	RESRKLOETKEBOYA	QVEEMLMNQLEEDV	VSARRSDLYESERRESLAAEERK	600		
QY	601	RK	ATECOHKLIAKXQ	QKPEVGEYAKLEKINA	EQOLQIOLQEOLEKIAKVA	STEAATELLQ	660	
Db	601	RK	ATECOHKLIAKXQ	QKPEVGEYAKLEKINA	EQOLQIOLQEOLEKIAKVA	STEAATELLQ	660	
QY	661	NI	ROKKEAERLEKLO	NREDSSEGI	RKKLVAEERPRHSL	ENKVRLFTMERRENRLKOD	720	
Db	661	NI	ROKKEAERLEKLO	NREDSSEGI	RKKLVAEERPRHSL	ENKVRLFTMERRENRLKOD	720	
QY	721	IOTS	SOQIQOAMADK	LELEEKREAOVSAOHL	EVHLKQEQHYEERIKY	LDNQIKDOLAD	780	
Db	721	IOTS	SOQIQOAMADK	LELEEKREAOVSAOHL	EVHLKQEQHYEERIKY	LDNQIKDOLAD	780	
QY	781	KET	LENMQORHEEAEH	EGKILSEQKAMIN	AMDSKIRSL	IEORIVELSEANKLA	ANSSLFT	840
Db	781	KET	LENMQORHEEAEH	EGKILSEQKAMIN	AMDSKIRSL	IEORIVELSEANKLA	ANSSLFT	840
QY	841	Q	RNMKAQEMISEL	RQKFYLETOAGKLEA	QNRKLEBQLEKISHQD	HSQKXRLLELFRLL	900	
Db	841	Q	RNMKAQEMISEL	RQKFYLETOAGKLEA	QNRKLEBQLEKISHQD	HSQKXRLLELFRLL	900	
QY	901	REV	SLHEEQKLEKRL	TELOSTIQERESQ	LTALQAA	RAALESQOLRAKTELETTABA	960	
Db	901	REV	SLHEEQKLEKRL	TELOSTIQERESQ	LTALQAA	RAALESQOLRAKTELETTABA	960	
QY	961	EE	EOALTAHDEI	ORFKFDALRNSCTV	ITDLEBQNLTEB	AEALNNQNFYLSKOLDAS	1020	
Db	961	EE	EOALTAHDEI	ORFKFDALRNSCTV	ITDLEBQNLTEB	AEALNNQNFYLSKOLDAS	1020	
QY	1021	GAN	DEIVOLRSEVDH	LREITEREMQ	LTOSQOTMEAL	KTTCTMLEBQVMDLEALNDELLE	1080	
Db	1021	GAN	DEIVOLRSEVDH	LREITEREMQ	LTOSQOTMEAL	KTTCTMLEBQVMDLEALNDELLE	1080	
QY	1081	KE	ROWEARSV	VLGDEKSO	FEGRVRELQ	MLDTEKOSRAPADORT	IESQVVELAYEKHA	1140
Db	1081	KE	ROWEARSV	VLGDEKSO	FEGRVRELQ	MLDTEKOSRAPADORT	IESQVVELAYEKHA	1140

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QY      1141  ETLLAQALTKQKLAESLSDKUNDEKHAMLENNARSLOOKLETREBELKORLLEBOAK  1200
Db      1141  ETLLAQALTKQKLAESLSDKUNDEKHAMLENNARSLOOKLETREBELKORLLEBOAK  1200
QY      1201  LOOQMDLOKNHIFRLTQGLQELADPADLTKTERSDLEQLENTIOVLVSHEKVKMEGTISQ  1266
Db      1201  LOOQMDLOKNHIFRLTQGLQELADPADLTKTERSDLEQLENTIOVLVSHEKVKMEGTISQ  1266
QY      1261  QTKLIDFLQAKMDOPAKKKKVPLOQYNELKALBEKKAQAELEALQKTRIELNSAREEA  1320
Db      1261  QTKLIDFLQAKMDOPAKKKKVPLOQYNELKALBEKKAQAELEALQKTRIELNSAREEA  1320
QY      1321  AHRKATDHPHSTPATPAQAQIAMSAYNSPEHOSANS LAPPESSRKESTPEEFSSRL  1380
Db      1321  AHRKATDHPHSTPATPAQAQIAMSAYNSPEHOSANS LAPPESSRKESTPEEFSSRL  1380
QY      1381  KERMHNNI PPHFNGGLNMRATKCAVCLDTYHFGQASCLCEQWCHPKCSTCLPATCGL  1440
Db      1381  KERMHNNI PPHFNGGLNMRATKCAVCLDTYHFGQASCLCEQWCHPKCSTCLPATCGL  1440
QY      1441  PAEYATHTTEAFPCRDKNMSPELQTKPESSSLHLEGGMMVPANNRRGOOGMDRKITYLEGS  1500
Db      1441  PAEYATHTTEAFPCRDKNMSPELQTKPESSSLHLEGGMMVPANNRRGOOGMDRKITYLEGS  1500
QY      1501  KVL IYDNEARABAGORPVEEFELCLPDGDVS IHGAVGASELANATAKADVPYILKMEHSPT  1560
Db      1501  KVL IYDNEARABAGORPVEEFELCLPDGDVS IHGAVGASELANATAKADVPYILKMEHSPT  1560
QY      1561  TCWPERTIYLLAPSPFDKQWVWTALLESVYAGGRVSRKAEADACLGNLSLKEGGDRLD  1620
Db      1561  TCWPERTIYLLAPSPFDKQWVWTALLESVYAGGRVSRKAEADACLGNLSLKEGGDRLD  1620
QY      1621  MNCTLPFSDOVVLVGTREGLYALNVLKSLTFHVIGIGAFQIYIYIKOLEKMLTAGEBRA  1680
Db      1621  MNCTLPFSDOVVLVGTREGLYALNVLKSLTFHVIGIGAFQIYIYIKOLEKMLTAGEBRA  1680
QY      1681  LCLVDVKKVKQSLAQSHLPAQPDISPNIPEAVKGCGLFGAGKIEINGCLICAMPSKVYIL  1740
Db      1681  LCLVDVKKVKQSLAQSHLPAQPDISPNIPEAVKGCGLFGAGKIEINGCLICAMPSKVYIL  1740
QY      1741  RYNNELSKYCIKRKIETSEPCSHFTNYSILIGTNKFYEIDMQOYTLLEFLDKNDHSLA  1800
Db      1741  RYNNELSKYCIKRKIETSEPCSHFTNYSILIGTNKFYEIDMQOYTLLEFLDKNDHSLA  1800
QY      1801  PAVFAASNSFPVSIYOVNSAGOREEYLLCFHERGCVVDVSGRRSRTDILKWSRLPLAFA  1860
Db      1801  PAVFAASNSFPVSIYOVNSAGOREEYLLCFHERGCVVDVSGRRSRTDILKWSRLPLAFA  1860
QY      1861  YREBYLFTYTHNSLEVEIEIQARSSAGTPAAYLIDIPNRYLGPALISSGAIYLASSYODKL  1920
Db      1861  YREBYLFTYTHNSLEVEIEIQARSSAGTPAAYLIDIPNRYLGPALISSGAIYLASSYODKL  1920
QY      1921  RVICCKGNLVKESGTEHHRGPSTSR  1945
Db      1921  RVICCKGNLVKESGTEHHRGPSTSR  1945

RESULT 3
US-09-804-471A-2
; Sequence 2, Application US/09804471A
; Patent No. 6479269
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al]
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001164
; CURRENT APPLICATION NUMBER: US/09/804,471A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 497

```

TYPE: PRT
ORGANISM: Human
US-09-804-471A-2

Query Match 23.3%; Score 2440; DB 4; Length 497;
Best Local Similarity 99.6%; Pred. No. 1,1e-118;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNDLGAAPLPIASRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60
DB 1 MLKFKYGARNDLGAAPLPIASRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60
QY 61 ECGSPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVSILVCGGFAEVQVVERKATG 120
DB 61 ECGSPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVSILVCGGFAEVQVVERKATG 120
QY 121 DIYAMKVMKKKALLAOQVVSFFEEERNILSRSTSPMIPOQYAFODKNHLYLWMEYOPGG 180
DB 121 DIYAMKVMKKKALLAOQVVSFFEEERNILSRSTSPMIPOQYAFODKNHLYLWMEYOPGG 180
QY 181 DLISLNRVEDQDENLQFYLAELILAVSHVLMGVHRDIPENILVDRTHIKLVDF 240
DB 181 DLISLNRVEDQDENLQFYLAELILAVSHVLMGVHRDIPENILVDRTHIKLVDF 240
QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMSVGVIAVEM1YGR 300
DB 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMSVGVIAVEM1YGR 300
QY 301 SPFAEGTSARTFNINNFQRLKFPDDPKVSDPLDLOSLLCGQKRLKFEGLCCHPFF 360
DB 301 SPFAEGTSARTFNINNFQRLKFPDDPKVSDPLDLOSLLCGQKRLKFEGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 420
DB 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSQDKCHK 468
DB 421 YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSQDKCHK 468

RESULT 4
US-10-238-709-2
Sequence 2, Application US/10238709
Patent No. 6680188
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: C0001164DI
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 497
TYPE: PRT
ORGANISM: Human
US-10-238-709-2

Query Match 23.3%; Score 2440; DB 4; Length 497;
Best Local Similarity 99.6%; Pred. No. 1,1e-118;
Matches 466; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLKFKYGARNDLGAAPLPIASRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60
DB 1 MLKFKYGARNDLGAAPLPIASRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60
QY 61 ECGSPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVSILVCGGFAEVQVVERKATG 120
DB 61 ECGSPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVSILVCGGFAEVQVVERKATG 120

QY 121 DIYAMKVMKKKALLAOQVVSFFEEERNILSRSTSPMIPOQYAFODKNHLYLWMEYOPGG 180
DB 121 DIYAMKVMKKKALLAOQVVSFFEEERNILSRSTSPMIPOQYAFODKNHLYLWMEYOPGG 180
QY 181 DLISLNRVEDQDENLQFYLAELILAVSHVLMGVHRDIPENILVDRTHIKLVDF 240
DB 181 DLISLNRVEDQDENLQFYLAELILAVSHVLMGVHRDIPENILVDRTHIKLVDF 240
QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMSVGVIAVEM1YGR 300
DB 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMSVGVIAVEM1YGR 300
QY 301 SPFAEGTSARTFNINNFQRLKFPDDPKVSDPLDLOSLLCGQKRLKFEGLCCHPFF 360
DB 301 SPFAEGTSARTFNINNFQRLKFPDDPKVSDPLDLOSLLCGQKRLKFEGLCCHPFF 360
QY 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 420
DB 361 SKIDMNNIRNSPPFPVTLKSDDDTSNFDPEKNSWSSPCQSPSGFSGEELPFVGF 420
QY 421 YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSQDKCHK 468
DB 421 YSKALGILGRSESVSGLDSPAKTSMKKLLIKSKELQDSQDKCHK 468

RESULT 5
US-09-804-471A-4
Sequence 4, Application US/09804471A
Patent No. 6479269
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: C0001164
CURRENT APPLICATION NUMBER: US/09/804,471A
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 494
TYPE: PRT
ORGANISM: Mus Musculus
US-09-804-471A-4

Query Match 20.7%; Score 2175.5; DB 4; Length 494;
Best Local Similarity 88.2%; Pred. No. 5,2e-105;
Matches 413; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

QY 1 MLKFKYGARNDLGAAPLPIASRASRLNLFQGGKPPMTQQQMSPLSREGILDALFVLFE 60
DB 1 MLKFKYGVNRPPASASEPIASRASRLNLFQGGKPPMTQQQMSALSREGILDALFVLFE 60
QY 61 ECGSPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVSILVCGGFAEVQVVERKATG 120
DB 61 ECGSPALMKIKHVSNFVRKYSDDTIAELQELQPSAKDFEVSILVCGGFAEVQVVERKATG 120
QY 121 DIYAMKVMKKKALLAOQVVSFFEEERNILSRSTSPMIPOQYAFODKNHLYLWMEYOPGG 180
DB 121 DIYAMKVMKKKALLAOQVVSFFEEERNILSRSTSPMIPOQYAFODKNHLYLWMEYOPGG 180
QY 181 DLISLNRVEDQDENLQFYLAELILAVSHVLMGVHRDIPENILVDRTHIKLVDF 240
DB 181 DLISLNRVEDQDENLQFYLAELILAVSHVLMGVHRDIPENILVDRTHIKLVDF 240
QY 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMSVGVIAVEM1YGR 300
DB 241 GSAAKNSNMVNAKLPIGTPDYMAPEVLTVMNGDGKTYGLDCDMSVGVIAVEM1YGR 300
QY 301 SPFAEGTSARTFNINNFQRLKFPDDPKVSDPLDLOSLLCGQKRLKFEGLCCHPFF 360
DB 301 SPFAEGTSARTFNINNFQRLKFPDDPKVSDPLDLOSLLCGQKRLKFEGLCCHPFF 360

Qy 361 SKIDMNNIRNSPPFPVPTLKSDDDTNSNDEPKNSWSSPCQLSPSGSGEELPFVGF 420
Db 360 ARTMNNIRNSPPFPVPTLKSDDDTNSNDEPKNSWSSPCQLSPSGSGEELPFVGF 419
Qy 421 YSKALGILGRSESVVSGIDSPAKTSMEKLLIKSKELQSDQCKHKM 468
Db 420 YSKALGILGRSESVVSGIDSPAKTSMEKLLIKSKELQSDQCKHKM 467

RESULT 6

US-10-238-709-4
Sequence 4, Application US/10238709
Patent No. 6680188
GENERAL INFORMATION:
APPLICANT: WEBSTER, Marion et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: C001164D1V
CURRENT APPLICATION NUMBER: US/10/238,709
CURRENT FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 494
TYPE: PRT
ORGANISM: Mus Musculus
US-10-238-709-4

Query Match 20.7%; Score 2175.5; DB 4; Length 494;

Best Local Similarity 88.2%; Pred. No. 5.2e-105; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MLKFKYGARNPLDGAAPLIRASRLNLFQGGKPPMTQOQMSPLSREGILDLFVLFE 60
Db 1 MLKFKYGARNPLDGAAPLIRASRLNLFQGGKPPMTQOQMSPLSREGILDLFVLFE 60
Qy 61 ECSQPALMKIKHVSNFVRKTSYDTIAELOPSAKDFEVRSLVCGHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKTSYDTIAELOPSAKDFEVRSLVCGHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKKALLAQOVSFEEERNILSRSTSPWIPQIYAFQDKNHLVLYMEYOPGG 180
Db 121 DIYAMKVMKKKALLAQOVSFEEERNILSRSTSPWIPQIYAFQDKNHLVLYMEYOPGG 180
Qy 181 DLSLRLRYEDQDENLQIYLAELILAVSHVHMGVYHVDIKENILVDTGHIKLVDF 240
Db 181 DLSLRLRYEDQDENLQIYLAELILAVSHVHMGVYHVDIKENILVDTGHIKLVDF 240
Qy 241 GSAAKNNSKKNVAKLPIGTEDYNAPEVLTVMNGDGKGTGJLDCDMSVGVAYEMITGR 300
Db 241 GSAAKNNSKKNVAKLPIGTEDYNAPEVLTVMNGDGKGTGJLDCDMSVGVAYEMITGR 299
Qy 301 SPFAEGTSARTENNINMFORFLKFPDDPKVSSDFDLIQLSLCGQKRLKEGLCCHPF 360
Db 300 TPFTGTSARTENNINMFORFLKFPDDPKVSSDFDLIQLSLCGQKRLKEGLCCHPF 359
Qy 361 SKIDMNNIRNSPPFPVPTLKSDDDTNSNDEPKNSWSSPCQLSPSGSGEELPFVGF 420
Db 360 ARTMNNIRNSPPFPVPTLKSDDDTNSNDEPKNSWSSPCQLSPSGSGEELPFVGF 419
Qy 421 YSKALGILGRSESVVSGIDSPAKTSMEKLLIKSKELQSDQCKHKM 468
Db 420 YSKALGILGRSESVVSGIDSPAKTSMEKLLIKSKELQSDQCKHKM 467

RESULT 7

US-09-916-204-2
Sequence 2, Application US/09916204
Patent No. 6638745
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

;; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;; FILE REFERENCE: THEREOF
;; FILE REFERENCE: C001164C1P
;; CURRENT APPLICATION NUMBER: US/09/916,204
;; CURRENT FILING DATE: 2001-07-24
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 2
;; LENGTH: 257
;; TYPE: PRT
;; ORGANISM: Human
US-09-916-204-2

Query Match 12.3%; Score 1287; DB 4; Length 257;

Best Local Similarity 100.0%; Pred. No. 2.1e-59; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDGAAPLIRASRLNLFQGGKPPMTQOQMSPLSREGILDLFVLFE 60
Db 1 MLKFKYGARNPLDGAAPLIRASRLNLFQGGKPPMTQOQMSPLSREGILDLFVLFE 60
Qy 61 ECSQPALMKIKHVSNFVRKTSYDTIAELOPSAKDFEVRSLVCGHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKTSYDTIAELOPSAKDFEVRSLVCGHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKKALLAQOVSFEEERNILSRSTSPWIPQIYAFQDKNHLVLYMEYOPGG 180
Db 121 DIYAMKVMKKKALLAQOVSFEEERNILSRSTSPWIPQIYAFQDKNHLVLYMEYOPGG 180
Qy 181 DLSLRLRYEDQDENLQIYLAELILAVSHVHMGVYHVDIKENILVDTGHIKLVDF 240
Db 181 DLSLRLRYEDQDENLQIYLAELILAVSHVHMGVYHVDIKENILVDTGHIKLVDF 240
Qy 241 GSAAKNNSKKNV 252
Db 241 GSAAKNNSKKNV 252

RESULT 8

US-10-282-048-2
Sequence 2, Application US/10282048
Patent No. 6692948
GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: C001164C1P-D1V
CURRENT APPLICATION NUMBER: US/10/282,048
CURRENT FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 257
TYPE: PRT
ORGANISM: Human
US-10-282-048-2

Query Match 12.3%; Score 1287; DB 4; Length 257;

Best Local Similarity 100.0%; Pred. No. 2.1e-59; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLKFKYGARNPLDGAAPLIRASRLNLFQGGKPPMTQOQMSPLSREGILDLFVLFE 60
Db 1 MLKFKYGARNPLDGAAPLIRASRLNLFQGGKPPMTQOQMSPLSREGILDLFVLFE 60
Qy 61 ECSQPALMKIKHVSNFVRKTSYDTIAELOPSAKDFEVRSLVCGHFAEVQVVRKATG 120
Db 61 ECSQPALMKIKHVSNFVRKTSYDTIAELOPSAKDFEVRSLVCGHFAEVQVVRKATG 120
Qy 121 DIYAMKVMKKKALLAQOVSFEEERNILSRSTSPWIPQIYAFQDKNHLVLYMEYOPGG 180
Db 121 DIYAMKVMKKKALLAQOVSFEEERNILSRSTSPWIPQIYAFQDKNHLVLYMEYOPGG 180

QY 1152 OKTAEISLDTKNDLEKKHMLMNNARSLOQKLETERELKOLLEBOAKLOQONDLOKXH 1211
Db 1028 RFLTKQAVNKLAETINRKEPVKRGNDTVRRKREKRLHMLKSEREKLTOQM----- 1081
QY 1212 IFRLTQGLQALDRADILKTERSDLEQLENIQVLYSHEKVMESTIQOTKLDLFOAK 1271
Db 1082 -----ITQGLMNMQAQLEBSOI----- 1101
QY 1272 MDQAKKKKVPLOYNELKLALEKARCALEALOKTRIELRSAREBAHRKATDHP 1331
Db 1102 -----RLEQMLTDSKDSIQEQLRSLQALHIGLDS----- 1133
QY 1332 STPATARQOIMSAIVRSPHQPSAMSLAPSSRRKSSSTPEEBSRLKRMHNTPHR 1391
Db 1134 -----SIGSPGDTADDDGPES----- 1151
QY 1392 FNVGLNMRATKCAVCLDTVHFGRQASKLEQVOMCHPKSTCLPATGCLPABVATHPTFA 1451
Db 1152 ----- 1151
QY 1452 FCRDKMNSPGLQTEPSSSLHEGMKVPRNNKSGQOQMDRKYIVLEGSXYLIYDNEARE 1511
Db 1152 -----RLEGWLSLPVRNNTKKPGWVKYIVVSSKILFYDSEQDK 1191
QY 1512 AGQRP 1516
Db 1192 EQSNP 1196

RESULT 10
US-08-685-871-2
Sequence 2, Application US/08685871
Patent No. 6013499
GENERAL INFORMATION:
APPLICANT: NARUMIVA, Shuh
TITLE OF INVENTION: RIO TARGET PROTEIN KINASE P160
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,871
FILING DATE: 24-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-184102
FILING DATE: 25-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-262553
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-685-871-2
Query Match 12.0%; Score 1260; DB 3; Length 1354;
Best Local Similarity 26.3%; Pred. No. 3.2e-57;
Matches 400; Conservative 293; Mismatches 531; Indels 296; Gaps 53;
QY 44 SPLRSGLDALFVLFEECSOPALMKI KAVSNFVRKYSDDTIAELOPSAKDEPVRSLV 103
Db 23 SEVNSDCLLDLADLVVDLPDPALRKNNKINIDFLSRKYDTINKIRDLRMKADEVVAVKI 82
QY 104 GCGHFAVQVVRKATAGTDIYMKYMKKKALLAQOVSFFEEBRNILSRSTPMLPOLOYA 163
Db 83 GRGAFGEVQLVRHSTKTKVYAMKLLSKFKEMIKRSDSAFFMEERIDIMAFANSPWVQLFYA 142
QY 164 FQDKNHLVLMVEYQPGDGLSLNRYDQDENTLOFPLAEILAAVSHVMGTVHRDIK 223
Db 143 FQDRYILVMWEIYFPGDVLVLMNSYD--VEKARFYTAEVLALDAIHSMGFIRHDVK 200
QY 224 PENILVDRTHIKLVDEGSAKONSNINOVNAKLPITGPDYMAPEVLTVMNGDGKTYGLD 283
Db 201 PDNMLDKSGHLKADPOTGCMKMKEGMVCDTAVGTPDVISPEVLKSGGD--GYGRE 258
QY 284 CDWWSGVIAVEMTYGSPPAEGTSARTFNINMFORFLKPPDDPKVSDFLDIQSLLC 343
Db 259 CDWWSGVFLYEMLVGDTPEYADSLVGTGKIMNHKSLTFPPDNDISKEAKNLCIFLT 318
QY 344 GQKERLKFEG---LCCHPFSKID--WNTRNSPPRPVPLTKSDPDTSNPEPKSNVWS 398
Db 319 DREYLRGNVGEELKRLPFENQDQWAEETLDYAPVLPDLSDDITSNDLEEDGEE 378
QY 399 SS-PCQLSPSGFSGEELPFVGFSSYKALGILGSESVSGDSPAFTSKMEKLLIKSKE 457
Db 379 ETFFI---PKAFVGNQLPVGFY---YSNRRTYSANPNRRTSSN-----ADKS 423
QY 458 LQDS-QDKCHRMQEMTRLHRVSEVAIVLSQKEVELKASGTOR--SLLEQD-LATYIT 512
Db 424 LOESLQKTIYKLEBQL-----HNEMQLKDEMEQCRYSNIKLDKIMKELD 468
QY 513 EGSLSKLSLQANREVOEDDKALQLLHDIREQSKIQELKEQYQOVE-EMLMNQL 571
Db 469 EEGNQRRNLST--VSQIKERKLLQHRINEYORKAQ--ENKRNANVEVSTLQDL 523
QY 572 EEDLVASRRSDLYESELRESRLAABEFKRAKTECQHLKAKQDQKPEVGEVYALKIN 631
Db 524 EDLAKTYSQNSQL-----AND---KLSQLQQLSEANDLRTESDPAVRLKSH 568
QY 632 AEOQLKIQELOEKLEKAVKASTATELLONIROAKERABELEKQONREDSSEGRKKLV 691
Db 569 TEMSKSISQL--ESLNRELQ--ERNRILEN--SKSQTDVQYQLQ-----AIL 610
QY 692 EAEBRRSLSENKVKRLTMRERNRLLKODIQTK---SQOIQOMADKILEBEKREAOV 747
Db 611 EAERDRG-----HDSMIGDQARTTSLOEBEVKHLKHLLEKVEGERKSAOD 657
QY 748 SAQLEVYHLKQKQHYBEKIKVLDNOIKDLADETELNNMORHEBAHE--KGTILS 803
Db 658 MLNHSF---KEK-----NLEITLNTK--LKSLOQRLEQGVNHHKTKYKARLTD 700
QY 804 EOKAMINAMDSKIRSEORIVELSEANKLANGLSFLTORNMKAQOEMIS--ELROQKYLE 862
Db 701 KHQISBEAKSVANCMCEKKLKEBEBAEKENRV---QIEKQCSMLVDVLQSQQKLE 756
QY 863 TQAGKLEAQRKLEBQLEKISHQDSDKRLLELFTRLREVSLSLHEBQK----- 911
Db 757 HLTGNK---RMEDEVKNLTQLQEBQSNRLLQLNELKTOAREADLKGLEKQMKQEIN 812
QY 912 --LELKROLTELETS-----LOERESQLTALQAAABAASQLEQATTELEBET 957
Db 813 TLLEAKR-LLEFELAQTQYRGNEGOMRELQQLLEBOYFSTLYKTQVLEKEEBEKN 871
QY 958 ABAEBEIQALTARDEIQRFDALRNSCTVITDLBEOJNQLTEBDNMLNNQNFYLSKQD 1017


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Db      679 LEKESNMEDMTYQVKTIQOS-----LEQEAENKA-----TAKRLADKKKIYESIEEA 728
Qy      765 --EKIYVLDNQIKKOLADKETLENMORHE-----EAEHEKGIUSEQAMINAM 812
Db      729 KSEAMKEMEKELBERTLKQKVENILLAEKRGSLDDCDLQSQKINELLKQDVAN-- 786
Qy      813 DSKIRSLBQRIVEISEANKLAANSLLFTQRMKAQOEIMISLRQOKFYLETQAGKLEAQN 872
Db      787 --EDVRNLTLKIEQETQKCL-----TQNDLKMQTQOVNLTAKMS----- 823
Qy      873 RKLEQLEKISHQSHSDKNRLLETLERLREVSLEHEEQKLEKQKQLELOLSQERESQ 932
Db      824 --EKQKQ-----ENHLMEMKMNL-----EKQNAELRKERQADQOMKELDPOL 866
Qy      933 TALQAAALAESQURQAKTELEETT---AEAEEIQTALTARDEIQKFDALRNSCTVIT 989
Db      867 EAEYFSTLYTQVRELKEBCEKTKQKELQOKQKQELQDERDSLQGLE-----IT 918
Qy      990 DLEBQNLQLEEDNAELNNQNFYLSKQULDEASGANDETVOLRSEVDHLREITEREMQUTS 1049
Db      919 LTKADSEQLARSIABEQYSDLEKEKIMKE-----LEIEMMARHKOELTEKDATIAS 970
Qy      1050 QKQIMEALKTKCTMLEBQVMDLEALNDELLEKERQWEAMBSVLGE-----KSQFECR 1102
Db      971 LEEHNRITLTSVANILAN--EKELNNLKVQVQO---LSRLDEBISAAITAQPE-- 1021
Qy      1103 VRELQRMILDEKQSRARADQRTESRQVVELAVENKAKAILALQALKEQKLKAKESLSDK 1162
Db      1022 -----KQLTERTLKQAVNKL 1038
Qy      1163 LNDLEKKHAMLEMMNARSLOQKLETERELKQRLLEBQALQOQMDLQKNNHFRLTQGLQEA 1222
Db      1039 AEIMNRKEPVKRGNDTVRRKEKENRKLHMKELKEREKLTQOM----- 1081
Qy      1223 LDRADLKTESDLEFQULENIQVLYSHKVMGEGTISQCTKLIFPLQAKMDQPAKKKKVP 1282
Db      1082 -----IKYQKELNMQAIAESQI----- 1101
Qy      1283 LQVNELKALEKEKARCAELEBEALQKTRIEIARSABEAHAKATDHPHSTPATARQOIA 1342
Db      1102 --RELQMTLDSKQSDLEBQLSQJQALHIGLDS----- 1133
Qy      1343 MSALVRSPEHQPMSMLAPSSRRKESSTPEEFSRRLKERMHNITPHRFVNGVLMBATK 1402
Db      1134 -----SIGSGPGDAEADGPFES----- 1151
Qy      1403 CAVCLDTVHFGRQASKLEBQVCMCHPKCSTCLPATCGLPAEYATHTFEACFRDMNSPGL 1462
Db      1152 ----- 1151
Qy      1463 QTEKPSSSLHEGMKVPRNNKRGQGGMDRYIVLEBSKVLYDNEAREAGORP 1516
Db      1152 -----RLEGWLSLPEVRNNTKKFGWVKYIVSSKILFTYSEQDKQSNP 1196

RESULT 12
US-09-976-594-296
; Sequence 296, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 296
; LENGTH: 1388

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 064987CD1
US-09-976-594-296

Query Match      12.0%; Score 1257; DB 4; Length 1388;
Best Local Similarity 24.6%; Pred. No. 4,7e-57;
Matches 375; Conservative 279; Mismatches 485; Indels 388; Gaps 37;

Qy      24 ASRLNLFQOKPPEMTQOQMSPLSREGILDALFVLFECSCGPAIMTKIKNVSNFRKYSDT 83
Db      24 ASR-----QKLEALIDPPSPINVESLLGLNSLVLDLPFAPLRKKNKINDFNRIEKI 78
Qy      84 IAELOELQPAKQPEVASLVGCGHFAEVQVVRREKATGDIYAMKVMKKKALLAQEVSFFE 143
Db      79 VKIRIGIQMAEDVDYKVGIRGAFGVQVLRHNASQKVYAMKLSIFEMIKRDSAPFW 138
Qy      144 EERNILSRSTSPWIPQLOVAFQDKNHLVYVNEVOPGDDLILNRYEDQDLENLIQFYLA 203
Db      139 EERDIMAFAANSPMVQVLFYAFQDDRVLVYVMEVPGDDLVLNLSNYD--VEKMAKYTA 196
Qy      204 ELIAVSHVLMGVNHDIPENILVDRTHIKLVDSGAAXKMSNKNNAKLPITGPDY 263
Db      197 EVVIALDAISHMGLIHRDVKPDNNLIDKHGLKADGTCMKMDGTGMVHCOTVAVGTPDY 256
Qy      264 MAPEVLTVNMGDGGTGLDCDMWSVGVIAYEMIVGRSPPAEGTSARTFNNINMFORFLK 323
Db      257 ISPEVLKSGGD--GFYGRCDMWSVGVPFLYEMLVGTPFPADSLVGTYSKIMHKSILC 314
Qy      324 FPDDPKVSYDFLLIQLGQKEREKLEEG---LCCHPFF--SKIDMNNIRNSPPPVPT 378
Db      315 FPEDAEISKAKNULICAFILDRVRLGRNGVEIRQRPFFKNDQWMDNIRETAPVVE 374
Qy      379 LKSDDTNSNDDEPKNSW--VSSPCQLSPSGFSEELPEVGFYSKALGLIGRESVYVG 437
Db      375 LSSDIOSSNPDIEDDGADVETPEPI---PRAFVGNQLPFGFTYRRENLLIS----- 423
Qy      438 LQSPA--KTSMEKLLIKSKELQDSQDKCHKMOEOTRLHRRVSEVAVLSQKEVELKA 495
Db      424 -DSPSCRENDSTQR--KNEESOEIOKKLYTBEBHLS-----EQA 462
Qy      496 SETQRLSEODLATYITECSSLSKSLQAEVSOE-----DDKALQLHDIREQSRKL 549
Db      463 KEE---LEQ-----KCKSVMTREKTAKELEBEITLAKSVSALRQL---ERRKAL 507
Qy      550 QEIKQSYQAQVEEMRLMNNQLEEDLVASARRSDLYSELSRESRLAAEFKRAKATBCQHK 609
Db      508 LQHKNAEYQKRAHDHADKKNLENDVNSLKQQLLEDLKKKQNSQISTE---KVNQLOQ 563
Qy      610 LKAKQOGRKEVEGYALKEKINAEOQKIQLOEKLEKAKVASTAEATELLQNTROAKERA 669
Db      564 LDEFNALLRTESDPTAALRLTQAESSKOIQLSEN-----NRDLODKNCLLETA 612
Qy      670 ERELK-LQNRDSESGIRKKLVEAEERRHSLNKVLETERERENRLKDDIQTKSQOI 728
Db      613 KKLKEKFINLQALBESERRDRTHGSEIINDQIRIGLGEDLKNGKILAKVLEKQ 672
Qy      729 QQADKTLLEEKGRRAQVSAQ--HLEVHLKQKE-QHYEEKIKYLD--NQIKQD--ADKE 782
Db      673 QERFTD-LEKESNMEDMTYQVKTIQOSLEQEAENKAKTARLADKKIYESIEEAKSE 731
Qy      783 TLENMORHEEAHEKGI---LSEQAMINAMDSKIRSLBQRIVEISEANKLAANSLLF 839
Db      732 AKMEKMKLLLEERTLKQKVENILLAEKRGSLDDCDLQSQKQKINEL----- 778
Qy      840 TORNMKAQOEIMISLRQOKFYLETQAGKLEAQNRLKEEQLKISHQSHSDKNRLLEETR 899
Db      779 ----LKQKVLANDVNRNLTKIEQETQKCLTQNDLKMQQVQVNTLMSRK-QUKQENNH 833
Qy      900 LREVSLEHEQKLEKRLQTELOLSQERESQLTALQAAALAESQURQAKTELEETT-- 957

```

```

Db      834 LMEKKNLEKONAEIRKRRQADOGAMELOQLEAEQYFSTLYKTYQVELKEBCEBEXTKL 893
Qy      958 -AEAESEELQALTAHDEIQRRKFDALRNSCTVITDLEEQNLQTEDEMANQNPFYLSKOL 1016
Db      894 GKELQKKQKQELQDERDSLAAQLE-----ITTLKADSEQLASIAIEQYSDLEKEKIM 945
Qy      1017 DEAGANDEIYQLESEVHLAREITEREMOLTSQKQTEALKTCTYMLEEQVMELEAND 1076
Db      946 KE-----LEIKEMARHKKQELTEKATTAASIEETRTLLSDVANIAN--EKEELNN 994
Qy      1077 ELLEKERQEWAMRSVLAGDE-----KSQFECRAVELQRMLDTEKQSHARADCRITESRQ 1129
Db      995 KLKVOQEQ-----LSLTKDEEISAAIKQFE----- 1021
Qy      1130 VVELAVKENKAEILALQALKEQKKAESLSDKLNDEKKIAMLENNARSLQOKLETERE 1189
Db      1022 -----KQLTERTLTKQAVNKLAELNNRKEPVRKGNDDVRRKEKENRK 1065
Qy      1190 LKQRLLEEQAQLQOQMDLQKNHIFPLTQGLQELADRADLILTERSDELYQENIQVLYSH 1249
Db      1066 LHMELKESREKLTQOM-----IKYOK 1086
Qy      1250 EKVMKEGTISQOTKLIDFLQAKMQPAKKKIVPLQYNELKLALEKEKARCALEBALOKT 1309
Db      1087 ELNEMQADIAESQI-----RIELQMTLDSKQSDIDQLNSQIQAL 1126
Qy      1310 RIELSAREEAAHKKATHPHPSTPATKQOILMSAIVRSEPHQPSANSLAPSSRRKE 1369
Db      1127 HIGDSS-----SISGEGDAEAD 1145
Qy      1370 SSTPEEFERLKERHNNHNPFRFVGLNMRATKCAVCLDVTVHFGQASKCLGQVMCHPK 1429
Db      1146 DGFEPS----- 1151
Qy      1430 CSTCLPATCGLPAEYATHTEAFCDKKNSSBGLQTEKPBSSILHEGMNKPVRNNKRGQOG 1489
Db      1152 -----RLEGWLSLPLVRNNTKKFG 1169
Qy      1490 WDRKTYIVESKVLIDYNEAEAGQRP 1516
Db      1170 WKKRYVIVSSKKILFLYDSEQDKQSNP 1196

RESULT 13
US-09-916-204-4
; Sequence 4, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROP
; FILE REFERENCE: CL001164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-916-204-4

```

Query Match	11.3%	Score 1183	DB 4	Length 251
Best Local Similarity	90.8%	Pred. No. 4.9e-54		
Matches 228	Conservative 12	Mismatches 11	Indels 0	Gaps 0
QY	1	MLKPFYGGARNPLDGAARPIASPRASRLNLFPGQKPPFTQOQMSPLSREGTLDAFLVYFE	60	
Db	1	MLKPFYGGVNRNSENASAPPIASRSRLNLFPGQKPLMTQOQMSLSREGVLDALFVILE	60	
QY	61	ECSPALMLKKIKHVSFVVRKSDTIAELQELQPSANDFEVRSLVGCGFAEYQVVRKATG	120	

Db	61	ECSPALMKIKHVSSFAVKYEDTIAELRELQPSVDFEVRSLVGGCHAEVQVAREKATG	120
Qy	121	DIYAKVKKKATLALQEOVSFPEEERNILSRSTSPWIPOLQYAFODKNHLYLWMEYQPEG	180
Db	121	DYAMKMKKKALTRAQEOVSFPEEERNILSGSTSPWITQLQYAFODKNHLYLWMEYQPEG	180
Qy	181	DLSTLNRYEDQDLNTLQFYLAETILAVSHVHLMGYVHRDIKPNILVDRTHGILKYDF	240
Db	181	DLSTLNRYEDQDLNNTQFYLAETILAVSHVHMGYVHRDIKPNILIDRTHGILKYDF	240
Qy	241	GSAAMNSNKM 251	
Db	241	GSAAMNSNKM 251	

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RESULT 14
US-10-282-048-4
; Sequence 4, Application US/10282048
; Patent No. 6692948
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001164CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/282,048
; CURRENT FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-282-048-4

```

Query Match	Similarity	11.3%	Score 1183;	DB 4	Length 251;
Beet Local	Similarity	90.8%	Pred. No. 4.9e-54;		
Matches	Conservative	12;	Mismatches	11;	Indels 0; Gaps 0
QY	1	MLKFRYGRANPLDAGAAEPIASRASRLNLFGQKPEPMTQQOMSPLSRBGIDALFVLPF	60		
DB	1	MLKFRYGRANPESEASAPESIPASRASRLNLFGQKPEPLTQQOMSPLSRBGVIDALFVLLF	60		
QY	61	ECGSPALMKIKHVSFVARKYSDTLAELOLPASADFEVRSIVGCGHFAEYVAREKATG	120		
DB	61	ECSPALMKIKHVSFVARKYSDTLAELELPQSVARDFEVRSIVGCGHFAEYVAREKATG	120		
QY	121	DIYANKVKKKALLAQECVSPFEERNLNSTSPWIPOLQYAFODKNNLYLWMEYQRCG	180		
DB	121	DYAMAKIKKKKALLRAQECVSPFEERNLNSTSPWIPOLQYAFODKNNLYLWMEYQRCG	180		
QY	181	DLSLILANKYEQDLBNLIFQYLAELILVHVSYHLMGYVARDIKPENIILVDRGHIKLVDYF	240		
DB	181	DLSLILANKYEQDLBNMIFQYLAELILVHVSYHMGYVARDIKPENIILIDRGHIKLVDYF	240		
QY	241	GSAAKMNSNMK	251		
DB	241	GSAAKMNSNKV	251		

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RESULT 15
US-09-916-204-5
; Sequence 5, Application US/09916204
; Patent No. 6638745
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01164CIP
; CURRENT APPLICATION NUMBER: US/09/916,204
; CURRENT FILING DATE: 2001-07-24
; NUMBER OF SEQ. ID NOS: 6
;

```

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-916-204-5

Query Match 11.2%; Score 1180; DB 4; Length 251;
Best Local Similarity 90.4%; Pred. No. 7e-54; 9; Indels 0; Gaps 0;
Matches 227; Conservative 15; Mismatches 9;

Qy	1	MLKFEYGARNDPLDGAAPPIASRASRLNLPFGKPPFTQOOMSPLSREGIIDLFLVLE	60
Db	1	MLKFKYGVNPPPEASASERPIASRASRLNLPFGKPPFTQOOMSALSRGMLDALFLFE	60
Qy	61	ECSPALMKIKHVSNFVRKYSDTIAELQELQPSAKDFEVRSLVGCCHPAEYQVVRKATG	120
Db	61	ECSPALMKMKHVSFVQKYSDTIAELRELQPSARDFEVRSLVGCCHPAEYQVVRKATG	120
Qy	121	DIYAMKVKKKALLAQEQVSPFEERNTLSRSTSPWIPOLQYAFQDKNHLVLMKEYOPG	180
Db	121	DVYAMKIKKKALLAQEQVSPFEERNTLSRSTSPWIPOLQYAFQDKNHLVLMKEYCPG	180
Qy	181	DLSTLNRYEDQDENLLOFYLAELILAVSHVLMGYVHRDIKPENILVDRGTGHIKLVDF	240
Db	181	DFLSLNRYEDQLDSMTQFYLAELILAVSHVLMGYVHRDIKPENILIDRTGETIKLVDF	240
Qy	241	GSAAKMNSNM 251	
Db	241	GSAAKMNSNKV 251	

Search completed: May 11, 2005, 16:46:48
Job time : 65 secs

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OM protein - protein search, using sw model

Run on: May 11, 2005, 16:27:33 ; Search time 227 Seconds
(without alignments)
3499.585 Million cell updates/sec

Title: US-10-791-666-2

Perfect score: 10493

Sequence: 1 MLKFRYGARNPIDAGAAAPRI.....AGAVRTPISQVKNWQSSV 2054

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980a:*
2: geneseqp1990a:*
3: geneseqp2000a:*
4: geneseqp2001a:*
5: geneseqp2002a:*
6: geneseqp2003a:*
7: geneseqp2003bs:*
8: geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10493	100.0	2054	5	ABR81927 Human kin
2	10486	99.9	2054	5	AAE24150 Human kin
3	10486	99.9	2054	6	AAO26959 Human CRT
4	10464.5	99.7	2055	8	ADJ96610 Human cIt
5	10458.5	99.7	2053	5	ABG78363 RHO/RAC-i
6	10458.5	99.7	2053	6	ADA05642 Human NOV
7	10431.5	99.4	2053	4	AAU03501 Human pro
8	10425.5	99.4	2066	5	ABG78362 Human pro
9	10425.5	99.4	2066	6	ADA05654 Human NOV
10	10422.5	99.3	2053	8	ADN62807 Human NOV
11	10412.5	99.2	2053	8	ADN63228 Human NOV
12	10407.5	99.2	2066	8	ADN62819 Human NOV
13	10109.5	96.3	2055	6	ABP97683 Polypept
14	10109.5	96.3	2055	6	AAO26960 Human CRT
15	10022.5	95.5	2053	5	AAE24079 Human MDP
16	10022.5	95.5	2053	7	ADRF60994 Pain asso
17	10022.5	95.5	2053	8	ADG89100 Human tiro
18	9996	94.5	1958	5	ABR81928 Human kin
19	7851.5	74.8	1641	7	ADN62804 Mouse cIt
20	7851.5	74.8	1619	7	ADD48584 Rat Prote
21	7851.5	74.8	1619	7	ADD46616 Rat Prote
22	6575	62.7	1286	3	AAH43359 Human ORF
23	6575	62.7	1286	6	AAO26961 Human CRT
24	6575	62.7	1286	7	ADD48586 Human pro
25	6575	62.7	1286	7	ADD46618 Human pro

26	5037	48.0	999	4	ABR11117 Human RHO
27	4871	46.4	940	7	ADD89967 Human can
28	4601	43.8	883	8	ADM72201 Human TAS
29	4501	42.9	910	4	AAU31443 Novel hum
30	4303	41.0	853	7	ADG09957 Novel pro
31	4115	39.2	832	6	ADA05646 Human NOV
32	4115	39.2	832	6	ADN62811 Human NOV
33	4097.5	39.0	847	6	ADA05648 Human NOV
34	4093.5	39.0	847	6	ADN62813 Human NOV
35	3244	30.9	623	6	ADA05650 Human NOV
36	3226.5	30.7	638	6	ADA05652 Human NOV
37	3226.5	30.7	638	8	ADN62817 Human NOV
38	3219	30.7	623	8	ADN62815 Human NOV
39	3165	30.2	623	6	ADA05644 Human NOV
40	3104.5	29.6	620	8	ADN62809 Human NOV
41	2443	23.3	495	6	ABP97681 Amino ac1
42	2443	23.3	497	6	ABP97687 Amino ac1
43	2440	23.3	497	6	ABU10126 Novel hum
44	2440	23.3	497	7	AAE39504 Human kin
45	2440	23.3	497	8	ADA05992 Human kin

ALIGNMENTS

RESULT 1	
ABR81927	
ID	ABR81927 standard; protein; 2054 AA.
XX	
AC	ABR81927;
XX	
DT	10-OCT-2002 (first entry)
XX	
DE	Human kinase #1.
XX	
KW	Human; kinase; enzyme; serine-threonine kinase; nootropic; cytosolic;
KW	Citron rho-interacting kinase; gene therapy; mental disorder; cancer.
OS	Homo sapiens.
XX	
PN	WO200259325-A2.
XX	
PD	01-AUG-2002.
XX	
PF	20-DEC-2001; 2001WO-US050497.
XX	
PR	27-DEC-2000; 2000US-0258335P.
XX	
PA	(LEXI-) LEXICON GENETICS INC.
XX	
PI	Yu X, Miranda M, Fiddie CJ;
XX	
DR	WPI; 2002-599796/64.
XX	
PT	N-PSDB; ABQ78870.
XX	
PT	Novel polynucleotide encoding human proteins that are structurally
XX	similar to animal kinases, useful for drug screening, diagnosis, in gene
PT	therapy of disorders and diseases e.g. cancer and pharmacogenomic
XX	applications.
XX	
PS	Claim 2; Page 39-43; 50pp; English.
XX	
CC	The invention relates to a novel human protein that shares structural
CC	similarity with animal kinases, including serine-threonine kinases,
CC	particularly Citron rho-interacting kinases. The proteins of the
CC	invention have nootropic and cytosolic activity. The polynucleotides may
CC	have a use in gene therapy. The encoded novel polypeptides are useful for
CC	generating antibodies, as reagents in diagnostic assays, for identifying
CC	other cellular gene products related to NHP and as reagents in assays for
CC	screening for compounds that are useful in the treatment of mental,
CC	biological or medical disorders and diseases including cancer. The
CC	sequence represents a novel human kinase of the invention

Seq	Sequence	2054 AA;
	Query Match	100.0%; Score 10493; DB 5; Length 2054;
	Best Local Similarity	100.0%; Pred. No. 0;
	Matches 2054;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MKFPGYGAENPLDAGAEPIASRASRLNLFQGGKPPMTQOQMSPIRREGIILDAFLVLE	60
DB	1 MKFPGYGAENPLDAGAEPIASRASRLNLFQGGKPPMTQOQMSPIRREGIILDAFLVLE	60
QY	61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVGCSPHFAVOVVEKATG	120
DB	61 ECSOPALMKIKHVSNFVKYSDTIAELQELQPSAKDFEVRSLVGCSPHFAVOVVEKATG	120
QY	121 DIYAMKVMKKALLAQEOVSPFEEERNILSRSTSPMIPOLQYAFODKNH.YLVMEYOPG3	180
DB	121 DIYAMKVMKKALLAQEOVSPFEEERNILSRSTSPMIPOLQYAFODKNH.YLVMEYOPG3	180
QY	181 DLLSLINRYEDQDENLLOFYLAELILAVHSVHLMGYVRDIPKENILVDRGHIKLVDF	240
DB	181 DLLSLINRYEDQDENLLOFYLAELILAVHSVHLMGYVRDIPKENILVDRGHIKLVDF	240
QY	241 GSAAKMNSKMYNAKLPIGTPTYMAPEVLTVMNGDGKGTGGLDCDMSVGVIAEMITYGR	300
DB	241 GSAAKMNSKMYNAKLPIGTPTYMAPEVLTVMNGDGKGTGGLDCDMSVGVIAEMITYGR	300
QY	301 SPFAEGTSARTFNINMNFORFLKFPDDPKVSDFDLLIQSLLCQGERLKFEGLCCHPFF	360
DB	301 SPFAEGTSARTFNINMNFORFLKFPDDPKVSDFDLLIQSLLCQGERLKFEGLCCHPFF	360
QY	361 SKIDMNNIRNSPPFPVPTIKSDDDTNSFNPBPKNSVSSPCQLSPSGSGSEELPVGVS	420
DB	361 SKIDMNNIRNSPPFPVPTIKSDDDTNSFNPBPKNSVSSPCQLSPSGSGSEELPVGVS	420
QY	421 YSKALGILGRSSVYSGLDSPAKTSSMEKKLLIKSKELQDSODCKHMEQCTRLLHRYS	480
DB	421 YSKALGILGRSSVYSGLDSPAKTSSMEKKLLIKSKELQDSODCKHMEQCTRLLHRYS	480
QY	481 EYEAVALISQKEVELKASETORSLLEODLAYITECSSLKRSLEQARMEVSQEDDKALQLLH	540
DB	481 EYEAVALISQKEVELKASETORSLLEODLAYITECSSLKRSLEQARMEVSQEDDKALQLLH	540
QY	541 DIRBOSRKLQETKEOEYQAOVEEMRLMNOULEBDLVASARRSDLYSELSRESRLAAEEK	600
DB	541 DIRBOSRKLQETKEOEYQAOVEEMRLMNOULEBDLVASARRSDLYSELSRESRLAAEEK	600
QY	541 DIRBOSRKLQETKEOEYQAOVEEMRLMNOULEBDLVASARRSDLYSELSRESRLAAEEK	600
DB	541 DIRBOSRKLQETKEOEYQAOVEEMRLMNOULEBDLVASARRSDLYSELSRESRLAAEEK	600
QY	601 RKATSCOHKLAKXQOGKPEVGEYAKLEKINAEQOLKIQELOKLEKAYKASTEATELQ	660
DB	601 RKATSCOHKLAKXQOGKPEVGEYAKLEKINAEQOLKIQELOKLEKAYKASTEATELQ	660
QY	661 NIROAKERAERLEKLQNRDSESEGIKKLVAEAEERHSLLENKVKYLETMBERENRLKND	720
DB	661 NIROAKERAERLEKLQNRDSESEGIKKLVAEAEERHSLLENKVKYLETMBERENRLKND	720
QY	721 IOTKSQOQIQWADKILLEEKREBAVSAQHLVHLKQKEOHYBEKKIYULDNOIKDLAD	780
DB	721 IOTKSQOQIQWADKILLEEKREBAVSAQHLVHLKQKEOHYBEKKIYULDNOIKDLAD	780
QY	781 KETLENMNOHREHEAEHKKIILSEOKAMTNAMDSKIRSLERIVELSEANKLAANSSLT	840
DB	781 KETLENMNOHREHEAEHKKIILSEOKAMTNAMDSKIRSLERIVELSEANKLAANSSLT	840
QY	841 QRMNKAQEBEMISELNOQKFYLETOAGKLEAONRKLEBOULEKISHODHSKXNLLLEETLU	900
DB	841 QRMNKAQEBEMISELNOQKFYLETOAGKLEAONRKLEBOULEKISHODHSKXNLLLEETLU	900
QY	901 REVSLHEHEOQKLELRQULTEQLSLQERESQUTALQAPALAESQLRQAKTELEETTABA	960
DB	901 REVSLHEHEOQKLELRQULTEQLSLQERESQUTALQAPALAESQLRQAKTELEETTABA	960
QY	961 REVSLEHEHEOQKLELRQULTEQLSLQERESQUTALQAPALAESQLRQAKTELEETTABA	960
DB	961 REVSLEHEHEOQKLELRQULTEQLSLQERESQUTALQAPALAESQLRQAKTELEETTABA	960
QY	961 REVSLEHEHEOQKLELRQULTEQLSLQERESQUTALQAPALAESQLRQAKTELEETTABA	960
DB	961 REVSLEHEHEOQKLELRQULTEQLSLQERESQUTALQAPALAESQLRQAKTELEETTABA	960

QY	1021 GANDEIVOLRSRVNDHLREBITEREMOULTSOQOTMEALKTCTCMLEBOVMDLEALNDELLE	1080
DB	1021 GANDEIVOLRSRVNDHLREBITEREMOULTSOQOTMEALKTCTCMLEBOVMDLEALNDELLE	1080
QY	1081 KERQWEAMRSVLDGSKSQPECEVRLEIORMLDEKOSRARADORITESHQVLEAVENKA	1140
DB	1081 KERQWEAMRSVLDGSKSQPECEVRLEIORMLDEKOSRARADORITESHQVLEAVENKA	1140
QY	1141 ETLALQALKEQKLAESISDKLNDLEKKHMLJMNASLSQOKLETERELKORLLEBOAK	1200
DB	1141 ETLALQALKEQKLAESISDKLNDLEKKHMLJMNASLSQOKLETERELKORLLEBOAK	1200
QY	1201 LOOQMDLOKNHIFRLTOGLOEALDADLILKTRSLLEYQLENIQVLYSHKXMGCTISQ	1260
DB	1201 LOOQMDLOKNHIFRLTOGLOEALDADLILKTRSLLEYQLENIQVLYSHKXMGCTISQ	1260
QY	1261 OTKLIDFLQAKMDQPAKKKKVPLQYNELKALEKKAKCALEBMLOKTRILARSAREBA	1320
DB	1261 OTKLIDFLQAKMDQPAKKKKVPLQYNELKALEKKAKCALEBMLOKTRILARSAREBA	1320
QY	1321 AHRKATDHPHPESTPATARQOAIMSAIVRSPEHQPSAMSLAPSSRRKESSTPEEFSRRL	1380
DB	1321 AHRKATDHPHPESTPATARQOAIMSAIVRSPEHQPSAMSLAPSSRRKESSTPEEFSRRL	1380
QY	1381 KERMEHNIIPHRPNVGLNMPATYCAVCLDTYHFGROASKLBEQVWCHRKCTCLPATGCL	1440
DB	1381 KERMEHNIIPHRPNVGLNMPATYCAVCLDTYHFGROASKLBEQVWCHRKCTCLPATGCL	1440
QY	1441 PAEYATHTFEACRGRKMSPGLOTEPESSSLHEGMVPRNNKSGQOGMDRKYIVLEGS	1500
DB	1441 PAEYATHTFEACRGRKMSPGLOTEPESSSLHEGMVPRNNKSGQOGMDRKYIVLEGS	1500
QY	1501 KYLIDYNEAREBAQRPVEEFELCLPDGDVSIHGAVGASELANTADAVPYILKMHSHPT	1560
DB	1501 KYLIDYNEAREBAQRPVEEFELCLPDGDVSIHGAVGASELANTADAVPYILKMHSHPT	1560
QY	1561 TCWPGRTTYLAPSPDPQORWTTALESVYAGRVSRKAEADAKILGNSILKLBEDDRID	1620
DB	1561 TCWPGRTTYLAPSPDPQORWTTALESVYAGRVSRKAEADAKILGNSILKLBEDDRID	1620
QY	1621 MNCTLPFSQOVVLYGTBERGLYALANVLYKNSLTVPGIGAVFOIYIYKDLKELMIAGEERA	1680
DB	1621 MNCTLPFSQOVVLYGTBERGLYALANVLYKNSLTVPGIGAVFOIYIYKDLKELMIAGEERA	1680
QY	1681 LCLVDVKVKYKOSLAOSHLPAPDISPNIPEAVKGCHLFGAGKIENGGLCI CAAMP SKVYL	1740
DB	1681 LCLVDVKVKYKOSLAOSHLPAPDISPNIPEAVKGCHLFGAGKIENGGLCI CAAMP SKVYL	1740
QY	1741 RYNNELSKYCIIRKEIETSEBPSCCHFTNYSLIGNNKYEIDMKQYTLBEFLDKNDHSLA	1800
DB	1741 RYNNELSKYCIIRKEIETSEBPSCCHFTNYSLIGNNKYEIDMKQYTLBEFLDKNDHSLA	1800
QY	1801 PAVFAASSNPFVSIYVONASAGOREEYLLCFHEBGFVPFDSYGRSRRTDLMKSRPLAFA	1860
DB	1801 PAVFAASSNPFVSIYVONASAGOREEYLLCFHEBGFVPFDSYGRSRRTDLMKSRPLAFA	1860
QY	1861 YREPLYTFTHFNSLEVIETIOARSSAGTPARAYLDIPNRYILGPALISSGAIYLAASSYQKL	1920
DB	1861 YREPLYTFTHFNSLEVIETIOARSSAGTPARAYLDIPNRYILGPALISSGAIYLAASSYQKL	1920
QY	1921 RYLCCKGNLVESGTEHHRGPSTSRSSPNKKGPPTYNEHITKRVASSPAPPGSPHPRP	1980
DB	1921 RYLCCKGNLVESGTEHHRGPSTSRSSPNKKGPPTYNEHITKRVASSPAPPGSPHPRP	1980
QY	1981 STPHRYRGRGTLELRDQSPGRPLERKSPGRILSTRRRSPARLPEDSSRGLPAGAVRT	2040
DB	1981 STPHRYRGRGTLELRDQSPGRPLERKSPGRILSTRRRSPARLPEDSSRGLPAGAVRT	2040
QY	2041 PLSQVKNYWDOSV 2054	
DB	2041 PLSQVKNYWDOSV 2054	


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Db      181  DILSLNLYEDDLDNLIOFYLAELILAVSHVLMGYHARDIKPENILVDRIGHIKLVDLF 240
Qy      241  GSAAKNSNKNVNAKLPICGPDYMAPEVLTVANGDGKGTGYGLDCMWSVGIYAYEMIYGR 300
Db      241  GSAAKNSNKNVNAKLPICGPDYMAPEVLTVANGDGKGTGYGLDCMWSVGIYAYEMIYGR 300
Qy      301  SPFAAGTSARPTNNIMNFQRFKPPDDPKVSSDFLDLISLCCGQKRLKEFGLCCHPFF 360
Db      301  SPFAAGTSARPTNNIMNFQRFKPPDDPKVSSDFLDLISLCCGQKRLKEFGLCCHPFF 360
Qy      361  SKIDNNNIRNSPPVPVPTLKSDDDTSNPEPEKSNWSSPCQSPSGSGEELPFVGS 420
Db      361  SKIDNNNIRNSPPVPVPTLKSDDDTSNPEPEKSNWSSPCQSPSGSGEELPFVGS 420
Qy      421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLTKSKELODSQDKCHKMEQENTRLHRRVS 480
Db      421  YSKALGILGRSESVVSGLDSPAKTSSMEKKLTKSKELODSQDKCHKMEQENTRLHRRVS 480
Qy      481  EYEAVLSQKEVVLKASETORSLLEODLATYITEGSLKRSLEQAMEVYSQEDDKALQOLIH 540
Db      481  EYEAVLSQKEVVLKASETORSLLEODLATYITEGSLKRSLEQAMEVYSQEDDKALQOLIH 540
Qy      541  DIRESRKLOETKEOEYQAVEEMRLMMQLEEDIVSARRSDLYESELRESRLAABEFK 600
Db      541  DIRESRKLOETKEOEYQAVEEMRLMMQLEEDIVSARRSDLYESELRESRLAABEFK 600
Qy      601  RKATCOHKLKAKOQKPEVEGYAKLEKINAQOLKIOELOEKLEKAVKASTEATELLO 660
Db      601  RKATCOHKLKAKOQKPEVEGYAKLEKINAQOLKIOELOEKLEKAVKASTEATELLO 660
Qy      661  NIRAQKAPARELEKLOQNRDSSSEGRKKLVABEERRHLENKVKRLTETMERENRLKXD 720
Db      661  NIRAQKAPARELEKLOQNRDSSSEGRKKLVABEERRHLENKVKRLTETMERENRLKXD 720
Qy      721  IOTKSOQIQWADKLTLEEKHREAVSAQHLFVHLKQKEQHYEEKIKYLDNQIKKDLAD 780
Db      721  IOTKSOQIQWADKLTLEEKHREAVSAQHLFVHLKQKEQHYEEKIKYLDNQIKKDLAD 780
Qy      781  KETLENMMQRRHEEAHEKGIKISEOKAMINAMDSKIRSLQRIIVELSEANKLAANSLETF 840
Db      781  KETLENMMQRRHEEAHEKGIKISEOKAMINAMDSKIRSLQRIIVELSEANKLAANSLETF 840
Qy      841  QRMNKAQEBMISELRQOKFYLETQAGKLEAONRKLBEQLEKISHODSHDNKFLLEETRL 900
Db      841  QRMNKAQEBMISELRQOKFYLETQAGKLEAONRKLBEQLEKISHODSHDNKFLLEETRL 900
Qy      901  REVSLHEBEQKLEKROLTELOLSIOERESQTLQAAPAALESQLRQKTELEETTAEA 960
Db      901  REVSLHEBEQKLEKROLTELOLSIOERESQTLQAAPAALESQLRQKTELEETTAEA 960
Qy      961  EEEIOALTARDEIORKFDALNSCTVITDLEEQNLQLTEDNAEILNNOFYLSKOLDAS 1020
Db      961  EEEIOALTARDEIORKFDALNSCTVITDLEEQNLQLTEDNAEILNNOFYLSKOLDAS 1020
Qy      1021  CANDEIVOLRSEVDHLRREITEREMQTSQOKTMEALKTCTMLEBQVMDLEALNDELIE 1080
Db      1021  CANDEIVOLRSEVDHLRREITEREMQTSQOKTMEALKTCTMLEBQVMDLEALNDELIE 1080
Qy      1081  KERQWEARSVYGDERSQPECEVRRELQORLDTREKSRAPADORTIESRQVAVLAKENKA 1140
Db      1081  KERQWEARSVYGDERSQPECEVRRELQORLDTREKSRAPADORTIESRQVAVLAKENKA 1140
Qy      1141  ETLALQOALKBOKLTAAESLSDKLNDEKKGAMLENNARSLOOKLETERELKORLLEBQAK 1200
Db      1141  ETLALQOALKBOKLTAAESLSDKLNDEKKGAMLENNARSLOOKLETERELKORLLEBQAK 1200
Qy      1201  LOQOMDLOKNHIFRLTQGLQEALDRAIDLKTERSDLEYOLENIQVLYSHHEKYMGGTISQ 1260
Db      1201  LOQOMDLOKNHIFRLTQGLQEALDRAIDLKTERSDLEYOLENIQVLYSHHEKYMGGTISQ 1260
Qy      1261  QTKLIDFLQAMKDOPAKKKKVPLOYNELKALBEKAKCAELEALQKTRIELRSAREEA 1320

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Db      1261  QTKLIDFLQAMKDOPAKKKKVPLOYNELKALBEKAKCAELEALQKTRIELRSAREEA 1320
Qy      1321  AHRKATDHPHSTPATTAQOIAMSAIVSPHROPSAMSLAPPSSRRKSSSTPEEFSSRL 1380
Db      1321  AHRKATDHPHSTPATTAQOIAMSAIVSPHROPSAMSLAPPSSRRKSSSTPEEFSSRL 1380
Qy      1381  KERMEHNTPHRPNVLANRATKCAVCLDTPVHFGRASCLBECQVWCHKCSTCLPATGCL 1440
Db      1381  KERMEHNTPHRPNVLANRATKCAVCLDTPVHFGRASCLBECQVWCHKCSTCLPATGCL 1440
Qy      1441  PAEYATHTTEAFRCRDKNKSPGLQTKBPPSSLHLEBGMKVPRNNKRGQOGMDRKYIVLEGS 1500
Db      1441  PAEYATHTTEAFRCRDKNKSPGLQTKBPPSSLHLEBGMKVPRNNKRGQOGMDRKYIVLEGS 1500
Qy      1501  KYLIYDNEAREAGQRPVEEFELCLPDGVSJHGAVGASELANTAAADVPYIIMKMSHPRT 1560
Db      1501  KYLIYDNEAREAGQRPVEEFELCLPDGVSJHGAVGASELANTAAADVPYIIMKMSHPRT 1560
Qy      1561  TCWPGRTLYLLAPSPDQORWYTLAESVYAGGRVREKAEADAKLLGNSLTKJEGDDRDL 1620
Db      1561  TCWPGRTLYLLAPSPDQORWYTLAESVYAGGRVREKAEADAKLLGNSLTKJEGDDRDL 1620
Qy      1621  MNCTLPFSDQVVLVGTBERGLVALNVLKNSLTHVPGIGAVFOIYIITKDEKLMIAGERA 1680
Db      1621  MNCTLPFSDQVVLVGTBERGLVALNVLKNSLTHVPGIGAVFOIYIITKDEKLMIAGERA 1680
Qy      1681  LCLVDVKVKOSLAQSHLPAOPDISPNIPEAVKGCHLFGAGKIENGLCICAMPSEKVYIL 1740
Db      1681  LCLVDVKVKOSLAQSHLPAOPDISPNIPEAVKGCHLFGAGKIENGLCICAMPSEKVYIL 1740
Qy      1741  RYNEMLSKYCIKKEIETSEPCSHFTNYSILIGNKRYEIDMKQYTLBEFLDKNDHSLA 1800
Db      1741  RYNEMLSKYCIKKEIETSEPCSHFTNYSILIGNKRYEIDMKQYTLBEFLDKNDHSLA 1800
Qy      1801  PAVFAASNSFPVSIYQVNSAGOREEYLLCFHEFGVFYDSYGRSRTDLMKSRJPLAFA 1860
Db      1801  PAVFAASNSFPVSIYQVNSAGOREEYLLCFHEFGVFYDSYGRSRTDLMKSRJPLAFA 1860
Qy      1861  YREPYLFTYHNSLEVEIIOARSSAGTPARAYLIDPNRYIGAPAISSGAIYASSYODKL 1920
Db      1861  YREPYLFTYHNSLEVEIIOARSSAGTPARAYLIDPNRYIGAPAISSGAIYASSYODKL 1920
Qy      1921  RYICCKGNLVESGTEHHRGSTSSPNKGPPTVNHITTRVAVSSPAPEGSHPREP 1980
Db      1921  RYICCKGNLVESGTEHHRGSTSSPNKGPPTVNHITTRVAVSSPAPEGSHPREP 1980
Qy      1981  STPHRYRGRTEIARDKSPGRPLEREKSPCHILSTRRRSPARLTFEDSSRGLPAGAVRT 2040
Db      1981  STPHRYRGRTEIARDKSPGRPLEREKSPCHILSTRRRSPARLTFEDSSRGLPAGAVRT 2040
Qy      2041  PLSQVNVKWDQSSV 2054
Db      2041  PLSQVNVKWDQSSV 2054

RESULT 3
AA026959
ID AA026959 standard; protein; 2054 AA.
XX
AC AA026959;
XX
DT 01-MAY-2003 (first entry)
XX
DE Human CR1K protein sequence, SEQ ID No 2.
XX
KW Anorectic; hypotensive; cardiast; antilipemic; cerebroprotective;
antigout; osteopathic; antiarthritic; cyostatic; antidepressant;
immunomodulator; antimanic; tranquiliser; antiparkinsonian; nootropic;
neuroprotective; antiinflammatory; antidiabetic; analgesic;
human citron rho/rac-interacting kinase; enzyme; CR1K; ameliorating;
obesity; comorbidity; cancer; anorexia; cachexia; bulimia;
central nervous system disorder; chronic obstructive pulmonary disease;
diabetes; pain.

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XX Homo sapiens.
OS
XX
XX WO2003004523-A1.
XX
XX 16-JAN-2003.
XX
XX 28-JUN-2002; 2002WO-EP007156.
XX
XX 02-JUL-2001; 2001US-0301841P.
XX 11-DEC-2001; 2001US-0338651P.
XX 25-APR-2002; 2002US-0375014P.
XX
XX (FARB) BAYER AG.
XX
XX Zhu Z;
XX
XX MPI; 2003-221576/21.
XX N-PSDB; MAL55214.
XX
XX New human citron rho/rac-interacting kinase (CRIK) polypeptide and
PT polynucleotide, useful in preventing, ameliorating or treating diseases
PT associated with human CRIK dysfunction, e.g. obesity, diabetes or
PT Alzheimer's disease.
XX
XX
XX Claim 1; Fig 2; 237pp; English.

The invention relates to an isolated polynucleotide encoding a human
CC citron rho/rac-interacting kinase polypeptide. The isolated
CC polynucleotide comprises a 6165 or 8603 base pair sequence, given in the
CC specification. The human citron rho/rac-interacting kinase (CRIK)
CC polypeptide and polynucleotide are useful in preventing, ameliorating, or
CC treating diseases associated with human CRIK dysfunction such as obesity
CC and obesity-associated comorbidities (e.g. hypertension, coronary artery
CC disease, hyperlipidemia, stroke, gout, osteoarthritis, some types of
CC cancer, including endometrial, breast, prostate and colon cancer),
CC anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
CC disorders, anxiety disorders, Parkinson's disease or Alzheimer's
CC disease), chronic obstructive pulmonary disease, or diabetes. These can
CC also be used to treat pain associated with the disorders. The human CRIK
CC polypeptide is also useful in diagnostic assays or in genetic testing.
CC The expression vector or the reagent is useful in preparing a medicament
CC for modulating the activity of a human CRIK in a disease, e.g. obesity, a
CC central nervous system disorder, or chronic obstructive pulmonary
CC disease. The fusion protein is useful for generating antibodies against a
CC CRIK polypeptide and for use in various assay systems. The methods are
CC useful in producing and detecting the polynucleotide and polypeptide and
CC in screening for agents that modulate the activity of the human CRIK
CC polypeptide. This sequence represents the human CRIK protein of the
CC invention
XX
XX
XX Sequence 2054 AA;

Query Match 99.9%; Score 10486; DB 6; Length 2054;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2052; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLKFFYGRNPLDGAAPRIASRLNLFQGRKPPMTQOOMSLSEGLIDALFVLF 60
DB 1 MLKFFYGRNPLDGAAPRIASRLNLFQGRKPPMTQOOMSLSEGLIDALFVLF 60
QY 61 ECSOPALMKIKHVSNFVKYSDDTIAELOPSADFEVRSIVGCGHAEVQVVEKKTG 120
DB 61 ECSOPALMKIKHVSNFVKYSDDTIAELOPSADFEVRSIVGCGHAEVQVVEKKTG 120
QY 121 DIYAMKVKKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQCG 180
DB 121 DIYAMKVKKKALLAQEOVSFFEEERNILSRSTSPWIPOLQYAFQDKNHLVLMVEYQCG 180
QY 181 DLSTLNVYEDQDENLLOFTIAELLAVHSHLMGVYHRDVKENIILVDRGHKLVDF 240
DB 181 DLSTLNVYEDQDENLLOFTIAELLAVHSHLMGVYHRDVKENIILVDRGHKLVDF 240

QY 241 GSAAMNSNKNVNAKLPIGTPDYAPBEVLTVMNGGKGTYGLDCCMWSVGVAYEMITYR 300
DB 241 GSAAMNSNKNVNAKLPIGTPDYAPBEVLTVMNGGKGTYGLDCCMWSVGVAYEMITYR 300
QY 301 SPFAEGTARTFNNTMNFORFLKFPDDPKVSDFDLLOSLCGQERKKEFGLCCHPFF 360
DB 301 SPFAEGTARTFNNTMNFORFLKFPDDPKVSDFDLLOSLCGQERKKEFGLCCHPFF 360
QY 361 SKIDNNNIRNSPPPEVPTLKSDDDTSNFDPEKNSWSSPCQSPSGSGEELPFVGRS 420
DB 361 SKIDNNNIRNSPPPEVPTLKSDDDTSNFDPEKNSWSSPCQSPSGSGEELPFVGRS 420
QY 421 YSKALGIIGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKMEQENTRLHRRVS 480
DB 421 YSKALGIIGRSESVVSGLDSPAKTSSMEKLLIKSKELQDSQDKCHKMEQENTRLHRRVS 480
QY 481 EVEAVLSQKEVELKASEFORSLLEODLATYTTESGLRSLSQAMWVSQEDDKALQLH 540
DB 481 EVEAVLSQKEVELKASEFORSLLEODLATYTTESGLRSLSQAMWVSQEDDKALQLH 540
QY 541 DIREQRKLOEIKEOEYQAYEEMRLMNOLEEDLVARRRSDLYESELSRESRLAAEPK 600
DB 541 DIREQRKLOEIKEOEYQAYEEMRLMNOLEEDLVARRRSDLYESELSRESRLAAEPK 600
QY 601 RKATECOHKLKAKDQGRPEVGEYAKLEKINABQQLKIQELOEKLEKAVKASTATELLQ 660
DB 601 RKATECOHKLKAKDQGRPEVGEYAKLEKINABQQLKIQELOEKLEKAVKASTATELLQ 660
QY 661 NITROAKEAELELELQNRRESSSEGRKLYAEERRRSLKRVRLTMEERRRLKDD 720
DB 661 NITROAKEAELELELQNRRESSSEGRKLYAEERRRSLKRVRLTMEERRRLKDD 720
QY 721 IOTSQOIQOAMDKILEEKKHREAOVSAOHLVELKQEOHYEERIKVLDNQIKKDLAD 780
DB 721 IOTSQOIQOAMDKILEEKKHREAOVSAOHLVELKQEOHYEERIKVLDNQIKKDLAD 780
QY 781 KETLENNMQRHEBEAHEKGLISEOKAMINAMDSKIRSLERQIVELSEANKLAANSUFT 840
DB 781 KETLENNMQRHEBEAHEKGLISEOKAMINAMDSKIRSLERQIVELSEANKLAANSUFT 840
QY 841 QRNKAQOEMISELRQOKFYLETQAKLEBAONRKLEBOLKESHODSDKRLLELRTL 900
DB 841 QRNKAQOEMISELRQOKFYLETQAKLEBAONRKLEBOLKESHODSDKRLLELRTL 900
QY 901 REVSLEHEBQKLEKROLTELOLSOERESQTLQAARALLESQRLORAKTELESTTAA 960
DB 901 REVSLEHEBQKLEKROLTELOLSOERESQTLQAARALLESQRLORAKTELESTTAA 960
QY 961 EEEIOALTNRHDEIQRKFDALRNSCTVITDLEBOLNQTEBNABEINMNOFVLSQDDEAS 1020
DB 961 EEEIOALTNRHDEIQRKFDALRNSCTVITDLEBOLNQTEBNABEINMNOFVLSQDDEAS 1020
QY 1021 GANDEIVOLRSEVDHLRREITEREMOLTSQKQTEALKTCTMLEEQVMDLEALNDELIE 1080
DB 1021 GANDEIVOLRSEVDHLRREITEREMOLTSQKQTEALKTCTMLEEQVMDLEALNDELIE 1080
QY 1081 KERQWEARSVLGPBKSGFECRVRELOMLDTEKQSRARAOORTESQOVELAYKEKA 1140
DB 1081 KERQWEARSVLGPBKSGFECRVRELOMLDTEKQSRARAOORTESQOVELAYKEKA 1140
QY 1141 EIALLOALKEOKLKAESLSKDLNDEKKHMLENNASLSQKLETERELKORLLEQAK 1200
DB 1141 EIALLOALKEOKLKAESLSKDLNDEKKHMLENNASLSQKLETERELKORLLEQAK 1200
QY 1201 LOQOMDLQKNHI FRLTGLQELADRADILKTERSDELYOLENIOVLYSHBEKVMEGTSQ 1260
DB 1201 LOQOMDLQKNHI FRLTGLQELADRADILKTERSDELYOLENIOVLYSHBEKVMEGTSQ 1260
QY 1261 QTKLIDFLQAMDDPAKKKKVPLQYNELKALBEKKAQALBEALQCTRIELRSAREEA 1320
DB 1261 QTKLIDFLQAMDDPAKKKKVPLQYNELKALBEKKAQALBEALQCTRIELRSAREEA 1320
QY 1321 AHRKATDHPHPSTATAARQOIAMSAIVSPHQPASMSLAPPSRRKESSTPEEFRRLL 1380

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Db      1321 AHRATDHPSTPTAQAQIAMSATVRSPEHQPSMILLAPSSRRRESSTPEEFSSRL 1380
Qy      1381 KERHNNIPHRPNVGLNRRATKCAVCLDTVHFGROASKLECOVWCHPCKSTCLPATGCL 1440
Db      1381 KERHNNIPHRPNVGLNRRATKCAVCLDTVHFGROASKLECOVWCHPCKSTCLPATGCL 1440
Qy      1441 PAEYATHTFEAPCRDKXNSPGIQTEKPESSSLHEGMMKVPNNKRGQGGQMDRKTYVLEGS 1500
Db      1441 PAEYATHTFEAPCRDKXNSPGIQTEKPESSSLHEGMMKVPNNKRGQGGQMDRKTYVLEGS 1500
Qy      1501 KVLVYDNARABAGQPVVEEFELCPDGDVSIHGAGSELANTADVPYLLKXMSHHT 1560
Db      1501 KVLVYDNARABAGQPVVEEFELCPDGDVSIHGAGSELANTADVPYLLKXMSHHT 1560
Qy      1561 TCWPGRTLYLLAPSPDKQRTWTALLESVAVAGRVREKAEADAKLLGNSLLKLEGGDRLD 1620
Db      1561 TCWPGRTLYLLAPSPDKQRTWTALLESVAVAGRVREKAEADAKLLGNSLLKLEGGDRLD 1620
Qy      1621 MNCCTLPSFDQVVLVGTSEGLYALNVLKNSLTHVPGIYIIKDLKELIMAGEBRA 1680
Db      1621 MNCCTLPSFDQVVLVGTSEGLYALNVLKNSLTHVPGIYIIKDLKELIMAGEBRA 1680
Qy      1681 LCLVDYKVKVKGSLAOSHHPADPDISPNTFEAVKGCGLFGAGKIENGCLICAMPKSVYL 1740
Db      1681 LCLVDYKVKVKGSLAOSHHPADPDISPNTFEAVKGCGLFGAGKIENGCLICAMPKSVYL 1740
Qy      1741 RYNNELSKYCKRKEIETSEPCSCIFPTVNSILIGTNKFEIDMKOYTLSEFLDKNDHSLA 1800
Db      1741 RYNNELSKYCKRKEIETSEPCSCIFPTVNSILIGTNKFEIDMKOYTLSEFLDKNDHSLA 1800
Qy      1801 PAVFAASSNPSPVSIYQVNSAGQREBYLLCFHEFGVPVDSYGRSRRTDLKMSRLPLAFA 1860
Db      1801 PAVFAASSNPSPVSIYQVNSAGQREBYLLCFHEFGVPVDSYGRSRRTDLKMSRLPLAFA 1860
Qy      1861 YREPLFTYTHNSLEVTIQARSSAGTPARATLDPNRYLYGPAISSAATYASGYOKL 1920
Db      1861 YREPLFTYTHNSLEVTIQARSSAGTPARATLDPNRYLYGPAISSAATYASGYOKL 1920
Qy      1921 RVICCKGNLVKESGTEHHRGPSTSSPNKGRPPTYNEHITKRVASSAPAPGEPSPREP 1980
Db      1921 RVICCKGNLVKESGTEHHRGPSTSSPNKGRPPTYNEHITKRVASSAPAPGEPSPREP 1980
Qy      1981 STPHRYRGRTLELRDKSPGRPLEREKSPGRILSTRRRSPARLFEDESSRGRLPAGAVRT 2040
Db      1981 STPHRYRGRTLELRDKSPGRPLEREKSPGRILSTRRRSPARLFEDESSRGRLPAGAVRT 2040
Qy      2041 PLSQVNTKVMDOSSV 2054
Db      2041 PLSQVNTKVMDOSSV 2054

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RESULT 4

ADJ96610 standard; protein; 2055 AA.

ADJ96610;

06-MAY-2004 (first entry)

Human citron Rho-interacting kinase CRK protein SeqID 67.

kinase; human; SNP; single nucleotide polymorphism;
 tyrosine protein kinase; serine/threonine protein kinase; PTK; STK;
 gene therapy; cancer; immune-related disease; cardiovascular disease;
 brain; neuronal associated disease; metabolic; inflammatory disorder;
 cytosolic; neuroprotective; immunomodulator; antiinflammatory; enzyme;
 citron Rho-interacting kinase; CRK.

Homo sapiens.

OS 57.

Key Location/Qualifiers

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FT      Misc-difference 961
FT      /note= "Wild type Ala substituted for Glu by single
FT      nucleotide polymorphism"
PN      WO2004006838-A2.
PD      22-JAN-2004.
PF      15-JUL-2003; 2003WO-US021730.
PR      15-JUL-2002; 2002US-0395632P.
PA      (SUGEN-) SUGEN INC.
PI      Whyte D, Manning G, Caenepeel S;
DR      WPI; 2004-122753/12.
DR      N-PSDB; ADJ96544.
XX      New nucleic acid molecule encoding a kinase polypeptide, useful for
XX      preparing a composition for treating diseases or disorders, e.g., cancer,
XX      or neurological, immunological or inflammatory disorders.
XX      Claim 1; SEQ ID NO 67; 366pp; English.

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This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytosolic, neuroprotective, immunomodulator and antiinflammatory activities. This polypeptide sequence is a human kinase protein sequence of the invention.

Sequence 2055 AA;

Query Match 99.7%; Score 10464.5; DB 8; Length 2055;

Beet Local Similarity 99.8%; Pred. No. 0; Mismatches 2; Indels 1; Gaps 1;

Matches 2050; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

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Qy      1 MLKFRYGRNPLDGAAPISRASRLNLFQGRKPEFTQQMSPLSEGLDALFVLFE 60
Db      1 MLKFRYGRNPLDGAAPISRASRLNLFQGRKPEFTQQMSPLSEGLDALFVLFE 60
Qy      61 EGSQPALMKIKGVNSFVRK-YSDTIAELQELQPSAKDPEVRSLYGCCGFPAVQVREKAT 119
Db      61 EGSQPALMKIKGVNSFVRK-YSDTIAELQELQPSAKDPEVRSLYGCCGFPAVQVREKAT 119
Qy      120 GDIYAMKVMKKKALLAQQVSEFFSEERNILSRSTSPWIPOLQYAFODGNHLYLWMEYQPG 179
Db      120 GDIYAMKVMKKKALLAQQVSEFFSEERNILSRSTSPWIPOLQYAFODGNHLYLWMEYQPG 179
Qy      121 GDIYAMKVMKKKALLAQQVSEFFSEERNILSRSTSPWIPOLQYAFODGNHLYLWMEYQPG 180
Db      121 GDIYAMKVMKKKALLAQQVSEFFSEERNILSRSTSPWIPOLQYAFODGNHLYLWMEYQPG 180
Qy      180 GDLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVRDIXENILVDRGTGIKLV 239
Db      180 GDLLSLNRYEDQDENLQFYLAELILAVSHVLMGYVRDIXENILVDRGTGIKLV 239
Qy      240 FGSAAKNNSNRVNAKLPIGTPDYNAPEVLTVMNGDGKGYGLDCDMSVGVIAEMLYG 299
Db      240 FGSAAKNNSNRVNAKLPIGTPDYNAPEVLTVMNGDGKGYGLDCDMSVGVIAEMLYG 299
Qy      241 FGSAAKNNSNRVNAKLPIGTPDYNAPEVLTVMNGDGKGYGLDCDMSVGVIAEMLYG 300
Db      241 FGSAAKNNSNRVNAKLPIGTPDYNAPEVLTVMNGDGKGYGLDCDMSVGVIAEMLYG 300
Qy      300 RSPFAEGTSARTFNINMFORFLKPPDDPKYSSDFLILQSLGQKXRLKFEGLCCHPF 359
Db      300 RSPFAEGTSARTFNINMFORFLKPPDDPKYSSDFLILQSLGQKXRLKFEGLCCHPF 359
Qy      301 RSPFAEGTSARTFNINMFORFLKPPDDPKYSSDFLILQSLGQKXRLKFEGLCCHPF 360
Db      301 RSPFAEGTSARTFNINMFORFLKPPDDPKYSSDFLILQSLGQKXRLKFEGLCCHPF 360
Qy      360 FSKIDMNNIRNSPPFPVFTLLKSDDDTSNFDPEKNSWSSSPCOLSPSGFSGEBLPEVGF 419
Db      360 FSKIDMNNIRNSPPFPVFTLLKSDDDTSNFDPEKNSWSSSPCOLSPSGFSGEBLPEVGF 419
Qy      361 FSKIDMNNIRNSPPFPVFTLLKSDDDTSNFDPEKNSWSSSPCOLSPSGFSGEBLPEVGF 420
Db      361 FSKIDMNNIRNSPPFPVFTLLKSDDDTSNFDPEKNSWSSSPCOLSPSGFSGEBLPEVGF 420

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QY 420 SYSKALGILGRSESVVSGLDSPAKTSMEEKLLIKSKELQSDQCHKMEQEMTLHRRV 479
DB 421 SYSKALGILGRSESVVSGLDSPAKTSMEEKLLIKSKELQSDQCHKMEQEMTLHRRV 480
QY 480 SEVEAVLSQKEVELKASETORSLSLEODLATYITTECSLSKRSLEQARMEVSQEDDALQTL 539
DB 481 SEVEAVLSQKEVELKASETORSLSLEODLATYITTECSLSKRSLEQARMEVSQEDDALQTL 540
QY 540 HDIRQSKRLQETIKQOEYQAOVEEMRLMNQLEBDLVSARRSDLYESLRSRLAAEEF 599
DB 541 HDIRQSKRLQETIKQOEYQAOVEEMRLMNQLEBDLVSARRSDLYESLRSRLAAEEF 600
QY 600 KRKATECOHKLKADQOGKPEVGEYAKLEKINABOOLKIQELOEKLKRAVKRSTATEL 659
DB 601 KRKATECOHKLKADQOGKPEVGEYAKLEKINABOOLKIQELOEKLKRAVKRSTATEL 660
QY 660 QNIRQAKRABERLEKLNQNRDESGIRKCLVEAEERHSLNKYRLETMRERENRLKD 719
DB 661 QNIRQAKRABERLEKLNQNRDESGIRKCLVEAEERHSLNKYRLETMRERENRLKD 720
QY 720 DIQTSQOIQOMADKILEEKHREAOVSAOHLBVHLKQEQHYEKKIVLDNQIKDIA 779
DB 721 DIQTSQOIQOMADKILEEKHREAOVSAOHLBVHLKQEQHYEKKIVLDNQIKDIA 780
QY 780 DKETLENNMORHEEBAHEKGLISBOKAMINAMDSKISLBQRIVELSEBANKLANSSIF 839
DB 781 DKETLENNMORHEEBAHEKGLISBOKAMINAMDSKISLBQRIVELSEBANKLANSSIF 840
QY 840 TORNNKAOBEMISELRQOKFYLETOAGKLEAONRKLBEOLKISHQSDSDKRLLEETR 899
DB 841 TORNNKAOBEMISELRQOKFYLETOAGKLEAONRKLBEOLKISHQSDSDKRLLEETR 900
QY 900 LREVSLEHEBOXLBEKROLTELQLSLOERESQJTLQARALJESQLQAKTELEETAAE 959
DB 901 LREVSLEHEBOXLBEKROLTELQLSLOERESQJTLQARALJESQLQAKTELEETAAE 960
QY 960 AABEIQALTARHDETORPFDALRNSCTVIITDEEOLNQLTEBNALNNQNFILSQDLBA 1019
DB 961 AABEIQALTARHDETORPFDALRNSCTVIITDEEOLNQLTEBNALNNQNFILSQDLBA 1020
QY 1020 SGANDEIVOLRSEVHLRREITEREMOJTSQKOTHEALKTCTMLEEQVMDLEALNDEL 1079
DB 1021 SGANDEIVOLRSEVHLRREITEREMOJTSQKOTHEALKTCTMLEEQVMDLEALNDEL 1080
QY 1080 EKERQWEAMRSVLDGKESQFECRVRELQRLDTEKQSPARADORTTESROVVELAVKHX 1139
DB 1081 EKERQWEAMRSVLDGKESQFECRVRELQRLDTEKQSPARADORTTESROVVELAVKHX 1140
QY 1140 AEIILALQALKEQKLIKASLSIDKNDLEKIAMLEMMARSLQOKLETREBELKQRLLEBOA 1199
DB 1141 AEIILALQALKEQKLIKASLSIDKNDLEKIAMLEMMARSLQOKLETREBELKQRLLEBOA 1200
QY 1200 KLQOQMDLOKNIHIFLTQGLQDALRADLKTERSDLYOULENOIYVSHKEVVMKEGITS 1259
DB 1201 KLQOQMDLOKNIHIFLTQGLQDALRADLKTERSDLYOULENOIYVSHKEVVMKEGITS 1260
QY 1260 QOTKLIDFLQAKMDQPAKKKQVPLQYNELKLALEKAKACALBEALQKTRITELASABE 1319
DB 1261 QOTKLIDFLQAKMDQPAKKKQVPLQYNELKLALEKAKACALBEALQKTRITELASABE 1320
QY 1320 AAHRKATDHPHSPATARQOISAMSAIVRSPHOPASMSLAPSSRRKESSTPEESFRR 1379
DB 1321 AAHRKATDHPHSPATARQOISAMSAIVRSPHOPASMSLAPSSRRKESSTPEESFRR 1380
QY 1380 LKERMHNIHPRFNVGLMRAATKAVCLDTVHFGQASKCEQVMCHPKSTCIPATCG 1439
DB 1381 LKERMHNIHPRFNVGLMRAATKAVCLDTVHFGQASKCEQVMCHPKSTCIPATCG 1440
QY 1440 LPAEYATHTFEAFCDKKNNSPGLQTKEPSSSLHLEGMKVPANNRGGQGMDRKTYIVLEG 1499
DB 1441 LPAEYATHTFEAFCDKKNNSPGLQTKEPSSSLHLEGMKVPANNRGGQGMDRKTYIVLEG 1500
QY 1500 SKVLIYDNEABAGORPVEBEFELCLPDGDVSIHGAVGASELANAKADVPIYLKMHSPH 1559

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DB 1501 SKVLIYDNEABAGORPVEBEFELCLPDGDVSIHGAVGASELANAKADVPIYLKMHSPH 1560
QY 1560 TTCWPGRTLYILAPSPFDKORWVTALLESVAVAGRVSRXEAADAKLGNLSLLKEGDDRL 1619
DB 1561 TTCWPGRTLYILAPSPFDKORWVTALLESVAVAGRVSRXEAADAKLGNLSLLKEGDDRL 1620
QY 1620 DMNCTLPSPDQVVLVGTREBGLYALNVLKNSLTHVIGICAVPQIYIILKOLEKLMLAGERR 1679
DB 1621 DMNCTLPSPDQVVLVGTREBGLYALNVLKNSLTHVIGICAVPQIYIILKOLEKLMLAGERR 1680
QY 1680 ALCLVDVKKVQSLAQSHLPAQPDISPNIPEAVKGCCHFGAGKIENGCLICAMPSSKYVI 1739
DB 1681 ALCLVDVKKVQSLAQSHLPAQPDISPNIPEAVKGCCHFGAGKIENGCLICAMPSSKYVI 1740
QY 1740 LRYMENLSKYCIKRIETSEPCSIHFTNYSILGTNKFYEIDMKOYTLLEFLDKNDHSL 1799
DB 1741 LRYMENLSKYCIKRIETSEPCSIHFTNYSILGTNKFYEIDMKOYTLLEFLDKNDHSL 1800
QY 1800 APAYFAASSNSFPVSIYOVNSAGQREBYLTCFHEGCVFVDSYGRSRITDDLKMSRLPLAF 1859
DB 1801 APAYFAASSNSFPVSIYOVNSAGQREBYLTCFHEGCVFVDSYGRSRITDDLKMSRLPLAF 1860
QY 1860 AYREBYLFTVTHNSLEVEIQARSSAGTPARAYLIDIPNRYLGPALISSGATYLAASYDK 1919
DB 1861 AYREBYLFTVTHNSLEVEIQARSSAGTPARAYLIDIPNRYLGPALISSGATYLAASYDK 1920
QY 1920 LRVLCCKNLVYSGSTEHRGPTSRSSPNKRGPTVMEHTIKRAVSSPAPEGSHPRE 1979
DB 1921 LRVLCCKNLVYSGSTEHRGPTSRSSPNKRGPTVMEHTIKRAVSSPAPEGSHPRE 1980
QY 1980 PSTPHRYEGRTTELRRDYSPPGRPLEREXSPGRILSTRERSPARLPESSGRRLPAGAVR 2039
DB 1981 PSTPHRYEGRTTELRRDYSPPGRPLEREXSPGRILSTRERSPARLPESSGRRLPAGAVR 2040
QY 2040 TPLSQVNVKMDQSSV 2054
DB 2041 TPLSQVNVKMDQSSV 2055

RESULT 5
ABG78363
ID ABG78363 standard; protein, 2053 AA.
XX
AC ABG78363;
XX
AC XX
XX
DT 15-NOV-2002 (first entry)
XX
DE RHO/RAC-interacting citron kinase-like human protein, designated NOV3b.
XX
XX Human; NOV; NOVX; NOVX-associated disorder; cardiomyopathy;
XX atherosclerosis; diabetes; cell signaling; metabolic pathway;
XX cellular receptor; downstream effector; cancer; gene therapy;
XX hypertension; congenital heart defect; aortic stenosis; obesity;
XX infectious disease; anorexia; Alzheimer's disease; Parkinson's disease;
XX neurodegenerative disorder; haemophilia; dyslipidemia; vaccine;
XX haematopoietic disease; scleroderma; fertility; immunogen;
XX idiopathic thrombocytopenic purpura; graft versus host disease;
XX Crohn's disease; multiple sclerosis; cirrhosis; autoimmune disease;
XX systemic lupus erythematosus; asthma; arthritis; psoriasis; allergy;
XX stroke; anxiety; Leisch-Nyhan syndrome; schizophrenia; cerebellar ataxia;
XX pain; alcoholism; transgenic.
OS
XX Homo sapiens.
XX
XX PN W0200226826-A2.
XX
XX PD 04-APR-2002.
XX
XX PF 27-SEP-2001; 2001WO-US042336.
XX
XX PR 27-SEP-2000; 2000US-0235631P.
XX
XX PR 27-SEP-2000; 2000US-0235633P.
PR

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PR 27-SEP-2000; 2000US-0235808P.
 PR 27-SEP-2000; 2000US-0236064P.
 PR 27-SEP-2000; 2000US-0236065P.
 PR 27-SEP-2000; 2000US-0236066P.
 PR 28-SEP-2000; 2000US-0236135P.
 PR 03-OCT-2000; 2000US-0237434P.
 PR 05-OCT-2000; 2000US-0238321P.
 PR 06-OCT-2000; 2000US-0238396P.
 PR 06-OCT-2000; 2000US-0238399P.
 PR 16-MAR-2001; 2001US-0276667P.
 PR 31-MAY-2001; 2001US-0294823P.
 PR 12-JUL-2001; 2001US-0304868P.
 PR 26-SEP-2001; 2001US-00235631.
 XX (CURA-) CURAGEN CORP.

PA Gerlach VL, Macdougall JR, Smithson G, Millet I, Stone D;
 PI Gunther E, Ellerman K, Grose WM, Alsobrook JP, Leplay DM;
 PI Burgess CE, Padigara W, Kekuda R, Spytek KA, Leach MD, Shinkens RA;
 XX WPI; 2002-499860/53.
 DR N-PSDB; ABS63436.

PT Novel isolated NOVX polypeptides and polynucleotides homologous to
 PT attractin, plexin, pappin-like family of proteins, useful for treating
 PT atherosclerosis, diabetes, cancer, Alzheimer's disease, hemophilia and
 PT stroke.

PS Claim 1; Page 44-45; 308bp; English.

XX The invention discloses the isolated human polypeptides, and
 CC polynucleotides encoding them, that have been designated NOVX. The
 CC polypeptides, polynucleotides and antibodies are useful in treating or
 CC preventing a NOVX-associated disorder which is cardiomyopathy,
 CC atherosclerosis and diabetes in a human, where the disorder is related to
 CC cell signal processing and metabolic pathway modulation. They can also be
 CC used in determining the presence of, or predisposition to, a disease
 CC associated with altered levels of the polypeptides and polynucleotides of
 CC any one of the 13 sequences (NOV1-NOV8), for raising antibodies, for
 CC identifying an agent that binds to, or that modulates the expression or
 CC activity of the polypeptide, for identifying an agent which is cellular
 CC receptor or downstream effector, for treating or preventing a NOVX-
 CC associated disorder and as a pharmaceutical composition comprising the
 CC polypeptide, polynucleotide or the antibody. The polypeptides and
 CC polynucleotides are useful in diagnostic applications (e.g. as a marker
 CC for cancerous cells or tissue types) where their amounts are assessed, or
 CC for the manufacture of a medicament (e.g. gene therapy) for treating or
 CC preventing disorders or syndromes such as hypertension, congenital heart
 CC defects, aortic stenosis, obesity, infectious disease, anorexia, cancer,
 CC Alzheimer's disease, Parkinson's disorders, neurodegenerative disorders,
 CC haemophilia, dyslipidemias, haematopoietic diseases, scleroderma,
 CC fertility, idiopathic thrombocytopenic purpura, graft versus host
 CC diseases, Crohn's disease, multiple sclerosis, cirrhosis, autoimmune
 CC disease, systemic lupus erythematosus, asthma, arthritis, psoriasis,
 CC allergy, stroke, anxiety, Lesch-Nyhan syndrome, schizophrenia, cerebellar
 CC ataxia, pain and alcoholism. They may also be used as immunogens to
 CC produce antibodies specific for the invention, and as vaccines.
 CC Transgenic cells containing a NOVX expressing construct are useful to
 CC produce non-human transgenic animals for studying the function and/or
 CC activity of the NOVX proteins and for identifying and/or evaluating
 CC modulators of NOVX protein activity. Transgenic cells containing a NOVX
 CC expressing construct are useful to produce non-human transgenic animals
 CC for studying the function and/or activity of the NOVX proteins and for
 CC identifying and/or evaluating modulators of NOVX protein activity. The
 CC sequences presented in ABG78359-ABG78371 are the human NOV1-NOV8 proteins
 XX
 SQ Sequence 2053 AA;

Query Match 99.7%; Score 10458.5; DB 5; Length 2053;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 2049; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MLKFRYGARNPIDAGAEPIASRASRLNLFQGGKPPFTMQQMSPLSREGLIDALFVLFE 60

Db 1 MLKFRYGARNPIDAGAEPIASRASRLNLFQGGKPPFTMQQMSPLSREGLIDALFVLFE 60
 QY 61 ECSQPALMKIKHVSFPAKYSDDTIAEIQELPSAXDFEVRSLVGGHFAEYQVYREKATG 120
 Db 61 ECSQPALMKIKHVSFPAKYSDDTIAEIQELPSAXDFEVRSLVGGHFAEYQVYREKATG 120
 QY 121 DIYAMKWKKKALLAQEVSFFEEERNLSTSPWIPQLDYAPQDKHLYLVMEYQGG 180
 Db 121 DIYAMKWKKKALLAQEVSFFEEERNLSTSPWIPQLDYAPQDKHLYLVMEYQGG 180
 QY 181 DLSLNRKEDQDENLQFYLAELILAVSHVLMGVHARDIKPENILVDRTHIKLYDF 240
 Db 181 DLSLNRKEDQDENLQFYLAELILAVSHVLMGVHARDIKPENILVDRTHIKLYDF 240
 QY 241 GSAAKMNSNMVNAKLPIGTPDYAPVYLTVNAGDGKGTGLDCDMSVGIAYIMTYGR 300
 Db 241 GSAAKMNSNMVNAKLPIGTPDYAPVYLTVNAGDGKGTGLDCDMSVGIAYIMTYGR 300
 QY 301 SPFAEGTSARTFNINMFQRLKFPDDPKVSSDFLDLIQSLCCQKELKEGKCHPFF 359
 Db 301 SPFAEGTSARTFNINMFQRLKFPDDPKVSSDFLDLIQSLCCQKELKEGKCHPFF 359
 QY 361 SKIDNNIRNSPPFPVFTLKSDDDTSNFBPEKNSWSSPCQSPSGSGEELPFVGS 420
 Db 361 SKIDNNIRNSPPFPVFTLKSDDDTSNFBPEKNSWSSPCQSPSGSGEELPFVGS 420
 QY 420 YSKALGILGRSESVVSGDSPAITSMEKLLIKSKELQDSQDKCHKEQEMTRILHRVS 480
 Db 420 YSKALGILGRSESVVSGDSPAITSMEKLLIKSKELQDSQDKCHKEQEMTRILHRVS 480
 QY 481 EVEAVLSQKVELKASEFQRLBODLATYTTGSSLSKRSLEQARMEVSQDDKXLOLH 540
 Db 481 EVEAVLSQKVELKASEFQRLBODLATYTTGSSLSKRSLEQARMEVSQDDKXLOLH 540
 QY 540 DIREOSRLQELKEQVYQAVYEMKLMNNOLEBDIVSARRSDYSESLRESRLAAEFK 600
 Db 540 DIREOSRLQELKEQVYQAVYEMKLMNNOLEBDIVSARRSDYSESLRESRLAAEFK 600
 QY 601 RKATECOHKLKANDQGEVGEYAKLEKINAQOLKIQELQEKLEKAVKASTATELILQ 660
 Db 601 RKATECOHKLKANDQGEVGEYAKLEKINAQOLKIQELQEKLEKAVKASTATELILQ 660
 QY 660 NIRQAKFAEPELEKQNRBDSSEIRIKCLVEAERRRSLNKVRLTETMERERRLKDD 719
 Db 660 NIRQAKFAEPELEKQNRBDSSEIRIKCLVEAERRRSLNKVRLTETMERERRLKDD 719
 QY 721 IOTKSQOIQMAADKILIEKHREAVSAHLEVLKQEQHYBEKIKVLDNQIKKDLAD 780
 Db 721 IOTKSQOIQMAADKILIEKHREAVSAHLEVLKQEQHYBEKIKVLDNQIKKDLAD 780
 QY 780 KETLENMMQREBEAHEKGLTISEQKAMINAMDSKIRSLBQRIYVLSANKLAANSLSFT 840
 Db 780 KETLENMMQREBEAHEKGLTISEQKAMINAMDSKIRSLBQRIYVLSANKLAANSLSFT 840
 QY 841 QRNMKAQEBMSIELRQKQFYLETQAGKLEAQRKLEBQLEKISHPDHDKRLLETRL 900
 Db 841 QRNMKAQEBMSIELRQKQFYLETQAGKLEAQRKLEBQLEKISHPDHDKRLLETRL 900
 QY 840 QRNMKAQEBMSIELRQKQFYLETQAGKLEAQRKLEBQLEKISHPDHDKRLLETRL 899
 Db 840 QRNMKAQEBMSIELRQKQFYLETQAGKLEAQRKLEBQLEKISHPDHDKRLLETRL 899
 QY 901 REVSLEHEQKLEKQLELQSLQESRESQTLQAARALLESQRLQAKTELEETTAB 960
 Db 901 REVSLEHEQKLEKQLELQSLQESRESQTLQAARALLESQRLQAKTELEETTAB 960
 QY 900 REVSLEHEQKLEKQLELQSLQESRESQTLQAARALLESQRLQAKTELEETTAB 959
 Db 900 REVSLEHEQKLEKQLELQSLQESRESQTLQAARALLESQRLQAKTELEETTAB 959
 QY 961 EEEIQALTAHDEIQRKFDALNSCTVITDLEBQNLQTEDNAELNNQFYLXKQLEBAS 1020
 Db 961 EEEIQALTAHDEIQRKFDALNSCTVITDLEBQNLQTEDNAELNNQFYLXKQLEBAS 1020
 QY 960 EEEIQALTAHDEIQRKFDALNSCTVITDLEBQNLQTEDNAELNNQFYLXKQLEBAS 1019
 Db 960 EEEIQALTAHDEIQRKFDALNSCTVITDLEBQNLQTEDNAELNNQFYLXKQLEBAS 1019
 QY 1021 GANDEIVQLRSEVDHLREITEREQMQLTSQQTMEALKTCTMLEBQVMDLEALDELLE 1080
 Db 1021 GANDEIVQLRSEVDHLREITEREQMQLTSQQTMEALKTCTMLEBQVMDLEALDELLE 1080
 QY 1020 GANDEIVQLRSEVDHLREITEREQMQLTSQQTMEALKTCTMLEBQVMDLEALDELLE 1079
 Db 1020 GANDEIVQLRSEVDHLREITEREQMQLTSQQTMEALKTCTMLEBQVMDLEALDELLE 1079
 QY 1081 KERQWEARSVLQPEKSGPEQCRVRELQMLDTEKQSRARQORITESHQVVELAVKEKA 1140
 Db 1081 KERQWEARSVLQPEKSGPEQCRVRELQMLDTEKQSRARQORITESHQVVELAVKEKA 1140

Db 1080 KEROMENASVLDEKSEQFECRVELQRMIDTEKOSRARDQRTESRQVVELAVKENKA 1139
 Qy 1141 EILALQOALKEQKLKAESLSDKLNDEKKAEMENARSIOQKLETERELKQBLEBOAK 1200
 Db 1140 EILALQOALKEQKLKAESLSDKLNDEKKAEMENARSIOQKLETERELKQBLEBOAK 1199
 Qy 1201 LQOQMDLOKXNHLRLTQGLQOALDRADDLKTERSDELYQLENIQVLYSHKXVMEGTISQ 1260
 Db 1200 LQOQMDLOKXNHLRLTQGLQOALDRADDLKTERSDELYQLENIQVLYSHKXVMEGTISQ 1259
 Qy 1261 QTKLIDELQAKMOOPAKKKKVPLOYNEMLKALEKEXARGCELEALQKTEILRSAREEA 1320
 Db 1260 QTKLIDELQAKMOOPAKKKKVPLOYNEMLKALEKEXARGCELEALQKTEILRSAREEA 1319
 Qy 1321 AHRKATDHPHSTPATARQOIAMSAIVRSBEHOPSAISLAPPSRKSSTPEERSRL 1380
 Db 1320 AHRKATDHPHSTPATARQOIAMSAIVRSBEHOPSAISLAPPSRKSSTPEERSRL 1379
 Qy 1381 KERHNNIPIHRENVGLNMRATKCAVCLDVTNFGROASKLECOVMCHPKSTCIPATCGL 1440
 Db 1380 KERHNNIPIHRENVGLNMRATKCAVCLDVTNFGROASKLECOVMCHPKSTCIPATCGL 1439
 Qy 1441 PARVATHFTEAFGRDKNSPGLQTKEPSSSLHLEGMMKVRRNKGQGGMDRKYTVLEGS 1500
 Db 1440 PARVATHFTEAFGRDKNSPGLQTKEPSSSLHLEGMMKVRRNKGQGGMDRKYTVLEGS 1499
 Qy 1501 KVLIIYDNEAREAGORPVEEFELCLPDGVSIGHAVGASELANTAKADVPIYILKXESHPT 1560
 Db 1500 KVLIIYDNEAREAGORPVEEFELCLPDGVSIGHAVGASELANTAKADVPIYILKXESHPT 1559
 Qy 1561 TCWPGRTLYLLAPSPDKQKRWVTALLESVAGRVSRKAKADAKLLGNSLLKLEGGDRLD 1620
 Db 1560 TCWPGRTLYLLAPSPDKQKRWVTALLESVAGRVSRKAKADAKLLGNSLLKLEGGDRLD 1619
 Qy 1621 MNCITLPPSDQVNVGTEBEGYALNVLKNSLTHVPGIGAVQIYIILKOLEKLLMAGEERA 1680
 Db 1620 MNCITLPPSDQVNVGTEBEGYALNVLKNSLTHVPGIGAVQIYIILKOLEKLLMAGEERA 1679
 Qy 1681 LCLVDYKVKVQSLAOSHLPAPDISPNIPEAVKGCMLFGAGKLENGLCICAMPKSVIL 1740
 Db 1680 LCLVDYKVKVQSLAOSHLPAPDISPNIPEAVKGCMLFGAGKLENGLCICAMPKSVIL 1739
 Qy 1741 RYNNENSKYCIKREIETSEPCSCIFHTNYSILIGTNKFYEDIMKQYTLLEFELDKNDSLA 1800
 Db 1740 RYNNENSKYCIKREIETSEPCSCIFHTNYSILIGTNKFYEDIMKQYTLLEFELDKNDSLA 1799
 Qy 1801 PAVFAASNSFPVSIYOVNSAGOREEYLLCFHEGCVFVDSYGRSRITDDIKMSRLPLAFA 1860
 Db 1800 PAVFAASNSFPVSIYOVNSAGOREEYLLCFHEGCVFVDSYGRSRITDDIKMSRLPLAFA 1859
 Qy 1861 YREBPVLFVTHPNSLEVEIEIARSSAGTPARAYLDIPNRYLGPATISSGATYLAASYDYL 1920
 Db 1860 YREBPVLFVTHPNSLEVEIEIARSSAGTPARAYLDIPNRYLGPATISSGATYLAASYDYL 1919
 Qy 1921 RYVCKKGNLVKESGTEHHRGPSTSRSSPNKRGPTVNEHTTKRYVASSPAPPEGSHPREP 1980
 Db 1920 RYVCKKGNLVKESGTEHHRGPSTSRSSPNKRGPTVNEHTTKRYVASSPAPPEGSHPREP 1979
 Qy 1981 STPHRYREGTELRDCKSPGRPLERKSPGRILSTRERSPARLFEDSSRGRLPAQAVRT 2040
 Db 1980 STPHRYREGTELRDCKSPGRPLERKSPGRILSTRERSPARLFEDSSRGRLPAQAVRT 2039
 Qy 2041 PLSOVNVWMOSSV 2054
 Db 2040 PLSOVNVWMOSSV 2053

RESULT 6

ADA05642

ID ADA05642 standard; protein: 2053 AA.

XX AC ADA05642;

XX

DT 06-NOV-2003 (first entry)
 DE Human NOVA protein SEQ ID NO:2.
 XX human; NOVA; antidiabetic; anorectic; antibacterial; virocidic;
 KW immunomodulator; cytostatic; neuroprotective;
 KW antiparkinsonian; antidiabetic; gene therapy; human disease;
 KW metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW immune disorder; haematopoietic disorder; dyslipidaemia.
 XX Homo sapiens.
 OS
 PN WO2003029424-A2.
 XX 10-APR-2003.
 PD
 XX 02-OCT-2002; 2002WO-US031373.
 PF
 XX 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327435P.
 PR 09-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 17-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 PR 01-OCT-2002; 2002US-00262511.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Smitheon G, Miller I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Paturajan M, Spytek KA, Bainger SR, Ellerman K, Malvankar UM;
 PI Ot T, Gorman L, Zetunuen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SC;
 PI Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Bergins C, DiIppio VA;
 PI Eisen AJ, Gangoli EA, Rieger DK, Spaderna SK;
 XX WPI; 2003-381626/36.
 DR N-PSDB; ADA05641.
 XX
 PT New NOVA polypeptides and nucleic acids, useful for diagnosing,
 PT preventing or treating NOVA-associated disorders, e.g. diabetes, obesity,
 PT cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 PS Claim 1; Page 99-100; 586pp; English.
 XX
 CC The present invention describes NOVA proteins, where X can be 1 to 55
 CC (e.g. NOVA). Also described: (1) a composition comprising a polypeptide
 CC described above and a carrier; (2) a kit comprising, in one or more
 CC containers, the composition described above; (3) an isolated nucleic acid

molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NOVX sequences have anti-diabetic, anorectic, antibacterial, virocidic, immunomodulator, cytostatic, neurotropic, neuroprotective, antiparkinsonian and antilipemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, hematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.

XX Sequence 2053 AA;

Query Match 99.7%; Score 10458.5; DB 6; Length 2053;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2049; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MKFKYGANPLDAGAAEPPLASASRLNFPQCKPPPTQOQSPLSRSGILDALVLE 60
DB 1 MKFKYGANPLDAGAAEPPLASASRLNFPQCKPPPTQOQSPLSRSGILDALVLE 60
QY 61 ECSOPALMKIKHVSNFVKYSDPTIAELOPSAKDFEVRSLVGCCHPAVQVVRKKA 120
DB 61 ECSOPALMKIKHVSNFVKYSDPTIAELOPSAKDFEVRSLVGCCHPAVQVVRKKA 120
QY 121 DIYAMKVMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNLVLMEXOPG 180
DB 121 DIYAMKVMKKALLAQEQVSPFEERNILSRSTSPWIPOLQYAFQDKNLVLMEXOPG 180
QY 181 DLISLNRKEDQDENLLOFYLAELILAVSHVLMGYVHRDIKPNILVDRGHIKLVDF 240
DB 181 DLISLNRKEDQDENLLOFYLAELILAVSHVLMGYVHRDIKPNILVDRGHIKLVDF 240
QY 241 GSAAMKNSKMNNAKLPFGTDPYMAPEVLTVMNGDGKGYGLDCMWSGVAVEMTYR 300
DB 241 GSAAMKNSKMNNAKLPFGTDPYMAPEVLTVMNGDGKGYGLDCMWSGVAVEMTYR 300
QY 301 SPFAGTSARTNNINNFQFLKFPDDPKVSSDFDLIQSLCGQKRLKFEGLCCHPF 360
DB 301 SPFAGTSARTNNINNFQFLKFPDDPKVSSDFDLIQSLCGQKRLKFEGLCCHPF 360
QY 361 SKIDNNNIRNSPPPVFTLKSDDDTSNFDPEKNSWSSPCOLSPSGSGEELPVG 420
DB 361 SKIDNNNIRNSPPPVFTLKSDDDTSNFDPEKNSWSSPCOLSPSGSGEELPVG 420
QY 421 YSKALGIIIGRSRVSGLDSPAKTSMKKLTKSKELODSODCKHMEQETRLHRRVS 480
DB 421 YSKALGIIIGRSRVSGLDSPAKTSMKKLTKSKELODSODCKHMEQETRLHRRVS 480
QY 481 EYEAVTLQKEVEELKASETORSLLEODLATYITEGSSLKRSLEQAMMEVSQEDKALQLH 540
DB 481 EYEAVTLQKEVEELKASETORSLLEODLATYITEGSSLKRSLEQAMMEVSQEDKALQLH 540

QY 541 DIREQSKLOEIKGEYQAVSEMRLLMNOLEDLYSARRSDLYSESLAESEFK 600
DB 540 DIREQSKLOEIKGEYQAVSEMRLLMNOLEDLYSARRSDLYSESLAESEFK 599
QY 601 RKATECOHLLKAKDQKPEVGYALKLEKINAAQOLKIOELQKLEKAVASTAETELL 660
DB 600 RKATECOHLLKAKDQKPEVGYALKLEKINAAQOLKIOELQKLEKAVASTAETELL 659
QY 661 NIRAERARELEKLONRDSSGIRKLVAEERRHSLNKVRLIETMERRENRKLD 720
DB 660 NIRAERARELEKLONRDSSGIRKLVAEERRHSLNKVRLIETMERRENRKLD 719
QY 721 IQRSQOIQMADKTIIEBKHEAOVSAQHEVHLKQEQHYBEKIKVLDNOIKDLD 780
DB 720 IQRSQOIQMADKTIIEBKHEAOVSAQHEVHLKQEQHYBEKIKVLDNOIKDLD 779
QY 781 KETLENNORHEEAHEKGTISEQAMNAMSRTSRFORVETSEANKLAANSLEFT 840
DB 780 KETLENNORHEEAHEKGTISEQAMNAMSRTSRFORVETSEANKLAANSLEFT 839
QY 841 ORNMKAQEMISLROQKTYLETOAGKLEAONRKLEBOLEKISHODSPKNRLLEETRL 900
DB 840 ORNMKAQEMISLROQKTYLETOAGKLEAONRKLEBOLEKISHODSPKNRLLEETRL 899
QY 901 REYSLHEBQKLEKQTLTELQSLQERESQULTALOAPALLESQURQAKTELETTAA 960
DB 900 REYSLHEBQKLEKQTLTELQSLQERESQULTALOAPALLESQURQAKTELETTAA 959
QY 961 EBEIOALTARBEIOKFPALNSCTVITDLSEQONLVEDNAELNNQNPYLSKIDP 1020
DB 960 EBEIOALTARBEIOKFPALNSCTVITDLSEQONLVEDNAELNNQNPYLSKIDP 1019
QY 1021 GANDEIVQLRSEVDHLRREITEREMQITSOQOTMEALKTCTMLEBQVMDLEALNDEL 1080
DB 1020 GANDEIVQLRSEVDHLRREITEREMQITSOQOTMEALKTCTMLEBQVMDLEALNDEL 1079
QY 1081 KERQWEAMRSVIGDEKSOPECEVRRELQRMLDTEKOSRAPADORTESROVVELAVEHKA 1140
DB 1080 KERQWEAMRSVIGDEKSOPECEVRRELQRMLDTEKOSRAPADORTESROVVELAVEHKA 1139
QY 1141 ETLALQALKEQKLAESLSDKLNLEKKNALENNARSLQOKLETERELKORLEBOAK 1200
DB 1140 ETLALQALKEQKLAESLSDKLNLEKKNALENNARSLQOKLETERELKORLEBOAK 1199
QY 1201 LOOQMDLOKNHIFRLTOGLQALADRADILKTERSDLEYLENIQVLYSHEKYMESTISQ 1260
DB 1200 LOOQMDLOKNHIFRLTOGLQALADRADILKTERSDLEYLENIQVLYSHEKYMESTISQ 1259
QY 1261 QTKLIDFLQAKMDQPAKKKVPLOYNELKALEKKAQALIEEALQKTRIELRSAREBA 1320
DB 1260 QTKLIDFLQAKMDQPAKKKVPLOYNELKALEKKAQALIEEALQKTRIELRSAREBA 1319
QY 1321 AHRKATDHPHSTPTATQAQIAMSALVRSPEHQPAMSLAPPSSRRKESSTPEEF 1380
DB 1320 AHRKATDHPHSTPTATQAQIAMSALVRSPEHQPAMSLAPPSSRRKESSTPEEF 1379
QY 1381 KERMEHNTIPIHFNVYGNARATCAVCLPTVHFGRASCLIEQWCHPKCSTCLPATGCL 1440
DB 1380 KERMEHNTIPIHFNVYGNARATCAVCLPTVHFGRASCLIEQWCHPKCSTCLPATGCL 1439
QY 1441 PAEYATHTTEAFGRDKMNSPGIQTEKPESSLHLEGMKVPRNNKRGQOGMDRKYTVLBS 1500
DB 1440 PAEYATHTTEAFGRDKMNSPGIQTEKPESSLHLEGMKVPRNNKRGQOGMDRKYTVLBS 1499
QY 1501 KYLTYDNEAREAGQRPVEFEFLCLPDGVYSIHGAVGASELANTAKADVPYIILKMSHPHT 1560
DB 1500 KYLTYDNEAREAGQRPVEFEFLCLPDGVYSIHGAVGASELANTAKADVPYIILKMSHPHT 1559
QY 1561 TCMPCRLLYTLAPSPDPKORWYTLAESVAVAGRSRREABADAKLIGNSLLTLEBDDDL 1620
DB 1560 TCMPCRLLYTLAPSPDPKORWYTLAESVAVAGRSRREABADAKLIGNSLLTLEBDDDL 1619
QY 1621 MNCITLFPSDQVVLVGTBERGLYALNVLKNSLTHVPGI GAVPQIYIIKDLEKLMLAGEBRA 1680

Db 1620 MNCTLPEDQVVLVTEEGVLALNVLKNSLTHVPEIGAVFOYITKDKLEKLMINGERA 1679
 Qy 1681 LCLVDVKKVKQSLAQSLLPAOPDISPNI FEAVKGCFLFGAGKIENGLCICAMPSEKVVIL 1740
 Db 1680 LCLVDVKKVKQSLAQSLLPAOPDISPNI FEAVKGCFLFGAGKIENGLCICAMPSEKVVIL 1739
 Qy 1741 RYNNENLSKYCIKKEIETSEPCSCIFHTVYSLILGINKVEYLDKQYTLLEFLDKNDHSLA 1800
 Db 1740 RYNNENLSKYCIKKEIETSEPCSCIFHTVYSLILGINKVEYLDKQYTLLEFLDKNDHSLA 1799
 Qy 1801 PAVEAASNSPSPVSIQVNSAGOREEYLLCFHEFGVFPDSYGRSRTDMLKMSRLPLAFA 1860
 Db 1800 PAVEAASNSPSPVSIQVNSAGOREEYLLCFHEFGVFPDSYGRSRTDMLKMSRLPLAFA 1859
 Qy 1861 YREPYLFTVHNSLEVIIBIOARSSAGTPARAYLDIPNRYLGPALISSGAIYLAASSYQDKL 1920
 Db 1860 YREPYLFTVHNSLEVIIBIOARSSAGTPARAYLDIPNRYLGPALISSGAIYLAASSYQDKL 1919
 Qy 1921 RVICCKGNLVKESGTEHHRGPSTSSPNKGGPPYNNHITKRVASSPAPBEGSHPREP 1980
 Db 1920 RVICCKGNLVKESGTEHHRGPSTSSPNKGGPPYNNHITKRVASSPAPBEGSHPREP 1979
 Qy 1981 STPHRYREGTETLRDCKSPGRPLEREKSGRILSTRRERSPARLPEDSSRGRLPAGAVT 2040
 Db 1980 STPHRYREGTETLRDCKSPGRPLEREKSGRILSTRRERSPARLPEDSSRGRLPAGAVT 2039
 Qy 2041 PLSQVNMKVMQSSV 2054
 Db 2040 PLSQVNMKVMQSSV 2053

RESULT 7 AAU03501

ID AAU03501 standard; protein; 2053 AA.

XX AC AAU03501;
 XX DT 12-SEP-2001 (first entry)
 XX DE Human protein kinase #1.
 XX KM Human, protein kinase; PTK; STK; cancer; cardiovascular disease;
 KM metabolic disorder; immune related disease; neurological disorder;
 KM neurodegenerative disorder; inflammatory disorder; infectious disease;
 KM reproductive disorder.
 XX OS Homo sapiens.
 XX PN MO200138503-A2.
 XX PD 31-MAY-2001.
 XX PF 22-NOV-2000; 2000MO-US032085.
 XX PR 24-NOV-1999; 99US-0167482P.
 XX PA (SUGC-) SUGEN INC.
 XX PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX DR MPI; 2001-343950/36.
 XX DR N-PSDB; AAS06701.
 XX PT Nucleic acid encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX PS Claim 7; Fig 2; 433pp; English.
 XX CC AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or

CC serine/threonine kinase (PK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity

Sequence 2053 AA:

Query Match 99.4%; Score 10431.5; DB 4; Length 2053;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 2045; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 1 MLKRYGARNPLDGAAPPIASRSLNLFPGKPPFTQOOMPSLREGILDLFLVFE 60
 Db 1 MLKRYGARNPLDGAAPPIASRSLNLFPGKPPFTQOOMPSLREGILDLFLVFE 60
 Qy 61 ECSQPALMKIKGVNPFYRK-YSDTIAELOLPASAKDFEVLVCGCFHFAVQVVERKAT 119
 Db 61 ECSQPALMKIKGVNPFYRK-YSDTIAELOLPASAKDFEVLVCGCFHFAVQVVERKAT 120
 Qy 120 GDIYAMKVMKKALLAOEVSFFEEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPG 179
 Db 121 GDIYAMKVMKKALLAOEVSFFEEERNILSRSTSPWIPOLQYAFQDNHLYLVMEYQPG 180
 Qy 180 GDLSILNRYEDQDENLLOFYLAELITAVSVHLMGVHNDIRENLTVPRTGHIKVD 239
 Db 181 GDLSILNRYEDQDENLLOFYLAELITAVSVHLMGVHNDIRENLTVPRTGHIKVD 240
 Qy 240 FGSAAKNSNMVNAKLPIGTPTYMAPEVLTVNMGDGKGTGLDGDWMSVGIAYEMTYG 299
 Db 241 FGSAAKNSNMVNAKLPIGTPTYMAPEVLTVNMGDGKGTGLDGDWMSVGIAYEMTYG 300
 Qy 300 RSPFAEGTSATFNNINMFORFLKFPDDPKVSDFLDIQSLCGQKERLKEGICHPF 359
 Db 301 RSPFAEGTSATFNNINMFORFLKFPDDPKVSDFLDIQSLCGQKERLKEGICHPF 360
 Qy 360 FSKIDMNNIRNSPPPPVPTLKSDDTSNPDPEKNSWSSSPCQLSPGFGSEELPFVGF 419
 Db 361 FSKIDMNNIRNSPPPPVPTLKSDDTSNPDPEKNSWSSSPCQLSPGFGSEELPFVGF 420
 Qy 420 SYSKALGILGRSESVSGLDSPAKTSSWEKKLITKSKELQDSODKCHMEDEMTLRHRV 479
 Db 421 SYSKALGILGRSESVSGLDSPAKTSSWEKKLITKSKELQDSODKCHMEDEMTLRHRV 480
 Qy 480 SEVEAVLSQKEVELKASGTORSLLEODLATYITECSSLKSLLEQARMEVSQEDDKALQTL 539
 Db 481 SEVEAVLSQKEVELKASGTORSLLEODLATYITECSSLKSLLEQARMEVSQEDDKALQTL 540
 Qy 540 HDIREQSRKLOETIEQOYQAOVEEMRLMMNOLBEDLVASRRSDLYESELLEESRLAEEF 599
 Db 541 HDIREQSRKLOETIEQOYQAOVEEMRLMMNOLBEDLVASRRSDLYESELLEESRLAEEF 600
 Qy 600 KRKATCOHKLLAKDDGKPEVGYALKETNAEQOLKIOELQKLEKAVASTBATELL 659
 Db 601 KRKATCOHKLLAKDDGKPEVGYALKETNAEQOLKIOELQKLEKAVASTBATELL 660
 Qy 660 QNTRQAKERARELEKLOINEDSSEGIRKKLVEAEERHSLLENKYKLETMERENRRLKD 719
 Db 661 QNTRQAKERARELEKLOINEDSSEGIRKKLVEAEERHSLLENKYKLETMERENRRLKD 720
 Qy 720 DIQTKSQOIQOMADKTIILEBKREAOVSAOHLVHLKQEQHYEEKIKVLNDQIKKOLA 779
 Db 721 DIQTKSQOIQOMADKTIILEBKREAOVSAOHLVHLKQEQHYEEKIKVLNDQIKKOLA 780

QY 780 DKETLENNMQRHEEBAHEKGIKILSEOKAMINAMDskIRSLSEORIVELSEANKLAANSLSF 839
 DB 781 DKETLENNMQRHEEBAHEKGIKILSEOKAMINAMDskIRSLSEORIVELSEANKLAANSLSF 840
 QY 840 TORNNKAOEEMIISLROQKFLYLETOAGLEBONKRLKEBQLEKISHOHSDKORLLEETR 899
 DB 841 TORNNKAOEEMIISLROQKFLYLETOAGLEBONKRLKEBQLEKISHOHSDKORLLEETR 900
 QY 900 LREVSLEHEBQKLEKORLTLOLSTLOERESOLFTALQARAALESQLOAKTELEETAE 959
 DB 901 LREVSLEHEBQKLEKORLTLOLSTLOERESOLFTALQARAALESQLOAKTELEETAE 960
 QY 960 AAEIIOALTARDEIORKFDALRNSCTVITDLBEOALNQTEDNALNNONYLSKOLDEA 1019
 DB 961 AAEIIOALTARDEIORKFDALRNSCTVITDLBEOALNQTEDNALNNONYLSKOLDEA 1020
 QY 1020 SGANDEIVOLRSEVDHLREITEREMOLTSQKQTEALKTCTMLEBEOVMDLEALNDELL 1079
 DB 1021 SGANDEIVOLRSEVDHLREITEREMOLTSQKQTEALKTCTMLEBEOVMDLEALNDELL 1080
 QY 1080 EKERQWEMRSVLDGKESQFECRVRELQRMLDTEKQSPARADQRTESROVVELAVKEHK 1139
 DB 1081 EKERQWEMRSVLDGKESQFECRVRELQRMLDTEKQSPARADQRTESROVVELAVKEHK 1140
 QY 1140 AEIILALQALKEOKLKAKESLSDKINDLEKHAMLEMNARSLOQKLETERELKORLLEBQA 1199
 DB 1141 AEIILALQALKEOKLKAKESLSDKINDLEKHAMLEMNARSLOQKLETERELKORLLEBQA 1200
 QY 1200 KLQOQMDIOKNHIFLITQGLBOLDRADLILTERSDELTYOLBNIOVLYSHEKVMKEGITS 1259
 DB 1201 KLQOQMDIOKNHIFLITQGLBOLDRADLILTERSDELTYOLBNIOVLYSHEKVMKEGITS 1260
 QY 1260 QOTKLIDLOAKMOPAKKKKVPLOYNELKALBEXKRCOLELEBALKTRIELRSAREE 1319
 DB 1261 QOTKLIDLOAKMOPAKKKKVPLOYNELKALBEXKRCOLELEBALKTRIELRSAREE 1320
 QY 1320 AAHRKATDHPSTPATAROOIAMSIVRSPEHQSASMLAPSSRRKESSTPEEFERR 1379
 DB 1321 AAHRKATDHPSTPATAROOIAMSIVRSPEHQSASMLAPSSRRKESSTPEEFERR 1380
 QY 1380 LKERMHNI PHRFVNLNMRATKCAVCLDTVHFGQASKLECYQWCHPKSCTCLPATCG 1439
 DB 1381 LKERMHNI PHRFVNLNMRATKCAVCLDTVHFGQASKLECYQWCHPKSCTCLPATCG 1440
 QY 1440 LPAEYATFTFAFCDCDKANSRGLQTKERSSSLHLEGMKVPRNNRGOQMDRKYIVLEG 1499
 DB 1441 LPAEYATFTFAFCDCDKANSRGLQTKERSSSLHLEGMKVPRNNRGOQMDRKYIVLEG 1500
 QY 1500 SKVLIYDNEABAGORPVEBPELCLPDGVSIGHAVGASELANATAKADVPYILKMKESHPH 1559
 DB 1501 SKVLIYDNEABAGORPVEBPELCLPDGVSIGHAVGASELANATAKADVPYILKMKESHPH 1560
 QY 1560 TTCWPGRTLYLLAPSPDKORWVTALBSVAVAGRVSRKEADAKULANSILKLEGGDRL 1619
 DB 1561 TTCWPGRTLYLLAPSPDKORWVTALBSVAVAGRVSRKEADAKULANSILKLEGGDRL 1620
 QY 1620 DMNCTLPSSDQVYVGTBEGLYALNVLKNSLTHVGCIGAVPOIYIIXLEKILMTAGBER 1679
 DB 1621 DMNCTLPSSDQVYVGTBEGLYALNVLKNSLTHVGCIGAVPOIYIIXLEKILMTAGBER 1680
 QY 1680 ALCLVDVKKVKSLOSLQASHLPAPODISPNIPEAVKCGHLFGAKIENGCLICAMPSKYVI 1739
 DB 1681 ALCLVDVKKVKSLOSLQASHLPAPODISPNIPEAVKCGHLFGAKIENGCLICAMPSKYVI 1740
 QY 1740 LRYNENLSKYCIKRIEITSEPCSIHFTNYSILIGTNKFEYIDMKOYTLLEFLDKNDHSL 1799
 DB 1741 LRYNENLSKYCIKRIEITSEPCSIHFTNYSILIGTNKFEYIDMKOYTLLEFLDKNDHSL 1800
 QY 1800 APAVAASNSFPVSIYOVSAGOREBYILCFHEGCVFVDSIGRSRDTDLKMSKLPALF 1859
 DB 1801 APAVAASNSFPVSIYOVSAGOREBYILCFHEGCVFVDSIGRSRDTDLKMSKLPALF 1860

QY 1860 AYREPYLFVTHNSLEVIIEIOASSAGTPARAYLDINPPIYGLPAISSGALTYLASSYODK 1919
 DB 1861 AYREPYLFVTHNSLEVIIEIOASSAGTPARAYLDINPPIYGLPAISSGALTYLASSYODK 1920
 QY 1920 LRVICCKGNLVKESGTEHHRGPTSRSSPNKRGPTTYNEHITTKRVASSPAPPEGSPHRE 1979
 DB 1921 LRVICCKGNLVKESGTEHHRGPTSRSSPNKRGPTTYNEHITTKRVASSPAPPEGSPHRE 1980
 QY 1980 PSTPHRYREGRTELRDRKSPGRPLEREKSPGRITISTRENSPARLFFDSSRGRLPAGAVR 2039
 DB 1981 PSTPHRYREGRTELRDRKSPGRPLEREKSPGRITISTRENSPARLFFDSSRGRLPAGAVR 2040
 QY 2040 TPPLSQVKNWMDOS 2052
 DB 2041 TPPLSQVKNWMDOS 2053
 RESULT 8
 ABG78362
 ID ABG78362 standard; protein; 2066 AA.
 XX ABG78362;
 AC
 XX
 XX
 XX 15-NOV-2002 (first entry)
 DE Human protein, homologous to kinases, designated NOV3A.
 XX
 XX Human; NOV; NOVX-associated disorder; cardiomyopathy;
 KW atherosclerosis; diabetes; cell signalling; metabolic pathway;
 KW cellular receptor; downstream effector; cancer; gene therapy;
 KW hypertension; congenital heart defect; aortic stenosis; obesity;
 KW infectious disease; anorexia; Alzheimer's disease; Parkinson's disease;
 KW neurodegenerative disorder; haemophilia; dyslipidemia; vaccine;
 KW haemopoietic disease; scleroderma; fertility; immunogen;
 KW idiopathic thrombocytopenic purpura; graft versus host disease;
 KW Crohn's disease; multiple sclerosis; cirrhosis; autoimmune disease;
 KW systemic lupus erythematosus; asthma; arthritis; psoriasis; allergy;
 KW stroke; anxiety; Leech-Nyman syndrome; schizophrenia; cerebellar ataxia;
 KW pain; alcoholism; transgenic.
 KW
 OS Homo sapiens.
 XX
 XX WO200226826-A2.
 PN
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-US042336.
 PR 27-SEP-2000; 2000US-0235631P.
 PR 27-SEP-2000; 2000US-0235633P.
 PR 27-SEP-2000; 2000US-0235808P.
 PR 27-SEP-2000; 2000US-0236064P.
 PR 27-SEP-2000; 2000US-0236065P.
 PR 27-SEP-2000; 2000US-0236066P.
 PR 28-SEP-2000; 2000US-0236135P.
 PR 03-OCT-2000; 2000US-0237434P.
 PR 05-OCT-2000; 2000US-0238321P.
 PR 06-OCT-2000; 2000US-0238396P.
 PR 06-OCT-2000; 2000US-0238399P.
 PR 16-MAR-2001; 2001US-0276667P.
 PR 31-MAY-2001; 2001US-0294823P.
 PR 12-JUL-2001; 2001US-0304868P.
 PR 26-SEP-2001; 2001US-02035631.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 XX Gerlach VL, MacDougall JR, Smithson G, Millet I, Stone D,
 PI Gunther E, Ellerman K, Grosse WM, Alsobrook JP, Lepley DM,
 PI Burgess CE, Padigaru M, Kikuda R, Spytek KA, Leach MD, Shimkets RA;
 XX WPI, 2002-499860/53.
 DR N-PsDB; ABS63435.
 XX

PT Novel isolated NOVX polypeptides and polynucleotides homologous to
PT attractin, plexin, papin-like family of proteins, useful for treating
PT atherosclerosis, diabetes, cancer, Alzheimer's disease, hemophilia and
PT stroke.

PS Claim 1; Page 42; 308pp; English.

XX The invention discloses the isolated human polypeptides, and
CC polynucleotides encoding them, that have been designated NOVX. The
CC polypeptides, polynucleotides and antibodies are useful in treating or
CC preventing a NOVX-associated disorder which is cardiomyopathy,
CC atherosclerosis and diabetes in a human, where the disorder is related to
CC cell signal processing and metabolic pathway modulation. They can also be
CC used in determining the presence of, or predisposition to, a disease
CC associated with altered levels of the polypeptides and polynucleotides of
CC any one of the 13 sequences (NOV1-NOV13), for raising antibodies, for
CC identifying an agent that binds to, or that modulates the expression or
CC activity of the polypeptide, for identifying an agent which is cellular
CC receptor or downstream effector, for treating or preventing a NOVX-
CC associated disorder and as a pharmaceutical composition comprising the
CC polypeptide, polynucleotide or the antibody. The polypeptides and
CC polynucleotides are useful in diagnostic applications (e.g. as a marker
CC for cancerous cells or tissue types) where their amounts are assessed, or
CC for the manufacture of a medicament (e.g. gene therapy) for treating or
CC preventing disorders or syndromes such as hypertension, congenital heart
CC defects, aortic stenosis, obesity, infectious disease, anorexia, cancer,
CC Alzheimer's disease, Parkinson's disorders, neurodegenerative disorders,
CC hemophilia, idiopathic thrombocytopenic purpura, graft versus host
CC disease, Crohn's disease, multiple sclerosis, cirrhosis, autoimmune
CC disease, systemic lupus erythematosus, asthma, arthritis, psoriasis,
CC allergy, stroke, anxiety, Lesch-Nyhan syndrome, schizophrenia, cerebellar
CC ataxia, pain and alcoholism. They may also be used as immunogens to
CC produce antibodies specific for the invention, and as vaccines.
CC Transgenic cells containing a NOVX expressing construct are useful to
CC produce non-human transgenic animals for studying the function and/or
CC activity of the NOVX proteins and for identifying and/or evaluating
CC modulators of NOVX protein activity. Transgenic cells containing a NOVX
CC expressing construct are useful to produce non-human transgenic animals
CC for studying the function and/or activity of the NOVX proteins and for
CC identifying and/or evaluating modulators of NOVX protein activity. The
CC sequences presented in ABG78359-ABG78371 are the human NOV1-NOV13 proteins
XX
SQ Sequence 2066 AA;

Query Match 99.4%; Score 10425.5; DB 5; Length 2066;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2044; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 MLKRYGARNPLDGAABPIASRASRLNLPFGKRPFTQOQMSPLSREGILDLAFVLF 60
Db 1 MLKRYGARNPLDGAABPIASRASRLNLPFGKRPFTQOQMSPLSREGILDLAFVLF 60
QY 61 ECGSPALMKIKHVNFPKRYSDTIAELOLPASAKDFEVRSLVCGHFAEYQVVRKATG 120
Db 61 ECGSPALMKIKHVNFPKRYSDTIAELOLPASAKDFEVRSLVCGHFAEYQVVRKATG 120
QY 121 DIYAMKVMKKKALLAEOVSFFEEERNILSRSTSPMIPOLQYAFODKNHLLVMEYOPGG 180
Db 121 DIYAMKVMKKKALLAEOVSFFEEERNILSRSTSPMIPOLQYAFODKNHLLVMEYOPGG 180
QY 181 DLISLNRVEDQDLENLLOFYLAELILAVSHVLMGVVHRDIKENLILVDRTHIKLVDF 240
Db 181 DLISLNRVEDQDLENLLOFYLAELILAVSHVLMGVVHRDIKENLILVDRTHIKLVDF 240
QY 241 GSAAKMSNMKNVAKLIGTPDYNAPEVLLYMGNDGKTYGLDCDWSVGYIAYEMTYGR 300
Db 241 GSAAKMSNMKNVAKLIGTPDYNAPEVLLYMGNDGKTYGLDCDWSVGYIAYEMTYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKPPDPKVSDFDLIQSLGCGKELKREGCCPFPF 360
Db 301 SPFAEGTSARTFNINMFORFLKPPDPKVSDFDLIQSLGCGKELKREGCCPFPF 360

QY 361 SKIDMNNIRNSPPFPVPTLKSDDDTSNPEPEKNSWSSPQSLSPSGSGEELPFVGRS 420
Db 360 SKIDMNNIRNAPPPVPLKSDDDTSNPEPEKNSWSSPQSLSPSGSGEELPFVGRS 419
QY 421 YSKALGILGRSESVSGIDSPAKTSMEKLLIKSKELQDSQDKCKHKEOEWRLHRRVS 480
Db 420 YSKALGILGRSESVSGIDSPAKTSMEKLLIKSKELQDSQDKCKHKEOEWRLHRRVS 479
QY 481 EVEAVLSQKEVELKASFTQSLLEODLATYITTEGSLKRSLEQARMEVSQEDDKALQLH 540
Db 480 EVEAVLSQKEVELKASFTQSLLEODLATYITTEGSLKRSLEQARMEVSQEDDKALQLH 539
QY 541 DIRQSRLOQIKQEOYQAOYEMRMNNOLEEDVSNRRSDLYESLRSRRLAAEFK 600
Db 540 DIRQSRLOQIKQEOYQAOYEMRMNNOLEEDVSNRRSDLYESLRSRRLAAEFK 599
QY 601 RKATCOGKLLKADQGEVGEYAKLEKINAEQOLKQEOELKEKAVKASTATELLQ 660
Db 600 RKATCOGKLLKADQGEVGEYAKLEKINAEQOLKQEOELKEKAVKASTATELLQ 659
QY 661 NIRAQERARELEKLONRSDSSGIRKQVLAERHSLBNKYRLTMRERNRLKOD 720
Db 660 NIRAQERARELEKLONRSDSSGIRKQVLAERHSLBNKYRLTMRERNRLKOD 719
QY 721 IQTSQOIQMAADKILIEEKHREAVSAQHLVHLKQKEQHYBEKTYVLNDQIKQDLAD 780
Db 720 IQTSQOIQMAADKILIEEKHREAVSAQHLVHLKQKEQHYBEKTYVLNDQIKQDLAD 779
QY 781 KETLENNMQRHEEBAHEKGLTSBOKMINAMDKINSLEORIYELSRANKLAANSLFT 840
Db 780 KETLENNMQRHEEBAHEKGLTSBOKMINAMDKINSLEORIYELSRANKLAANSLFT 839
QY 841 QRNMKAQEMISLIRQOKFYLETQAGKLEAQRKLEBQLEKISHQDHSKXRLLELETRL 900
Db 840 QRNMKAQEMISLIRQOKFYLETQAGKLEAQRKLEBQLEKISHQDHSKXRLLELETRL 899
QY 901 REVSLHEBQCLEKROLTIELQSLQERESQTLQAARALBESQLOAKTELETTTAA 960
Db 900 REVSLHEBQCLEKROLTIELQSLQERESQTLQAARALBESQLOAKTELETTTAA 959
QY 961 EEEIQALTARHDEIQRFKFDLRNSCTVITDLEBQNLQTEENALNNQNFVLSQDLAS 1020
Db 960 EEEIQALTARHDEIQRFKFDLRNSCTVITDLEBQNLQTEENALNNQNFVLSQDLAS 1019
QY 1021 GANDEIVQNSEVHLRREITEREMQTSQKQTEALKTCTMLEBQVMDLEALNDELLE 1080
Db 1020 GANDEIVQNSEVHLRREITEREMQTSQKQTEALKTCTMLEBQVMDLEALNDELLE 1079
QY 1081 KERQWEAMRSVLDGKESQFECRVARELOMLDTERKOSPARADQRTTESRQVVELAVKHA 1140
Db 1080 KERQWEAMRSVLDGKESQFECRVARELOMLDTERKOSPARADQRTTESRQVVELAVKHA 1139
QY 1141 EITALLQALKEQKAKASLSKNDLEKKNAMLEMANRSLQOKLETREBELKORLLEBAK 1200
Db 1140 EITALLQALKEQKAKASLSKNDLEKKNAMLEMANRSLQOKLETREBELKORLLEBAK 1199
QY 1201 LQQQMDLOKNHIFRLTQGLQBALRADLLKTERSDLEXYOLENIQVLSHEKVKMEGTSIQ 1260
Db 1200 LQQQMDLOKNHIFRLTQGLQBALRADLLKTERSDLEXYOLENIQVLSHEKVKMEGTSIQ 1259
QY 1261 QTKLIDFLQAKMDQPAKKKKVPLQYNEIKLALREKARCAELBALQKTRILERSAREEA 1320
Db 1260 QTKLIDFLQAKMDQPAKKKKVPLQYNEIKLALREKARCAELBALQKTRILERSAREEA 1319
QY 1321 AHRKATHPHPSTPATARQOIAMSAIVRSPEHQSNASILAPSSRRKESSTPEEPFRL 1380
Db 1320 AHRKATHPHPSTPATARQOIAMSAIVRSPEHQSNASILAPSSRRKESSTPEEPFRL 1379
QY 1381 KERQHNNI PRRFVNGLMRATKCAVCLDTYVFGQAKCLEQVMCHPKCSTCLPATGCL 1440
Db 1380 KERQHNNI PRRFVNGLMRATKCAVCLDTYVFGQAKCLEQVMCHPKCSTCLPATGCL 1439
QY 1441 PAEYATHTFAFCRDKNMSPGLQTKPESSSLHLEGMMKVPRNNKRGQOGMDRKYIVLEGS 1500

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Db      1440 PAEYATHTTEAFCDKDKMSPELQTKPESSSLHLEGMKVPENNRKRGQGMGRKXIVLEGS 1499
Qy      1501 KVLIVDEARARAGRPVBEPELCLPDGVSTHGA VGASELANTKADVPYLLKMEHPHT 1560
Db      1500 KVLIVDEARARAGRPVBEPELCLPDGVSTHGA VGASELANTKADVPYLLKMEHPHT 1559
Qy      1561 TCWGRLLYLLAPSPDKQKRWTALESYVAGRVSRKAEADAKLLGNSLLKLEGGDRLD 1620
Db      1560 TCWGRLLYLLAPSPDKQKRWTALESYVAGRVSRKAEADAKLLGNSLLKLEGGDRLD 1619
Qy      1621 MNCITLPPSDQVYVYTERBGLYALNVLNKSLTHVPGIGAVFOIYIIKLEKLLMAGEBRA 1680
Db      1620 MNCITLPPSDQVYVYTERBGLYALNVLNKSLTHVPGIGAVFOIYIIKLEKLLMAGEBRA 1679
Qy      1681 LCLVDVKKVKQSLAOSHLPAQPDISPNI FEAVKGCHLFGAKINGLCTICAMPSKVYIL 1740
Db      1680 LCLVDVKKVKQSLAOSHLPAQPDISPNI FEAVKGCHLFGAKINGLCTICAMPSKVYIL 1739
Qy      1741 RYNNELSKYCIKKEIETSEPCSIHFTNYSILIGTNKYEIDMKQYTLLEPFLDKNDHSLA 1800
Db      1740 RYNNELSKYCIKKEIETSEPCSIHFTNYSILIGTNKYEIDMKQYTLLEPFLDKNDHSLA 1799
Qy      1801 PAVFAASNSFPVSIYOVNSAGOREBYLLCFHEGVPYDYSIGRSRTDDLKWSRLPLAFA 1860
Db      1800 PAVFAASNSFPVSIYOVNSAGOREBYLLCFHEGVPYDYSIGRSRTDDLKWSRLPLAFA 1859
Qy      1861 YREBYLFTVTHENSLEVEIEIORSAGTPARAYLIDIPNRYIGPAISSGATLASSYODKL 1920
Db      1860 YREBYLFTVTHENSLEVEIEIORSAGTPARAYLIDIPNRYIGPAISSGATLASSYODKL 1919
Qy      1921 RVLCCKGNLVKESGTEHHRGSPSTRSSPNKRGPPTYNEHTIKRVASSPAPPEGSHPREP 1980
Db      1920 RVLCCKGNLVKESGTEHHRGSPSTRSSPNKRGPPTYNEHTIKRVASSPAPPEGSHPREP 1979
Qy      1981 STPHRYBGRTELARDKSPGRLPERKSPGRILSTRRRSPARLFEODSRRLPAGAVRT 2040
Db      1980 STPHRYBGRTELARDKSPGRLPERKSPGRILSTRRRSPARLFEODSRRLPAGAVRT 2039
Qy      2041 PLGQVNVKWDOS 2052
Db      2040 PLGQVNVKWDOS 2051

RESULT 9
ADA05654
ID      ADA05654 standard; proteoin: 2066 AA.
XX
AC      ADA05654;
XX
DT      06-NOV-2003 (first entry)
XX
DE      Human NOV1g protein SEQ ID NO:14.
XX
KW      human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
KW      immunomodulator; cytosolic; neuroprotective;
KW      antiparkinsonian; antilipemic; gene therapy; human disease;
KW      metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
KW      neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW      immune disorder; haematopoietic disorder; dyslipidaemia.
XX
OS      Homo sapiens.
XX
PN      WO2003029424-A2.
XX
PD      10-APR-2003.
XX
PE      02-OCT-2002; 2002WO-US031373.
XX
PR      02-OCT-2001; 2001US-0326483P.
PR      05-OCT-2001; 2001US-0327435P.
PR      05-OCT-2001; 2001US-0327449P.
PR      09-OCT-2001; 2001US-0327917P.

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PR      09-OCT-2001; 2001US-0328029P.
PR      09-OCT-2001; 2001US-0328044P.
PR      09-OCT-2001; 2001US-0328056P.
PR      12-OCT-2001; 2001US-0328849P.
PR      15-OCT-2001; 2001US-0329414P.
PR      17-OCT-2001; 2001US-0330142P.
PR      18-OCT-2001; 2001US-0330309P.
PR      22-OCT-2001; 2001US-0341058P.
PR      24-OCT-2001; 2001US-0339266P.
PR      24-OCT-2001; 2001US-0343629P.
PR      29-OCT-2001; 2001US-0349575P.
PR      01-NOV-2001; 2001US-0346357P.
PR      17-APR-2002; 2002US-0373260P.
PR      19-APR-2002; 2002US-0373815P.
PR      19-APR-2002; 2002US-0373817P.
PR      19-APR-2002; 2002US-0373826P.
PR      19-APR-2002; 2002US-0373884P.
PR      22-APR-2002; 2002US-0374977P.
PR      16-MAY-2002; 2002US-0381037P.
PR      16-MAY-2002; 2002US-0381038P.
PR      16-MAY-2002; 2002US-0381042P.
PR      17-MAY-2002; 2002US-0381642P.
PR      28-MAY-2002; 2002US-0383656P.
PR      29-MAY-2002; 2002US-0383831P.
PR      25-JUN-2002; 2002US-0391335P.
PR      01-OCT-2002; 2002US-00262511.

XX
PA      (CURA-) CURAGEN CORP.
XX
PI      Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI      Pattnayan M, Spytek KA, Bainger SR, Ellerman K, Malyankar UM;
PI      Ort T, Gorman L, Zetlusen BD, Anderson DW, Zhong M, Caterton E;
PI      Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI      Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, DiPippo VA;
PI      Eisen AJ, Gangolli BA, Rieger DK, Spaderna SK;
XX
DR      WPI; 2003-381626/36.
DR      N-PSDB; ADA05653.
XX
PT      New NOVX polypeptides and nucleic acids, useful for diagnosing,
PT      preventing or treating NOVX-associated disorders, e.g. diabetes, obesity,
PT      cancer or dyslipidemia, and in chromosome mapping, tissue typing or
PT      pharmacogenomics.
XX
PS      Claim 1; Page 105-106; 586pp; English.
XX
CC      The present invention describes NOVX proteins, where X can be 1 to 55
CC      (e.g. NOV1). Also described: (1) a composition comprising a polypeptide
CC      described above and a carrier; (2) a kit comprising, in one or more
CC      containers, the composition described above; (3) an isolated nucleic acid
CC      molecule which encodes a NOVX protein of the invention; (4) a vector
CC      comprising the nucleic acid molecule described above; (5) a cell
CC      comprising the above vector; (6) an antibody that immunospecifically
CC      binds to the polypeptide described above; (7) methods for determining the
CC      presence or amount of the above polypeptide or nucleic acid molecule in a
CC      sample; (8) methods for determining the presence of or predisposition to
CC      a disease associated with altered levels of expression of the above
CC      polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
CC      method of identifying an agent that binds to the polypeptide described
CC      above; (10) a method for identifying a potential therapeutic agent for
CC      use in treating a pathology that is related to an aberrant expression or
CC      aberrant physiological interactions of the polypeptide; (11) a method of
CC      screening for a modulator of activity or of latency or predisposition to
CC      a pathology associated with the polypeptide; (12) a method for modulating
CC      the activity of the polypeptide described above; (13) methods of treating
CC      or preventing a pathology associated with the above polypeptide in a
CC      mammal; and (14) a method for producing the above polypeptide. NOVX
CC      sequences have antidiabetic, anorectic, antibacterial, virucide,
CC      immunomodulator, cytosolic, anorectic, neuroprotective, antiparkinsonian
CC      and antilipemic activities, and can be used in gene therapy. The
CC      polypeptide is useful in manufacturing a medicament for treating a
CC      syndrome associated with a human disease. The polypeptide or the nucleic
CC      acid molecule may be used to diagnose, treat or prevent metabolic

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CC disorders such as diabetes or obesity, infections, cachexia, cancer,
CC neurodegenerative disorders such as Alzheimer's disease or Parkinson's
CC disease, immune disorders, haematopoietic disorders and various
CC dyplidemia. The nucleic acids can also be used as hybridisation
CC probes in chromosome mapping, tissue typing, preventive medicine and
CC pharmacogenomics. The present sequence represents a human NOVX from the
CC present invention.

SQ Sequence 2066 AA;

Query Match 99.4%; Score 10425.5; DB 6; Length 2066;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2044; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 MLKRYGARNPLDGAAPISASRLNLPFGKPPFTQOMSPISREGILDLFVLF 60
DB 1 MLKRYGARNPLDGAAPISASRLNLPFGKPPFTQOMSPISREGILDLFVLF 60
QY 61 ECSOPALMKIYVNSFVAKYSDTIAELOLOPSAKDFVRSLVGGGFAEVQVVRKATG 120
DB 61 ECSOPALMKIYVNSFVAKYSDTIAELOLOPSAKDFVRSLVGGGFAEVQVVRKATG 120
QY 121 DIYAMKWKKKKALLAOEVSFFEEERNLTSRSTSPWLPOLQYAFODKXHLVLMEXPGG 180
DB 121 DIYAMKWKKKKALLAOEVSFFEEERNLTSRSTSPWLPOLQYAFODKXHLVLMEXPGG 180
QY 181 DLSLRLRYEDOLDENLIQFYLAELILAVSHVLMGYVHRDIKPELILVDRTHIKLVDF 240
DB 181 DLSLRLRYEDOLDENLIQFYLAELILAVSHVLMGYVHRDIKPELILVDRTHIKLVDF 240
QY 241 GSAAKNSNKNVNAKLPIGTDYNAPEVLTVMGDGGKGTGLDCDWSVGVIAVEMTYGR 300
DB 241 GSAAKNSNKNVNAKLPIGTDYNAPEVLTVMGDGGKGTGLDCDWSVGVIAVEMTYGR 300
QY 301 SPFAEGTSARFNNINMFORFLKPPDPKVSDFDLIQLSLCGOKERLKEGLCCHPFF 360
DB 301 SPFAEGTSARFNNINMFORFLKPPDPKVSDFDLIQLSLCGOKERLKEGLCCHPFF 360
QY 361 SKIDMNNIRNAPFPFVFLKSDDDTSNFDPEKNSWVSSPCQSPSGFSGEELPFVGF 420
DB 361 SKIDMNNIRNAPFPFVFLKSDDDTSNFDPEKNSWVSSPCQSPSGFSGEELPFVGF 420
QY 421 YSKALGILGSESVVSGDSPAKTSSMEKLLIKSKELQDSQDCHKMEQMTLHRVRS 480
DB 421 YSKALGILGSESVVSGDSPAKTSSMEKLLIKSKELQDSQDCHKMEQMTLHRVRS 480
QY 481 EYEVAVLSQKEVELQASTQNSLEFODLATTYTCSSSLKSLKSLQARMVYSQDDYALQLH 540
DB 481 EYEVAVLSQKEVELQASTQNSLEFODLATTYTCSSSLKSLKSLQARMVYSQDDYALQLH 540
QY 541 DIRQSRKLOEIKOEYOAOVEEMRLMNNOLEEDLVASRRSDIYSESLRESRLAAEFK 600
DB 541 DIRQSRKLOEIKOEYOAOVEEMRLMNNOLEEDLVASRRSDIYSESLRESRLAAEFK 600
QY 601 RKATECHKLKAKDOQKPEVGEYAKLEKINAEOQLKQELQELKRAVAKSTATELILQ 660
DB 601 RKATECHKLKAKDOQKPEVGEYAKLEKINAEOQLKQELQELKRAVAKSTATELILQ 660
QY 661 NIRAQARAERELEKLNREDSSGIRKULVEABERHSLNKKYKRLFTMERENRLKD 720
DB 661 NIRAQARAERELEKLNREDSSGIRKULVEABERHSLNKKYKRLFTMERENRLKD 720
QY 721 IOTSGOQIQOQADKILEBEKREAOVSAOHLVHLMKOEQYBEKIKVLINOIKKDLAD 780
DB 721 IOTSGOQIQOQADKILEBEKREAOVSAOHLVHLMKOEQYBEKIKVLINOIKKDLAD 780
QY 781 KETLENNMORHEBAHEKGLISSEKAMINAMDSKISLEQRIYELSEANKLAANSILFT 840
DB 781 KETLENNMORHEBAHEKGLISSEKAMINAMDSKISLEQRIYELSEANKLAANSILFT 840
QY 841 ORNKAQOEMISELROOKFYLETQAGKLEAONRKLBEOLLEKISHQDSDKRRLLLELTRL 900
DB 841 ORNKAQOEMISELROOKFYLETQAGKLEAONRKLBEOLLEKISHQDSDKRRLLLELTRL 900

QY 901 REVSLEHEEQKLEBKROLTEILOLSLOERESQUTALQAARALBSQRLQAKTELEETAA 960
DB 901 REVSLEHEEQKLEBKROLTEILOLSLOERESQUTALQAARALBSQRLQAKTELEETAA 960
QY 961 EEEIOALTANDEIORKFDALRNSCTVITDEEQNLQNTENAEINNONFVLSKLDERS 1020
DB 961 EEEIOALTANDEIORKFDALRNSCTVITDEEQNLQNTENAEINNONFVLSKLDERS 1020
QY 1021 GANDEIVOLRSEVHLRREITEREMOLTSQKOTMEALKTTCMTLEBOVMDEALNDELLE 1080
DB 1021 GANDEIVOLRSEVHLRREITEREMOLTSQKOTMEALKTTCMTLEBOVMDEALNDELLE 1080
QY 1081 KERQWEAMRSLVGDKEQFECRVELQMLDTEKQSRARADQRTIESROYVELAVKEKA 1140
DB 1081 KERQWEAMRSLVGDKEQFECRVELQMLDTEKQSRARADQRTIESROYVELAVKEKA 1140
QY 1141 EILALQALKEQKIKASLSLKLNDLEKKHMLENNASLQOKLETBELLKORLLEBOAK 1200
DB 1141 EILALQALKEQKIKASLSLKLNDLEKKHMLENNASLQOKLETBELLKORLLEBOAK 1200
QY 1201 LQQQMDLOKNIIFRLTQGLQALDRADLLKTERSPLYQLENIQVLYSHEKYKMEGTISQ 1260
DB 1201 LQQQMDLOKNIIFRLTQGLQALDRADLLKTERSPLYQLENIQVLYSHEKYKMEGTISQ 1260
QY 1261 QTKLIDFLQAMMDPAKKKKVPLQYNEIKLALKEKARCAELBEALQKTRIELNSAREEA 1320
DB 1261 QTKLIDFLQAMMDPAKKKKVPLQYNEIKLALKEKARCAELBEALQKTRIELNSAREEA 1320
QY 1321 AHRKATHPHPSTPATARQOITAMSAIVRSPEHOPSMSLAPSSRRKESSTPEEFSSRL 1380
DB 1321 AHRKATHPHPSTPATARQOITAMSAIVRSPEHOPSMSLAPSSRRKESSTPEEFSSRL 1380
QY 1381 KERHNNHNPFRFNNGLMMARATKCAVCLDTVAFGQASCLCEQWCHPKSTCLPATGL 1440
DB 1381 KERHNNHNPFRFNNGLMMARATKCAVCLDTVAFGQASCLCEQWCHPKSTCLPATGL 1440
QY 1441 PAEYATFTFEAFCDKKNNSPGLQTKEPSSSLHLEGMKVPPNNRGGQGMKRYIVLEGS 1500
DB 1441 PAEYATFTFEAFCDKKNNSPGLQTKEPSSSLHLEGMKVPPNNRGGQGMKRYIVLEGS 1500
QY 1501 KVLIIYDNEARBAQGRPYEBEFLCLPDGDVSIHGAVGASELANTAKADVPIYLKMSHPHT 1560
DB 1501 KVLIIYDNEARBAQGRPYEBEFLCLPDGDVSIHGAVGASELANTAKADVPIYLKMSHPHT 1560
QY 1561 TCWPGRTLYLLAPSPDKQKRWVTALESVAGGRVSRKAEADAKLGNLSLKTLEGGDDRLD 1620
DB 1561 TCWPGRTLYLLAPSPDKQKRWVTALESVAGGRVSRKAEADAKLGNLSLKTLEGGDDRLD 1620
QY 1621 MNCTLPSPDOVVLVGTREGLYALNVLKNSLTHVPGIGAVFOIYIILKOLEKLMTAGERA 1680
DB 1621 MNCTLPSPDOVVLVGTREGLYALNVLKNSLTHVPGIGAVFOIYIILKOLEKLMTAGERA 1680
QY 1681 LCLVDVKKVQSLAQSHLPAQPDISPNIPEAVKCHLFGAKIENGCLCICAMPSSKVYL 1740
DB 1681 LCLVDVKKVQSLAQSHLPAQPDISPNIPEAVKCHLFGAKIENGCLCICAMPSSKVYL 1740
QY 1741 RYNNENLSKYCIKKEIETSEPCSHFTNYSILIGTNKFEYIDMKOYTLLEFLDKNDHSLA 1800
DB 1741 RYNNENLSKYCIKKEIETSEPCSHFTNYSILIGTNKFEYIDMKOYTLLEFLDKNDHSLA 1800
QY 1801 PAVFAASNSFPVSIYOVNSAGREBYLLCCHEGGVFVDSIGRSRTDLMKSRPLPLAFA 1860
DB 1801 PAVFAASNSFPVSIYOVNSAGREBYLLCCHEGGVFVDSIGRSRTDLMKSRPLPLAFA 1860
QY 1860 YREBYLFTVTHNSLEVIEIQARSSAGTPARAYLIDIPRRLYGPAISSGAIYLAASYQKL 1920
DB 1860 YREBYLFTVTHNSLEVIEIQARSSAGTPARAYLIDIPRRLYGPAISSGAIYLAASYQKL 1920
QY 1920 RVICCKGNLVKESGTEHHRGPTSSRSPNKGPTTYNEHTTKRVAASPAPREGSHPREP 1980
DB 1920 RVICCKGNLVKESGTEHHRGPTSSRSPNKGPTTYNEHTTKRVAASPAPREGSHPREP 1980

Matches 2043; Conservative 2; Mismatches 8; Indels 1; Gaps 1;

QY 1 MLKRTGARNPLDGAAPLIRASRLNLFQCKPPEMTQOQMSPLSEGLIDALFVLE 60
Db 1 MLKRTGARNPLDGAAPLIRASRLNLFQCKPPEMTQOQMSPLSEGLIDALFVLE 60
QY 61 ECSPALMKIKHVNFPVKYSDTIAEIQEOPSAKDFVRSVNGGHAEOVYVREKATG 120
Db 61 ECSPALMKIKHVNFPVKYSDTIAEIQEOPSAKDFVRSVNGGHAEOVYVREKATG 120
QY 61 ECSPALMKIKHVNFPVKYSDTIAEIQEOPSAKDFVRSVNGGHAEOVYVREKATG 120
Db 61 ECSPALMKIKHVNFPVKYSDTIAEIQEOPSAKDFVRSVNGGHAEOVYVREKATG 120
QY 121 DIYAMKMKKALLAOEVSFFEEERNLTSRSTPMIQLQYAFQDKHLLVMEYORG 180
Db 121 DIYAMKMKKALLAOEVSFFEEERNLTSRSTPMIQLQYAFQDKHLLVMEYORG 180
QY 181 DLSLNRYEDQDLENIQFYLAELILAVSHVLMGVYHARDIKENILVDRTHIKLVDF 240
Db 181 DLSLNRYEDQDLENIQFYLAELILAVSHVLMGVYHARDIKENILVDRTHIKLVDF 240
QY 241 GSAAKNMSNKVNAKPLIGTPDYAPPEVLTVMNGDGKTYGLDCDMSVGIYVEMTYGR 300
Db 241 GSAAKNMSNK-VNAKPLIGTPDYAPPEVLTVMNGDGKTYGLDCDMSVGIYVEMTYGR 299
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSDFLDIQSLCGOKERLKEGICCHPEF 360
Db 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSDFLDIQSLCGOKERLKEGICCHPEF 359
QY 361 SKIDMNNIRNSPPFVPTLSDDDTSNFDPEKNSWVSSPCQSPSGSGEELPFVQFS 420
Db 361 SKIDMNNIRNANPPFVPTLSDDDTSNFDPEKNSWVSSPCQSPSGSGEELPFVQFS 419
QY 421 YSKALGILGRSESVSGIDSPAKTSMEKKLISKELQDSQDKHKEOEMTLARRVS 480
Db 421 YSKALGILGRSESVSGIDSPAKTSMEKKLISKELQDSQDKHKEOEMTLARRVS 479
QY 481 EWEAVLSOKEVELKASETORSLEODLATYITECSSIKRSLKQARMVSOQDDALQULH 540
Db 481 EWEAVLSOKEVELKASETORSLEODLATYITECSSIKRSLKQARMVSOQDDALQULH 539
QY 541 DIRBOSKLOEIKOEYOAOYEENRMLMNOLEBDLVASRRSDLYESBLRESRLAAEFK 600
Db 541 DIRBOSKLOEIKOEYOAOYEENRMLMNOLEBDLVASRRSDLYESBLRESRLAAEFK 599
QY 601 RKATECOHKLKAKOQKPEYGEYAKLEKINAEOQLKIQEQLKRAVKASTATETLQ 660
Db 601 RKATECOHKLKAKOQKPEYGEYAKLEKINAEOQLKIQEQLKRAVKASTATETLQ 659
QY 661 NIQAOKRARARELEKONREDSSEGIKKLVAEERHSHLENKYRLJEMERRERLKD 720
Db 661 NIQAOKRARARELEKONREDSSEGIKKLVAEERHSHLENKYRLJEMERRERLKD 719
QY 721 IOTKSQOIQOMADKILEEKHREAOVSAOHLAEVHLKOEQHYBEKIKVLDNOIKKDLAD 780
Db 721 IOTKSQOIQOMADKILEEKHREAOVSAOHLAEVHLKOEQHYBEKIKVLDNOIKKDLAD 779
QY 781 KETLENNMOHHEEBAHEKGISBQKAMINAMDSKIRSLBORIVELSEANKLAANSLSFT 840
Db 781 KETLENNMOHHEEBAHEKGISBQKAMINAMDSKIRSLBORIVELSEANKLAANSLSFT 839
QY 841 QRMNKAQEMISERLOOKFYLETQAGKLEAONRKLSEOLEKISQODSDKRRLLLESTRL 900
Db 841 QRMNKAQEMISERLOOKFYLETQAGKLEAONRKLSEOLEKISQODSDKRRLLLESTRL 899
QY 901 REVSLHEEOQKLEKROLTTELQSLQERESQLTALQARALAESQLQOAKTELETTARA 960
Db 901 REVSLHEEOQKLEKROLTTELQSLQERESQLTALQARALAESQLQOAKTELETTARA 959
QY 961 EEEIQTARHDEIQRKFDALRNSCTVITDLEBQNLQTEBDNAELNNQNFYLSKQDAS 1020
Db 961 EEEIQTARHDEIQRKFDALRNSCTVITDLEBQNLQTEBDNAELNNQNFYLSKQDAS 1019
QY 1021 GANDEIYQLASEVDHLREITEREMOULTSQKQTEALKTCTMLEEOVMDEALNDELLE 1080
Db 1021 GANDEIYQLASEVDHLREITEREMOULTSQKQTEALKTCTMLEEOVMDEALNDELLE 1079

QY 1081 KERQWEAMRSVLDGEKQFECRVRBELQMLDTEKQSRADQRTESQVVELAVKEHKA 1140
Db 1081 KERQWEAMRSVLDGEKQFECRVRBELQMLDTEKQSRADQRTESQVVELAVKEHKA 1139
QY 1141 EILALQALKEOKXIKASLSDKNDLEKHAMLENNASLQOKLETERELKORLLEBQAK 1200
Db 1141 EILALQALKEOKXIKASLSDKNDLEKHAMLENNASLQOKLETERELKORLLEBQAK 1199
QY 1201 LOQOMDLOKXNHPULQGLQALDRADLLKTERSDLEQLENIQVLYSHEKVMGEGTISQ 1260
Db 1201 LOQOMDLOKXNHPULQGLQALDRADLLKTERSDLEQLENIQVLYSHEKVMGEGTISQ 1259
QY 1261 QTKLIDFLQAMQDPACKKKVPLQYNEIKALKEKARCAELBEALQTRIELSAREBA 1320
Db 1261 QTKLIDFLQAMQDPACKKKVPLQYNEIKALKEKARCAELBEALQTRIELSAREBA 1319
QY 1321 AHRKATDHPHSTATATARQOJLMSALYRSPHQSAMSLLAPSSRRKESSTPEEFSTRL 1380
Db 1321 AHRKATDHPHSTATATARQOJLMSALYRSPHQSAMSLLAPSSRRKESSTPEEFSTRL 1379
QY 1381 KERHNNHNPHEFNGLMNRATKCAVCLDTYHFGQASKLEQVWCHPKGCTCLPATGCL 1440
Db 1381 KERHNNHNPHEFNGLMNRATKCAVCLDTYHFGQASKLEQVWCHPKGCTCLPATGCL 1439
QY 1441 PAEYATHTTEAFCDKKNMSPGLQTKESPSSLHLEGMKVPNNNRQOQGMQDKTYVLEGS 1500
Db 1441 PAEYATHTTEAFCDKKNMSPGLQTKESPSSLHLEGMKVPNNNRQOQGMQDKTYVLEGS 1499
QY 1501 KVLTYNDPAREAGORPYEBEFLCLPDGDVSJHGAVASLANTAKADVPYILKMSHPHT 1560
Db 1501 KVLTYNDPAREAGORPYEBEFLCLPDGDVSJHGAVASLANTAKADVPYILKMSHPHT 1559
QY 1561 TQWPGRTLYLLAPSPKORVNTALASVAVGARSREKABADKLGSLKLTGSDDBLD 1620
Db 1561 TQWPGRTLYLLAPSPKORVNTALASVAVGARSREKABADKLGSLKLTGSDDBLD 1619
QY 1621 MNCTLPSPSDQVVLVGTGEGLYALNVLNNSLTHVAGIGAVFOIYIILKOLEKMLTAGEERA 1680
Db 1621 MNCTLPSPSDQVVLVGTGEGLYALNVLNNSLTHVAGIGAVFOIYIILKOLEKMLTAGEERA 1679
QY 1681 LCLVDVKKVQOSLAQSHLPAPODISEPNIPEAVKGCCHLFGAGKINGLCICAMPSKVYL 1740
Db 1681 LCLVDVKKVQOSLAQSHLPAPODISEPNIPEAVKGCCHLFGAGKINGLCICAMPSKVYL 1739
QY 1741 RYENENLSKYCIRKEIETSEBSCCHFTNYSTILGTNKFYEIDMKQYTLLEFLDKNDHSLA 1800
Db 1741 RYENENLSKYCIRKEIETSEBSCCHFTNYSTILGTNKFYEIDMKQYTLLEFLDKNDHSLA 1799
QY 1801 PAVFAASNSFPVSIYOVNSAGOREEYILCFHEFGVFVDSYGRSRITDDLKMSRLPLAFA 1860
Db 1801 PAVFAASNSFPVSIYOVNSAGOREEYILCFHEFGVFVDSYGRSRITDDLKMSRLPLAFA 1859
QY 1861 YREBYLFVTHFNLSLEVIEIQARSSAGTPARAYLIDIPNRYLGPALISSGAIYLAASYODKL 1920
Db 1861 YREBYLFVTHFNLSLEVIEIQARSSAGTPARAYLIDIPNRYLGPALISSGAIYLAASYODKL 1919
QY 1921 RVICCKNVLKESGTEHHRGPSTSRSSPNKRGPTTYNHEHTTKRVAASPAPEGSHPREP 1980
Db 1921 RVICCKNVLKESGTEHHRGPSTSRSSPNKRGPTTYNHEHTTKRVAASPAPEGSHPREP 1979
QY 1981 STPHRYEGRTELARDSPGRPLERKSPGRILSTRERSPARLFEDESSRGRLLPAGAVRT 2040
Db 1981 STPHRYEGRTELARDSPGRPLERKSPGRILSTRERSPARLFEDESSRGRLLPAGAVRT 2039
QY 2041 PLSQVNVWDQSSV 2054
Db 2041 PLSQVNVWDQSSV 2053

RESULT 11
ADN63228 standard; protein; 2053 AA.

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XX AC ADN63228;
XX DT 01-JUL-2004 (first entry)
XX DE Human NOVA variant.
XX KW human; NOVA; metabolic disorder; diabetes; obesity; infectious disease;
XX KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
XX KW Alzheimer's disease; Parkinson's disease; immune disorder;
XX KW haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
XX KW wasting disorder.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1440
XX FT /note= "Pro substituted by Leu as a result of single
XX FT nucleotide polymorphism"
XX PN US2004038223-A1.
XX PD 26-FEB-2004.
XX PF 01-OCT-2002; 2002US-00262511.
XX PR 02-OCT-2001; 2001US-0326483P.
XX PR 05-OCT-2001; 2001US-0327435P.
XX PR 05-OCT-2001; 2001US-0327449P.
XX PR 09-OCT-2001; 2001US-0327917P.
XX PR 09-OCT-2001; 2001US-0328029P.
XX PR 09-OCT-2001; 2001US-0328044P.
XX PR 09-OCT-2001; 2001US-0328056P.
XX PR 12-OCT-2001; 2001US-0328849P.
XX PR 15-OCT-2001; 2001US-0329414P.
XX PR 17-OCT-2001; 2001US-0330142P.
XX PR 18-OCT-2001; 2001US-0330309P.
XX PR 22-OCT-2001; 2001US-0341058P.
XX PR 24-OCT-2001; 2001US-0339268P.
XX PR 24-OCT-2001; 2001US-0343629P.
XX PR 29-OCT-2001; 2001US-0349575P.
XX PR 01-NOV-2001; 2001US-0346357P.
XX PR 17-APR-2002; 2002US-0373260P.
XX PR 19-APR-2002; 2002US-0373815P.
XX PR 19-APR-2002; 2002US-0373817P.
XX PR 19-APR-2002; 2002US-0373826P.
XX PR 19-APR-2002; 2002US-0373884P.
XX PR 22-APR-2002; 2002US-0374977P.
XX PR 16-MAY-2002; 2002US-0381037P.
XX PR 16-MAY-2002; 2002US-0381038P.
XX PR 16-MAY-2002; 2002US-0381042P.
XX PR 17-MAY-2002; 2002US-0381642P.
XX PR 28-MAY-2002; 2002US-0383656P.
XX PR 29-MAY-2002; 2002US-0383831P.
XX PR 25-JUN-2002; 2002US-0391335P.
XX SM (SMIT/) SMITHSON G.
XX PA (MILT/) MILLET I.
XX PA (PEYM/) PEYMAN J A.
XX PA (KEKU/) KEKUDA R.
XX PA (JUUJ/) JU J.
XX PA (LILL/) LI L.
XX PA (GUOX/) GUO X.
XX PA (PATU/) PATURAJAN M.
XX PA (SPYT/) SPYTEK K A.
XX PA (EDIN/) EDINGER S R.
XX PA (ELLE/) ELLERMAN K.
XX PA (MALY/) MALYANKAR U M.
XX PA (ORTT/) ORT T.
XX PA (GORM/) GORMAN L.
XX PA (ZERR/) ZERRHUSEN B D.
XX PA (ANDE/) ANDERSON D W.
XX PA (ZHON/) ZHONG M.

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PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILT/) MILLER C E.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIPI/) DIPIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
XX PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
PI Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE, Shenoy SG;
PI Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
XX DR WPI; 2004-213931/20.
XX DR N-PSDB; ADN62806.
XX PT Isolated NOVA polypeptides and nucleic acids, useful for preventing,
XX PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
XX PS Example 54; Page; 395pp; English.
XX CC The invention relates to isolated NOVA polypeptides and polynucleotides.
XX CC NOVA polypeptides and polynucleotides are used to prevent, diagnose or
XX CC treat a medical condition in human related to the aberrant expression and
XX CC activity of NOVA polypeptides. For example, NOVA polypeptides and
XX CC polynucleotides may be used to treat disorders associated with decreased
XX CC expression or activity of NOVA by supplementing the patient out
XX CC production or to rectify mutations. Conversely, antisense NA molecules
XX CC may be administered to down regulate expression of NOVA polypeptides by
XX CC binding with the cells own genes and preventing their expression. NOVA
XX CC polynucleotides and complementary sequences may also be used as DNA
XX CC probes in diagnostic assays to detect and quantify the presence of
XX CC similar sequences in samples, and so which patients may be in need of
XX CC restorative therapy. NOVA polypeptides may also be used as antigens in
XX CC the production of antibodies and in assays to identify modulators
XX CC (agonists and antagonists) of the expression and activity of NOVA. The
XX CC anti-NOVA polypeptide antibodies, agonists and antagonists may also be
XX CC used to modulate NOVA polynucleotide expression and activity of NOVA
XX CC polypeptides. The anti-NOVA polypeptide antibodies may also be used as
XX CC diagnostic agents for detecting the presence of NOVA in samples. NOVA
XX CC polypeptides and polynucleotides may be used in this way to prevent,
XX CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
XX CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
XX CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
XX CC haematopoietic disorders, and the various dyslipidaemias, metabolic
XX CC disturbances associated with obesity, the metabolic syndrome X and
XX CC wasting disorders associated with chronic diseases and various cancers.
XX CC They may also be used as antibacterial agents. The present sequence
XX CC represents the amino acid sequence of a human NOVA protein. Note the
XX CC present sequence is not shown in the specification but was created by the
XX CC indexer using the information given in example 54.
XX SQ Sequence 2053 AA:
SQ Query Match 99.2%; Score 10412.5; DB 8; Length 2053;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2042; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
QY 1 MLKFKYGARNPDLNAGAAEPFLASASASRLNLFQCKRPPTMOOQMSPLSRGIIALFLFE 60
Db 1 MLKFKYGARNPDLNAGAAEPFLASASASRLNLFQCKRPPTMOOQMSPLSRGIIALFLFE 60

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QY 61 ECGPALMKIYGVNFVFKYSDTTAELOELPSAKDFVRSIVGCGHFAVQVVEKATG 120
DB 61 ECGPALMKIKGVNFVFKYSDTTAELOELPSAKDFVRSIVGCGHFAVQVVEKATG 120
QY 121 DIYAMKWKKKALLAOEVOVSFFEEERNLSRSTSMIQLQYAPODKNHLYVMEYQGG 180
DB 121 DIYAMKWKKKALLAOEVOVSFFEEERNLSRSTSMIQLQYAPODKNHLYVMEYQGG 180
QY 181 DLILSLNRYEDQDLBNLIQFYLAELILAVHSHVLMGYVHRDIKPENIIVDRTHIKLYDF 240
DB 181 DLILSLNRYEDQDLBNLIQFYLAELILAVHSHVLMGYVHRDIKPENIIVDRTHIKLYDF 240
QY 241 GSAAMNSNKNVNAKLPIGTPDYNAPEVLTVMNGDGKGTGYGLDCMWSVGIYAYEMIYGR 300
DB 241 GSAAMNSNKNVNAKLPIGTPDYNAPEVLTVMNGDGKGTGYGLDCMWSVGIYAYEMIYGR 300
QY 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSDPLDLIQLSLCQKELKKEGJCCHFPF 360
DB 301 SPFAEGTSARTFNINMFORFLKFPDDPKVSDPLDLIQLSLCQKELKKEGJCCHFPF 360
QY 361 SKIDMNNIRNPPFPVPTLKSDDDTSNFDEPKNSWSSPCQSPSGFSGEELPFVGS 420
DB 361 SKIDMNNIRNPPFPVPTLKSDDDTSNFDEPKNSWSSPCQSPSGFSGEELPFVGS 420
QY 421 YSKALGILGRSESVSGIDSPAKTSSMEKULLIKSKELQDSQDKCHKXQEMTRLHRRVS 480
DB 421 YSKALGILGRSESVSGIDSPAKTSSMEKULLIKSKELQDSQDKCHKXQEMTRLHRRVS 480
QY 481 EVEVAVLSQKVEYELKASETORSLLEODLATYITEGSLKRSLEQARMEVSQDDYALQILH 540
DB 481 EVEVAVLSQKVEYELKASETORSLLEODLATYITEGSLKRSLEQARMEVSQDDYALQILH 540
QY 541 DIREQSRLOEIKEOEYOAOVEEMRLMNOLEBDLVASARRSDIYESELRESRLAAEFK 600
DB 541 DIREQSRLOEIKEOEYOAOVEEMRLMNOLEBDLVASARRSDIYESELRESRLAAEFK 600
QY 601 RKATECOHKLKAKDOGKEVEGYAKLEKINAEOQLKIOELOELKBAVKASTEATELLO 660
DB 601 RKATECOHKLKAKDOGKEVEGYAKLEKINAEOQLKIOELOELKBAVKASTEATELLO 660
QY 661 NIROAKRARELEKLONRDSSGICRKKLYEABERHSHENKYKLETMERENRLKD 720
DB 661 NIROAKRARELEKLONRDSSGICRKKLYEABERHSHENKYKLETMERENRLKD 720
QY 721 IOTKSQOIQOMADKILEBKHREAOVSACHLEVHLKQKQHYBEKIKVLDNOIKKDLAD 780
DB 721 IOTKSQOIQOMADKILEBKHREAOVSACHLEVHLKQKQHYBEKIKVLDNOIKKDLAD 780
QY 781 KETLENNMOHBEBAHEKGIKLSQKAMINAMDSKISRLEQRIYELSEANKLANSSILFT 840
DB 781 KETLENNMOHBEBAHEKGIKLSQKAMINAMDSKISRLEQRIYELSEANKLANSSILFT 840
QY 841 QORNKAOEEMISELROOKFYLETQAGKLEAONRKLBOLEKISHOQSDKNRLILETRL 900
DB 841 QORNKAOEEMISELROOKFYLETQAGKLEAONRKLBOLEKISHOQSDKNRLILETRL 900
QY 901 REVSLEHEBOKLEKROLTLELOSLORRESQLTALQARALAESQLOAKTELEETAA 960
DB 901 REVSLEHEBOKLEKROLTLELOSLORRESQLTALQARALAESQLOAKTELEETAA 960
QY 961 EEBEIOALTARDEIQRKFDALRNSCTVITDLEBOLNLTEDNAELNNQNFYLSKQLEBAS 1020
DB 961 EEBEIOALTARDEIQRKFDALRNSCTVITDLEBOLNLTEDNAELNNQNFYLSKQLEBAS 1020
QY 1021 GANDEIVOLASEVDHLREITEREMOULTSQKQINEALKTCTMLEBOVMDEALNDELLE 1080
DB 1021 GANDEIVOLASEVDHLREITEREMOULTSQKQINEALKTCTMLEBOVMDEALNDELLE 1080
QY 1081 KEROMEAMRSVLDGKESQFECRAVELQRMLDTEKOSARADQRTTESRQVVELAVKEHKA 1140
DB 1081 KEROMEAMRSVLDGKESQFECRAVELQRMLDTEKOSARADQRTTESRQVVELAVKEHKA 1140

QY 1141 EILALQALKEQKIKASLSLKDNLDEKHAMLENNARSLOQKLETERBELKORLLEBOAK 1200
DB 1140 EILALQALKEQKIKASLSLKDNLDEKHAMLENNARSLOQKLETERBELKORLLEBOAK 1199
QY 1201 LOOQMDLOKNIIFPLTQLOFALRADLLEKTERBDLEVOLENIQVLYSHEKVKMGSTISQ 1260
DB 1200 LOOQMDLOKNIIFPLTQLOFALRADLLEKTERBDLEVOLENIQVLYSHEKVKMGSTISQ 1259
QY 1261 QTKLIDFLOAMDOPAKKKKVPLQYNELKALKEKARCALEBEALQKTRIELRSAREBA 1320
DB 1260 QTKLIDFLOAMDOPAKKKKVPLQYNELKALKEKARCALEBEALQKTRIELRSAREBA 1319
QY 1321 AHRKATDHPDSTPATYARQOITAMSAIVSPHOPSAMSLAPSSRRKESSTPEEFSSRL 1380
DB 1320 AHRKATDHPDSTPATYARQOITAMSAIVSPHOPSAMSLAPSSRRKESSTPEEFSSRL 1379
QY 1381 KERHNNHNPFRFNGGLNRRATKCAVCLDTYHFGQASCLCEQWCHKSTCLPATGCL 1440
DB 1380 KERHNNHNPFRFNGGLNRRATKCAVCLDTYHFGQASCLCEQWCHKSTCLPATGCL 1439
QY 1441 PAEYATHTTEAFCDKKNNSPGLQTKPESSSLHSGMMKVPRNNKRGQOGMPRKTYVLEGS 1500
DB 1440 LAEYATHTTEAFCDKKNNSPGLQTKPESSSLHSGMMKVPRNNKRGQOGMPRKTYVLEGS 1499
QY 1501 KVLIIYDNEABARAGRPVEEFELCLPDGDSIHGAVGASELANTAKADVPYILKXESHPT 1560
DB 1500 KVLIIYDNEABARAGRPVEEFELCLPDGDSIHGAVGASELANTAKADVPYILKXESHPT 1559
QY 1561 TCWPGRTLYLLABFPFKORVNTALBESVAVAGRSREAEADAKLNGSLKLEGGDRILD 1620
DB 1560 TCWPGRTLYLLABFPFKORVNTALBESVAVAGRSREAEADAKLNGSLKLEGGDRILD 1619
QY 1621 MNCITLPPSDQVVLVGTBEGLYALNVLNKSLTHVIGIGAFQIYIILKOLEKLMTAGEBRA 1680
DB 1620 MNCITLPPSDQVVLVGTBEGLYALNVLNKSLTHVIGIGAFQIYIILKOLEKLMTAGEBRA 1679
QY 1681 LCILVDVKKVQSLAQSHLPAQPDISPNIPFAVKGCFLGAKIENGCLICAMPSSKVYL 1740
DB 1680 LCILVDVKKVQSLAQSHLPAQPDISPNIPFAVKGCFLGAKIENGCLICAMPSSKVYL 1739
QY 1741 RYENENSKYCIKKEIETSEPCSCIHFTNYSTILIGTNKFEYIDMKQYTLLEFLDKNDHSLA 1800
DB 1740 RYENENSKYCIKKEIETSEPCSCIHFTNYSTILIGTNKFEYIDMKQYTLLEFLDKNDHSLA 1799
QY 1801 PAVFAASSNSFPVSIYOVNSAGOREEYLLCPEHGFVVDSTGRRSRITDDLKMSRLPLAFA 1860
DB 1800 PAVFAASSNSFPVSIYOVNSAGOREEYLLCPEHGFVVDSTGRRSRITDDLKMSRLPLAFA 1859
QY 1861 YREBYLFTVTHFNSLEVEIEIQRSSAGTPADAYLDPMPRYLGPALISSGAYLAASYODKL 1920
DB 1860 YREBYLFTVTHFNSLEVEIEIQRSSAGTPADAYLDPMPRYLGPALISSGAYLAASYODKL 1919
QY 1921 RYICCKGNLVKESGTEHHRGBSTSRSSPNKRGPTTYEHITKRYASSAPAPGEGSHPREP 1980
DB 1920 RYICCKGNLVKESGTEHHRGBSTSRSSPNKRGPTTYEHITKRYASSAPAPGEGSHPREP 1979
QY 1981 STPHRYREGRTBLRDSKPGRLERKSPGRIILSTRERSPARLFEDESSRGRLLPAGAVRT 2040
DB 1980 STPHRYREGRTBLRDSKPGRLERKSPGRIILSTRERSPARLFEDESSRGRLLPAGAVRT 2039
QY 2041 PLSQVNVKMDQSSV 2054
DB 2040 PLSQVNVKMDQSSV 2053

RESULT 12
ADN62819
ID ADN62819 standard; protein; 2066 AA.
XX
AC ADN62819;
XX
DT 01-JUL-2004 (first entry)
XX

DE Human NOV1g.
 XX
 KW human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW hematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 KW wasting disorder.
 OS Homo sapiens.
 PN US2004038223-A1.
 XX
 PD 26-FEB-2004.
 XX
 PF 01-OCT-2002; 2002US-00262511.
 XX
 PR 02-OCT-2001; 2001US-0326483P.
 PR 05-OCT-2001; 2001US-0327443P.
 PR 09-OCT-2001; 2001US-0327449P.
 PR 09-OCT-2001; 2001US-0327917P.
 PR 09-OCT-2001; 2001US-0328029P.
 PR 09-OCT-2001; 2001US-0328044P.
 PR 09-OCT-2001; 2001US-0328056P.
 PR 12-OCT-2001; 2001US-0328849P.
 PR 15-OCT-2001; 2001US-0329414P.
 PR 17-OCT-2001; 2001US-0330142P.
 PR 18-OCT-2001; 2001US-0330309P.
 PR 22-OCT-2001; 2001US-0341058P.
 PR 24-OCT-2001; 2001US-0339266P.
 PR 24-OCT-2001; 2001US-0343629P.
 PR 29-OCT-2001; 2001US-0349575P.
 PR 01-NOV-2001; 2001US-0346357P.
 PR 17-APR-2002; 2002US-0373260P.
 PR 19-APR-2002; 2002US-0373815P.
 PR 19-APR-2002; 2002US-0373817P.
 PR 19-APR-2002; 2002US-0373826P.
 PR 19-APR-2002; 2002US-0373884P.
 PR 22-APR-2002; 2002US-0374977P.
 PR 16-MAY-2002; 2002US-0381037P.
 PR 16-MAY-2002; 2002US-0381038P.
 PR 16-MAY-2002; 2002US-0381042P.
 PR 18-MAY-2002; 2002US-0381642P.
 PR 28-MAY-2002; 2002US-0383656P.
 PR 29-MAY-2002; 2002US-0383831P.
 PR 25-JUN-2002; 2002US-0391335P.
 XX
 PA (SMIT/) SMITHSON G.
 PA (MILT/) MILLET I.
 PA (PEYM/) PEYMAN J A.
 PA (KEKU/) KEKUDA R.
 PA (JUUJ/) JU J.
 PA (LILL/) LI L.
 PA (GUOX/) GUO X.
 PA (PATR/) PATURAJAN M.
 PA (SPYT/) SPYTEK K A.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (MALY/) MALYANKAR V M.
 PA (ORTT/) ORT T.
 PA (GORM/) GORMAN L.
 PA (ZERR/) ZERRUSEN B D.
 PA (ANDR/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (CATT/) CATTERTON E.
 PA (JIMM/) JI W.
 PA (MILL/) MILLER C E.
 PA (RAST/) RASTELLI L.
 PA (STON/) STONE D J.
 PA (PENR/) PENR C B A.
 PA (SHEN/) SHENOY S G.
 PA (SHIM/) SHIMKETS R A.
 PA (ROTH/) ROTHENBERG M E.
 PA (LEAC/) LEACH M D.

PA (AGEE/) AGE E M L.
 PA (BERG/) BERGHS C.
 PA (DIP/) DIPOLPO V A.
 PA (EISE/) EISEN A.
 PA (GANG/) GANGOLLI E A.
 PA (RIEG/) RIEGER D K.
 PA (SPAD/) SPADERNA S K.
 XX
 PI Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
 PI Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyanakar VM,
 PI Ort T, Gorman L, Zerrusen BD, Anderson DW, Zhong M, Catterton E;
 PI Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Sheno Sg;
 PI Shimkets RA, Rothenberg ME, Leach MP, Agee ML, Berghs C, Dipolpo VA;
 PI Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 XX
 DR WPI; 2004-213931/20.
 DR N-PSDB; ADN62818.
 XX
 PT Isolated NOVX polypeptides and nucleic acids, useful for preventing,
 PT diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 XX
 PS Claim 1; SEQ ID NO 14; 395bp; English.
 XX
 CC The invention relates to isolated NOVX polypeptides and polynucleotides.
 CC NOVX polypeptides and polynucleotides are used to prevent, diagnose or
 CC treat a medical condition in human related to the aberrant expression and
 CC activity of NOVX polypeptides. For example, NOVX polypeptides and
 CC polynucleotides may be used to treat disorders associated with decreased
 CC expression or activity of NOVX by supplementing the patient our
 CC production or to rectify mutations. Conversely, antisense NA molecules
 CC may be administered to down regulate expression of NOVX polypeptides by
 CC binding with the cells own genes and preventing their expression. NOVX
 CC polynucleotides and complementary sequences may also be used as DNA
 CC probes in diagnostic assays to detect and quantitate the presence of
 CC similar sequences in samples, and so which patients may be in need of
 CC restorative therapy. NOVX polypeptides may also be used as antigens in
 CC the production of antibodies and in assays to identify modulators
 CC (agonists and antagonists) of the expression and activity of NOVX. The
 CC anti-NOVX polypeptide antibodies, agonists and antagonists may also be
 CC used to modulate NOVX polynucleotide expression and activity of NOVX
 CC polypeptides. The anti-NOVX polynucleotide antibodies may also be used as
 CC diagnostic agents for detecting the presence of NOVX in samples. NOVX
 CC polypeptides and polynucleotides may be used in this way to prevent,
 CC diagnose and treat: metabolic disorders, diabetes, obesity, infectious
 CC disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative
 CC disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders,
 CC haematopoietic disorders, and the various dyslipidaemias, metabolic
 CC disturbances associated with obesity, the metabolic syndrome X and
 CC wasting disorders associated with chronic diseases and various cancers.
 CC They may also be used as antibacterial agents. The present sequence
 CC represents the amino acid sequence of a human NOVX protein.
 CC
 XX
 SQ Sequence 2066 AA;
 Query Match 99.2%; Score 10407.5; DB 8; Length 2066;
 Best Local Similarity 99.5%; Pred. No. 0;
 Matches 2041; Conservative 2; Mismatches 8; Indels 1; Gaps 1;
 QY 1 MLKFKYGARNDPDAAGAPRIASRASRLNLFQGGKPPFTMQQMSPLSREGILDALFVLF 60
 DB 1 MLKFKYGARNDPDAAGAPRIASRASRLNLFQGGKPPFTMQQMSPLSREGILDALFVLF 60
 QY 61 ECGQPALMKIKHVSNFVRKYSPTIAELOIOPSAKFEVRSVLGCGHFAFVQVVRKATG 120
 DB 61 ECGQPALMKIKHVSNFVRKYSPTIAELOIOPSAKFEVRSVLGCGHFAFVQVVRKATG 120
 QY 121 DIYAMKVMKKKALLAEOVSFFEEERNILSRSTSPMIPOLQYAFQDKNHLVLYMEYOPGG 180
 DB 121 DIYAMKVMKKKALLAEOVSFFEEERNILSRSTSPMIPOLQYAFQDKNHLVLYMEYOPGG 180
 QY 181 DLSLNLRYEDQDENLIGFYLAELILAVSHVLMGVYHRDIPENILVDRTGHIKLVDF 240
 DB 181 DLSLNLRYEDQDENLIGFYLAELILAVSHVLMGVYHRDIPENILVDRTGHIKLVDF 240

QY	241	GSAAWNSNKNVNAKLPIGTDPYMAPEVLYVWNGDGKGTYGDCDWMVGVYIAEYMYGR	300
Db	241	GSAAWNSNKN-VNAKLPIGTDPYMAPEVLYVWNGDGKGTYGDCDWMVGVYIAEYMYGR	299
QY	301	SPFAGTSARFTNNIMNFQRLKFPDDPKVSGDFDLIQSLICQKELKTEBGLCHPEF	360
Db	300	SPFAGTSARFTNNIMNFQRLKFPDDPKVSGDFDLIQSLICQKELKTEBGLCHPEF	359
QY	361	SKIDNNNRNSPPVPFTLKSDDDTSNDEPEKNSWSSPQOLSPSGSEBEPFVYES	420
Db	360	SKIDNNNRNMPVPFTLKSDDDTSNDEPEKNSWSSPQOLSPSGSEBEPFVYES	419
QY	421	YSKALGILGRSESVSGDSPAKTYSMEKKLLIKSKELQDSQDKKHKOEOTRLHRRVS	480
Db	420	YSKALGILGRSESVSGDSPAKTYSMEKKLLIKSKELXSDGDKHKHXMTRLHRRVS	479
QY	481	EVEAVLSQKEVELKASETORSILLEDOLATYTTECSLGRSLBQARMEVSOEDKALQLH	540
Db	480	EVEAVLSQKEVELKASETORSILLEDOLATYTTECSLGRSLBQARMEVSOEDKALQLH	539
QY	541	DIREOSRLQELKOEYOAYOEWMNMNOLBEDVSAARRSDLYESLREBSRLAAEBFK	600
Db	540	DIREOSRLQELKOEYOAYOEWMNMNOLBEDVSAARRSDLYESLREBSRLAAEBFK	599
QY	601	RKATECQHLLKAKQOGRPEVGEYAKLEKINAEOQLKQOEQKLEKAVKASTEATELLQ	660
Db	600	RKATECQHLLKAKQOGRPEVGEYAKLEKINAEOQLKQOEQKLEKAVKASTEATELLQ	659
QY	661	NIROAKERAEERLEKLNREDSSBGRKKLYAEERHSLNNKYRLFTMERRENRLKOD	720
Db	660	NIROAKERAEERLEKLNREDSSBGRKKLYAEERHSLNNKYRLFTMERRENRLKOD	719
QY	721	IOTSQOIQOWADKLELEEKHREAYSAOHLVHLKQKEQHYEBKIKVLDNOIKDOLAD	780
Db	720	IOTSQOIQOWADKLELEEKHREAYSAOHLVHLKQKEQHYEBKIKVLDNOIKDOLAD	779
QY	781	KETLENNMQRHEBEAHEKGIKLESEKAMINMDSKIRSLGEORIVELSEANKLAANSLSFT	840
Db	780	KETLENNMQRHEBEAHEKGIKLESEKAMINMDSKIRSLGEORIVELSEANKLAANSLSFT	839
QY	841	QRNMKAQOEWISSELRQOKFYLETQAGKLEAONRKLEBQLEKISHODSDKNRLLELETRL	900
Db	840	QRNMKAQOEWISSELRQOKFYLETQAGKLEAONRKLEBQLEKISHODSDKNRLLELETRL	899
QY	901	REVLSEHEQKLEKROLTETOLSIQERESQUTLQARALLESQLOAKTELEBTTAE	960
Db	900	REVLSEHEQKLEKROLTETOLSIQERESQUTLQARALLESQLOAKTELEBTTAE	959
QY	961	EEESIALTAHDEIORKFDALRNSCTVTTDEBOLNQTENAEANNONFLSQOLDEAS	1020
Db	960	EEESIALTAHDEIORKFDALRNSCTVTTDEBOLNQTENAEANNONFLSQOLDEAS	1019
QY	1021	GANDEIVOLRSEVDHLRREITEREMOVLTSQOTMEALKTTCMLBEOVMDEALNDELLE	1080
Db	1020	GANDEIVOLRSEVDHLRREITEREMOVLTSQOTMEALKTTCMLBEOVMDEALNDELLE	1079
QY	1081	KERQWEARSVLGDSEKQSECEVRNLEQMLDTEKOSRAPADQRTTESQVVELAVKEHKA	1140
Db	1080	KERQWEARSVLGDSEKQSECEVRNLEQMLDTEKOSRAPADQRTTESQVVELAVKEHKA	1139
QY	1141	EILALQOLKXQKUKASELSDKLNDLEKHAMLENNANSLQKLETERELKORLLEBQAK	1200
Db	1140	EILALQOLKXQKUKASELSDKLNDLEKHAMLENNANSLQKLETERELKORLLEBQAK	1199
QY	1201	LQOQWDLQKNIIFRLTQGLQELRADLKLTERSDELEYOTENIQVLSHEKVKMEGTISQ	1260
Db	1200	LQOQWDLQKNIIFRLTQGLQELRADLKLTERSDELEYOTENIQVLSHEKVKMEGTISQ	1259
QY	1261	QTKLIDFLQAKMDQPAKKKKVPLQYNEKALAEKKKACAELEBALQKTRIELSARBEA	1320
Db	1260	QTKLIDFLQAKMDQPAKKKKVPLQYNEKALAEKKKACAELEBALQKTRIELSARBEA	1319

QY	131	AHRAKTDHPHSTATATACQIAMSALYRSPHOSMSLAPSPSSRRKESSTPEERFSRL	1308
Db	1320	AHRAKTDHPHSTATATACQIAMSALYRSPHOSMSLAPSPSSRRKESSTPEERFSRL	1379
QY	1381	KERNHNHNPHPFNGLNBRATKCAVCLDITVHFPGQASKCLEQWCHPKGCTCLPATGCL	1440
Db	1380	KERNHNHNPHPFNGLNBRATKCAVCLDITVHFPGQASKCLEQWCHPKGCTCLPATGCL	1435
QY	1441	PAEVAHTFEAFPCRDKNNSPGLQTEKPESSSLHLEGMMKVPNNNRNGOQGMRKTYIVLEGS	1500
Db	1440	PAEVAHTFEAFPCRDKNNSPGLQTEKPESSSLHLEGMMKVPNNNRNGOQGMRKTYIVLEGS	1499
QY	1501	KVLIIYDNEARAPAGORPVBEFELCLPDGVSIHGAVGASELANTAKADVPYILKMHESHPT	1560
Db	1500	KVLIIYDNEARAPAGORPVBEFELCLPDGVSIHGAVGASELANTAKADVPYILKMHESHPT	1559
QY	1561	TCWPERITLYILABPDKQKRWVTLLESVVAGGRVSRKAEADALCLNGLSKLEGGDRLD	1620
Db	1560	TCWPERITLYILABPDKQKRWVTLLESVVAGGRVSRKAEADALCLNGLSKLEGGDRLD	1619
QY	1621	MNCTLPFSDDQVVLVGTSEBGLYALNVLKNSLTHVVGIGAFQIYIYIKOLEKLMIAGEERA	1680
Db	1620	MNCTLPFSDDQVVLVGTSEBGLYALNVLKNSLTHVVGIGAFQIYIYIKOLEKLMIAGEERA	1679
QY	1681	LCLVDVKKVKQSLAQSHLPDAQDISPNIPEAVKGCCLFGAGKIBNGLCICAMPSKVYL	1740
Db	1680	LCLVDVKKVKQSLAQSHLPDAQDISPNIPEAVKGCCLFGAGKIBNGLCICAMPSKVYL	1739
QY	1741	RYNENLSKTCIRKSEIETSEBPCSHFTNYSLLIGTNKFEIEMQYTLBEFLDKNDHSLA	1800
Db	1740	RYNENLSKTCIRKSEIETSEBPCSHFTNYSLLIGTNKFEIEMQYTLBEFLDKNDHSLA	1799
QY	1801	PAVFAASNSPSPVIVQVNASGOREEYLLCFHEGCVFVDSYGRSRRTDCLKMSRLPLAFA	1860
Db	1800	PAVFAASNSPSPVIVQVNASGOREEYLLCFHEGCVFVDSYGRSRRTDCLKMSRLPLAFA	1859
QY	1861	YREPYLFVTHNSLVEIEIQARSAGTPARAYLIDIPNRYLGPALISSGAIYVLASSYODKL	1920
Db	1860	YREPYLFVTHNSLVEIEIQARSAGTPARAYLIDIPNRYLGPALISSGAIYVLASSYODKL	1919
QY	1921	RVICCKGNLVESGTEHHRGSTERSSPNKRGGPTYNHEITKRVASSPAPEGSGHPREP	1980
Db	1920	RVICCKGNLVESGTEHHRGSTERSSPNKRGGPTYNHEITKRVASSPAPEGSGHPREP	1979
QY	1981	STPHRYEGRETELRLDKSPGRPLERKSPGRILSTRERSPARLFEEDSRGRLPAGAVRT	2040
Db	1980	STPHRYEGRETELRLDKSPGRPLERKSPGRILSTRERSPARLFEEDSRGRLPAGAVRT	2039
QY	2041	PLSQVNKIKWQDS 2052	
Db	2040	PLSQVNKIKWQDS 2051	
RESULT 13			
ID	ABP97683		
ABP97683	standard; protein; 2055 AA.		
XX	ABP97683;		
XX	16-MAY-2003 (first entry)		
DE	Polypeptide similar to citron rho/rac-interacting kinase-short kinase.		
XX	Human; citron rho/rac-interacting kinase-short kinase; obesity;		
KW	chronic obstructive pulmonary disease; hypertension; diabetes;		
KW	coronary artery disease; hyperlipidaemia; stroke; gallbladder disease;		
KW	gout; osteoarthritis; sleep apnea; cancer; thrombolic disease;		
KW	polycystic ovarian syndrome; fertility; depression.		
XX	Homio sapiens.		
XX	MO2003004629-A2.		

PD 16-JAN-2003.
 XX 01-JUL-2002; 2002WC-EP007229.
 XX 02-JUL-2001; 2001US-0301853P.
 PR 10-DEC-2001; 2001US-0337130P.
 PR 25-APR-2002; 2002US-0375015P.
 XX (FARB) BAYER AG.
 PA Zhu Z;
 XX WPI; 2003-221595/21.
 DR New human citron rho/rac-interacting kinase-short kinase polypeptide and
 PT polynucleotide for preventing or treating diseases associated with the
 PT polypeptide dysfunction, e.g. obesity or chronic obstructive pulmonary
 PT disease.
 PS Disclosure; Fig 4; 145pp; English.
 XX The present sequence represents a polypeptide with some identity to a
 CC human citron rho/rac-interacting kinase-short kinase polypeptide. The
 CC polynucleotide and polypeptide of the invention are useful in preventing,
 CC ameliorating, or treating diseases associated with the polypeptide
 CC dysfunction. The expression vector or the reagent is useful in the
 CC preparation of a medication for modulating the activity of a human citron
 CC rho/rac-interacting kinase-short kinase in a disease, such as obesity or
 CC chronic obstructive pulmonary disease. These may also be used for
 CC treating obesity/overweight-associated comorbidities, such as
 CC hypertension, diabetes, coronary artery disease, hyperlipidaemia, stroke,
 CC gallbladder disease, gout, osteoarthritis, sleep apnea, cancer,
 CC thrombotic diseases, polycystic ovarian syndrome, reduced fertility, and
 CC depression
 XX Sequence 2055 AA;
 SO
 Query Match 96.3%; Score 10109.5; DB 6; Length 2055;
 Best Local Similarity 96.0%; Pred. No. 0;
 Matches 1974; Conservative 40; Mismatches 39; Indels 3; Gaps 2;

QY 481 EWEAVLSQKEVELKASETORSLLEODLATYITECSSLKXSLSEARMEVSQEDDKALQLH 540
 DB 480 EWEAVLSQKEVELKASETORSLLEODLATYITECSSLKXSLSEARMEVSQEDDKALQLH 539
 QY 541 DIREQSRKLOEIKEOEYQAOVEEMRLMNQLEEDLVASARRSDLYSELSRESLAAEFK 600
 DB 540 DIREQSRKLOEIKEOEYQAOVEEMRLMNQLEEDLVASARRSDLYSELSRESLAAEFK 599
 QY 601 RKATECOHKILKADQCKPEVGEYAKLEKINAEQOLKLOELQEKAYKASTEATELLQ 660
 DB 600 RKANECQHKLMKAKDQCKPEVGEYSKLEKINAEQOLKLOELQEKAYKASTEATELLQ 659
 QY 661 NIREQABERERLEKIONREDSSEGRKKLVAEERHSLNENVKRLETERENLKKOD 720
 DB 660 NIREQABERERLEKIONREDSSEGRKKLVAEERHSLNENVKRLETERENLKKOD 719
 QY 721 IOTKSQOIQOMADKILEBEKREAOVSQHLVEHLKQKQHYEEKIKVLNDQIKDQAD 780
 DB 720 IOTKSQOIQOMADKILEBEKREAOVSQHLVEHLKQKQHYEEKIKVLNDQIKDQAD 779
 QY 781 KETLENNMOHEBEAHEKGIUSEQYAMINANDSKTRSLFORIVELSEANKLAANSGLT 840
 DB 780 KETLENNMOHEBEAHEKGIUSEQYAMINANDSKTRSLFORIVELSEANKLAANSGLT 839
 QY 841 QRMKAKOEWISLROCKFYLETOAGKLEAONRKLSEOLEKISHODSPDKNRLLEETRL 900
 DB 840 QRMKAKOEWISLROCKFYLETOAGKLEAONRKLSEOLEKISHODSPDKNRLLEETRL 899
 QY 901 REVSLEHEQKLELQKLTLEQLSLOERSQUTALQAAABALESQURQAKTELEETTAEA 960
 DB 900 REVSLEHEQKLELQKLTLEQLSLOERSQUTALQAAABALESQURQAKTELEETTAEA 959
 QY 961 EEEIOALTARDEIQKFPALRNSCTVITDLEBOLNQTEDNAELNNOFFYLSKQIDEAS 1020
 DB 960 EEEIOALTARDEIQKFPALRNSCTVITDLEBOLNQTEDNAELNNOFFYLSKQIDEAS 1019
 QY 1021 GANDEIVQARSEVDHRRRTTEREMOLTQOKQMEALKTTCMTLEBQVMDLBNLELLE 1080
 DB 1020 GANDEIVQARSEVDHRRRTTEREMOLTQOKQMEALKTTCMTLEBQVMDLBNLELLE 1079
 QY 1081 KERQWEMRVSVLDEKSEOFECREVRLEQRMIDTEKQSRABADQRTESQVVELAVENHKA 1140
 DB 1080 KERQWEMRVSVLDEKSEOFECREVRLEQRMIDTEKQSRABADQRTESQVVELAVENHKA 1139
 QY 1141 EIALAQALKEQKLAESLSDKLNDEKXAMLENMARSIOQKLETERBEIKQRLLEBOAK 1200
 DB 1140 EIALAQALKEQKLAESLSDKLNDEKXAMLENMARSIOQKLETERBEIKQRLLEBOAK 1199
 QY 1201 LOQOMLOKNNHIFRLTOGLQEALDRADLLKTERSDLEYOLENTQVLYSHKVMGEGTISQ 1260
 DB 1200 LOQOMLOKNNHIFRLTOGLQEALDRADLLKTERSDLEYOLENTQVLYSHKVMGEGTISQ 1259
 QY 1261 QTKLIDFLQAKMDQPAKKKKVPQVNEVLKLALEKEXARCALEBEALQKTRIELSAREEA 1320
 DB 1260 QTKLIDFLQAKMDQPAKKKKVPQVNEVLKLALEKEXARCALEBEALQKTRIELSAREEA 1319
 QY 1321 AHRKATDHPHSTPATARQOIAMSAIVRSPEHOPSAMSLAPSSRRKSSSTPEEBSRL 1380
 DB 1320 AHRKATDHPHSTPATARQOIAMSAIVRSPEHOPSAMSLAPSSRRKSSSTPEEBSRL 1379
 QY 1381 KERMMHNIPIRRFVNGIMBATKCAVCLDVHFERQASKCLECQVMCHPCKSTCLPATCGI 1440
 DB 1380 KERMMHNIPIRRFVNGIMBATKCAVCLDVHFERQASKCLECQVMCHPCKSTCLPATCGI 1439
 QY 1441 PARYATHTEAPCRDQKNSPGLOTKEPSSILHEGMKATPRNNKRQOQGDWKYIYLEGS 1500
 DB 1440 PARYATHTEAPCRDQKNSPGLOTKEPSSILHEGMKATPRNNKRQOQGDWKYIYLEGS 1499
 QY 1501 KVLIDYNEAREAQORVEEPELCLPDGVSIRGAVASBELANTAKADVPIYILMESHPHT 1560
 DB 1500 KVLIDYNEAREAQORVEEPELCLPDGVSIRGAVASBELANTAKADVPIYILMESHPHT 1559
 QY 1561 TCMFGKTLIILAFSPFDKQRMWTALAESVVAAGRVSEKXKADAKKLGNSILKLEGGDRID 1620


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Db      1560 TCMGRITLYLAPSPDQKQWVTLAESVAGARVREVAEDAKLIGSLKLEGGDDLD
Qy      1621 MNCTLPSPDQVVLVGTBEGLYALNVLKNSLTHVPGIGAFQIYIITKDEKLMAGEERA
Db      1620 MNCTLPSPDQVVLVGTBEGLYALNVLKNSLTHVPGIGAFQIYIITKDEKLMAGEERA
Qy      1681 LCLVDVKKVKQSLAQSHLPAPDISPNI FEAVKGCHEFGACKIENGLCICAMPKSVIL
Db      1680 LCLVDVKKVKQSLAQSHLPAPDIVSPNIFEAVKGCHEFGACKIENGLCICAMPKSVIL
Qy      1741 RYNNELSKYCIKRIETSEPCSCIHFTMYSTLIGNKKEYIDMQYTLDEFLDKNDHSLA
Db      1740 RYNNELSKYCIKRIETSEPCSCIHFTMYSTLIGNKKEYIDMQYTLDEFLDKNDHSLA
Qy      1801 PAVEAASSNFPVSIIVQVNSAGOREYLLCFHEFGVFDVSGRSRTDLMKSRPLAFA
Db      1800 PAVEAASSNFPVSIIVQVNSAGOREYLLCFHEFGVFDVSGRSRTDLMKSRPLAFA
Qy      1861 YREPYLFVTNHSLEVIEIQARSSAGTPARAAYLDIPNRYLGPAISSGATYLAASYODKL
Db      1860 YREPYLFVTNHSLEVIEIQARSSAGTPARAAYLEIPNRYLGPAISSGATYLAASYODKL
Qy      1921 RVLCCKNLVKESTGHEHHRGPGSTSRSSPNKKGPTVYEHITKRYVASSAPPEGSHREP
Db      1920 RVLCCKNLVKESTGHEHHRGPGSTSRSSPNKKGPTVYEHITKRYVASSAPPEGSHREP
Qy      1981 STPHRY--REGRTLRDCKSPGRPLEREKSPGRILSTRERSPARLPEDSSRGRLPAGAV
Db      1980 STPHRYDREGRTELRLDKSPGRPLEREKSPGRILSTRERSPARLPEDSSRGRLPAGAV
Qy      2039 RTPLSQVNVKWDQSSV 2054
Db      2040 RTPLSQVNVKWDQSSV 2055

RESULT 14
AAO26960 standard; protein; 2055 AA.
XX
AC      AAO26960;
XX
DT      01-MAY-2003 (first entry)
DE
DE      Human CRK related protein sequence, SEQ ID No 3.
XX
KW      Anorectic; hypotensive; cardiatic; antilipemic; cerebroprotective;
KW      anti-gout; osteopathic; antiarthritic; cytosstatic; antidepressant;
KW      immunomodulator; antitumor; tranquilizer; antiparkinsonian; nootropic;
KW      neuroprotective; antiinflammatory; antidiabetic; analgesic;
KW      human citron rho/rac-interacting kinase; enzyme; CRK; ameliorating;
KW      obesity; comorbidity; cancer; anorexia; cachexia; bulimia;
KW      central nervous system disorder; chronic obstructive pulmonary disease;
KW      diabetes; pain.
XX
XX      Homo sapiens.
XX      OS
XX      MO2003004523-A1.
XX      PD
XX      16-JAN-2003.
XX
XX      28-JUN-2002; 2002MO-EP007156.
XX      PF
XX      02-JUL-2001; 2001US-0301841P.
XX      PR      11-DEC-2001; 2001US-0338651P.
XX      PR      25-APR-2002; 2002US-0375014P.
XX
XX      (FARB ) BAYER AG.
XX
XX      Zhu Z;
XX
XX      WPI; 2003-221576/21.

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PT      New human citron rho/rac-interacting kinase (CRK) polypeptide and
PT      polynucleotide, useful in preventing, ameliorating or treating diseases
PT      associated with human CRK dysfunction, e.g. obesity, diabetes or
PT      Alzheimer's disease.
XX
XX      Disclosure; Fig 3; 237pp; English.
XX
XX      The invention relates to an isolated polynucleotide encoding a human
XX      citron rho/rac-interacting kinase polypeptide. The isolated
XX      polynucleotide comprises a 6165 or 6603 base pair sequence, given in the
XX      specification. The human citron rho/rac-interacting kinase (CRK)
XX      polypeptide and polynucleotide are useful in preventing, ameliorating, or
XX      treating diseases associated with human CRK dysfunction such as obesity
XX      and obesity-associated comorbidities (e.g. hypertension, coronary artery
XX      disease, hyperlipidemia, stroke, gout, osteoarthritis, some types of
XX      cancer including endometrial, breast, prostate and colon cancer),
XX      anorexia, cachexia, bulimia, central nervous system disorders (e.g. mood
XX      disorders, anxiety disorders, Parkinson's disease or Alzheimer's
XX      disease), chronic obstructive pulmonary disease, or diabetes. These can
XX      also be used to treat pain associated with the disorders. The human CRK
XX      polypeptide is also useful in diagnostic assays or in genetic testing.
XX      The expression vector or the reagent is useful in preparing a medicament
XX      for modulating the activity of a human CRK in a disease, e.g. obesity, a
XX      central nervous system disorder, or chronic obstructive pulmonary
XX      disease. The fusion protein is useful for generating antibodies against a
XX      CRK polypeptide and for use in various assay systems. The methods are
XX      useful in producing and detecting the polynucleotide and polypeptide and
XX      in screening for agents that modulate the activity of the human CRK
XX      polypeptide. This sequence represents a protein relating to the human
XX      CRK protein of the invention
XX
XX      Sequence 2055 AA;
XX
XX      Query Match          96.3%; Score 10109.5; DB 6; Length 2055;
XX      Best Local Similarity 96.0%; Pred. No. 0;
XX      Matches 1974; Conservative 40; Mismatches 39; Indels 3; Gaps 2;
Qy      1 MLKFKYGARNPLDAGAAPIASRASRLNLFQCKPPTMQOQMSPLREGILDAFLVFE 60
Db      1 MLKFKYGVNRNPPASASBPISASRSRLNLFQCKPPTMQOQMSALREGMLDLFLALFE 60
Qy      61 ECGSPALMKIKHVSNFVRKYSDDTIAELQSLQPSAKDFEVSILVCGHFAEYQVVERKATG 120
Db      61 ECGSPALMKKHVSNFQVKYSDDTIAELRELQPSARDEVSILVCGHFAEYQVVERKATG 120
Qy      121 DIYAMKMKKKALLAQOVSFEEERNTLSRSTSPWIPQIQAQDKNHLVLMVEYQPGG 180
Db      121 DIYAMKMKKKALLAQOVSFEEERNTLSRSTSPWIPQIQAQDKNHLVLMVEYQPGG 180
Qy      181 DLISLNRVEDQDENLQFYLAELIYAVSVHLMGVVHRDIKENLIVRTGHIKLVDF 240
Db      181 DFLSLNRVEDQDENLQFYLAELIYAVSVHLMGVVHRDIKENLIVRTGHIKLVDF 240
Qy      241 GSAAKNSNMVNAKLPIGTDPYMAPEVLTVMNGDGKGYGLDGDWMSVGIAYEMTYGR 300
Db      241 GSAAKNSNMK-VDAKLPIGTDPYMAPEVLTVMNEDRGTGYGLDGDWMSVGVAEMTYGK 299
Qy      301 SPFAEGTSATFTNNIMNRFELKRPDDPKVSSDFLDLQSLCGQKRLKFEGLCHPFF 360
Db      300 TPFTGTSATFTNNIMNRFELKRPDDPKVSSDFLDLQSLCGQKRLKFEGLCHPFF 359
Qy      361 SKIDMNNIRNSPPFVFTLKSDDTSNFDPEPKNSWVSSPCQLSPGSGEELPFQFGS 420
Db      360 ARTDMNNIRNSPPFVFTLKSDDTSNFDPEPKNSWVSSPCQLSPGSGEELPFQFGS 419
Qy      421 YSKALGILGRSBSVSGLDSPATSSMEKLLIKSKELQDSQDKCHMEQEMTLHRVS 480
Db      420 YSKALGILGRSBSVSGLDSPATSSMEKLLIKSKELQDSQDKCHMEQEMTLHRVS 479
Qy      481 EYEAVALSQKEVELKASSETQSLLEQDLATYITTCSSLSKRLLEQARMEVSEDDKALQLH 540
Db      480 EYEAVALSQKEVELKASSETQSLLEQDLATYITTCSSLSKRLLEQARMEVSEDDKALQLH 539

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QY 541 DIBOSKLOEIKOEYOAOVEEMKLMNOJEBDLVSNRRSDLYESBLRESRLAEEFK 600
 DB 540 DIRQSOKLOEIKOEYOAOVEEMRLMMNOJEBDLVSARRSDLYESBLRESRLAEEFK 599
 QY 601 RKAECSOKLKLKADQCKPEYGEYAKLEKINAEOOLIOELQELKFAVKASTATELLO 660
 DB 600 RKANECOKHMKADQCKPEYGEYSKLEKINAEOOLIOELQELKFAVKASTATELLO 659
 QY 661 NIROKAEARELEKLONRDESSGIRKLVAEERHSLNNKVKLETERRENNRLKDD 720
 DB 660 NIROKAEARELEKLONRDESSGIRKLVAEERHSLNNKVKLETERRENNRLKDD 719
 QY 721 IQTSOQOIQOAMADKILBLEEKHRAOVSAGHLEHNLQCKGHYEKIKVLDNOJCKDLAD 780
 DB 720 IQTSOQOIQOAMADKILBLEEKHRAOVSAGHLEHNLQCKGHYEKIKVLDNOJCKDLAD 779
 QY 781 KETLENNMORHEEAHKGKILSEOKAMINAMDSKISLEORIVELSEANKLANSSLFT 840
 DB 780 KESLENNMORHEEAHKGKILSEOKAMINAMDSKISLEORIVELSEANKLANSSLFT 839
 QY 841 QRRNKAOEMISELROCKFYLETQAGKLEAONRKLBEQLEKISHQDHSKNNRLLEETRL 900
 DB 840 QRRNKAOEMISELROCKFYLETQAGKLEAONRKLBEQLEKISHQDHSKNNRLLEETRL 899
 QY 901 REVSLHEBOKLEKROULTELOLSLOBRESQUTLQARALAEOLQAKTELEETTAEA 960
 DB 900 REVSLHEBOKLEKROULTELOLSLOBRESQUTLQARALAEOLQAKTELEETTAEA 959
 QY 961 EEEIOALTARHDEIQRFPDALRNSCTVITDLEBOLNLTEDNALNNONFLSKOLBEAS 1020
 DB 960 EEEIOALTARHDEIQRFPDALRNSCTVITDLEBOLNLTEDNALNNONFLSKOLBEAS 1019
 QY 1021 GANDEIVOLRSEVDHLREITEREMOULTSQOKTWEALKTCTMLEBQVMDLEALNDELE 1080
 DB 1020 GANDEIVOLRSEVDHLREITEREMOULTSQOKTWEALKTCTMLEBQVMDLEALNDELE 1079
 QY 1081 KERQEMKRSVLDGKESQFECGRVRELQRMIDTEKOSARADQRTTESQVVELAVKHKA 1140
 DB 1080 KERQEMKRSVLDGKESQFECGRVRELQRMIDTEKOSARADQRTTESQVVELAVKHKA 1139
 QY 1141 EITLALQALKEOKKAKESLSPDKNDLEKKHMLEMNRSLQOKLETRELEKORLLEBOAK 1200
 DB 1140 EITLALQALKEOKKAKESLSPDKNDLEKKHMLEMNRSLQOKLETRELEKORLLEBOAK 1199
 QY 1201 LQOQMDLQKXHFILFTQLOEALDRADLKTERSDLEYOLENIOVLYSHEKVXNEGTSIQ 1260
 DB 1200 LQOQMDLQKXHFILFTQLOEALDRADLKTERSDLEYOLENIOVLYSHEKVXNEGTSIQ 1259
 QY 1261 QTKLIDFLQAKMDQPAKKKVPLOYNELKALBEKAKCALEBALQKTRIELRSABEEA 1320
 DB 1260 QTKLIDFLQAKMDQPAKKKVPLOYNELKALBEKAKCALEBALQKTRIELRSABEEA 1319
 QY 1321 AHRKATDHPHSTPATAROOIAMSATVRSPEHOPSAMSLAPSSRRKESSTPEEFSRRL 1380
 DB 1320 AHRKATDHPHSTPATAROOIAMSATVRSPEHOPSAMSLAPSSRRKESSTPEEFSRRL 1379
 QY 1381 KERHNNIPIHREFNVLNMRATKCAVCLDTVFHGRQASKLEQCYWCHPKCSTCLPATCGL 1440
 DB 1380 KERHNNIPIHREFNVLNMRATKCAVCLDTVFHGRQASKLEQCYWCHPKCSTCLPATCGL 1439
 QY 1441 PAEYATHTFAFCSDKXNSPGLQTKPEPSSSLHEGMKVPVRRNKRGQOQMDRKTYVLGGS 1500
 DB 1440 PAEYATHTFAFCSDKXNSPGLQTKPEPSSSLHEGMKVPVRRNKRGQOQMDRKTYVLGGS 1499
 QY 1501 KVLITYNEARBARAGRPVEEPELCPDGDVSIHGAVGASELANTAKADVPTILKMHSHPH 1560
 DB 1500 KVLITYNEARBARAGRPVEEPELCPDGDVSIHGAVGASELANTAKADVPTILKMHSHPH 1559
 QY 1561 TCWPGRTLYLAPSPDKORVVTALBSVVAAGRVSRKAEADAKILGNLSLKLJEGDRLD 1620
 DB 1560 TCWPGRTLYLAPSPDKORVVTALBSVVAAGRVSRKAEADAKILGNLSLKLJEGDRLD 1619
 QY 1621 MNCTLPSPDOVLVGTBEGLYALNVLNLSLTHPGIGAFQIYIIKOLEKLMITAGEERA 1680

DB 1620 MNCTLPSPDOVLVGTBEGLYALNVLNLSLTHPGIGAFQIYIIKOLEKLMITAGEERA 1679
 QY 1681 LCLVDVKVYKOSLQASHLPAQDIPSPNIFEAVKGCHLFGAGKILENGLCICAMPKRVIL 1740
 DB 1680 LCLVDVKVYKOSLQASHLPAQDIPSPNIFEAVKGCHLFGAGKILENGLCICAMPKRVIL 1739
 QY 1741 RYNNENSKYCIKREIETSEPCSCIHFTNYSILIGTKKFEYIDMKOYTLBEFLDKDHSIA 1800
 DB 1740 RYNNENSKYCIKREIETSEPCSCIHFTNYSILIGTKKFEYIDMKOYTLBEFLDKDHSIA 1799
 QY 1801 PAVFAASNSFPVSIYOVNSAGOREEYLCFHFEGYFVDSYGRSRSTDLDKMSRLPLAFA 1860
 DB 1800 PAVFAASNSFPVSIYOVNSAGOREEYLCFHFEGYFVDSYGRSRSTDLDKMSRLPLAFA 1859
 QY 1861 YREPVLFTVHFNLSLEYIEIQARSSAGTPARAYLDIPNPRYLGAISSGALYIASSYQDKL 1920
 DB 1860 YREPVLFTVHFNLSLEYIEIQARSSAGTPARAYLDIPNPRYLGAISSGALYIASSYQDKL 1919
 QY 1921 RYVCCGKLVKESGTEHHRGPTSRSSPNKRGPTTNEHTTKRVASSPAPPEGSPHREP 1980
 DB 1920 RYVCCGKLVKESGTEHHRGPTSRSSPNKRGPTTNEHTTKRVASSPAPPEGSPHREP 1979
 QY 1981 STEPHRY--RGRTELRRDSSPGRPLERKSPGRILSTRRERSPARLFEDESRGRPLPAGAV 2038
 DB 1980 STEPHRYRDRGRTELRRDSSPGRPLERKSPGRILSTRRERSPARLFEDESRGRPLPAGAV 2039
 QY 2039 RTPLSQNVKWDQSSV 2054
 DB 2040 RTPLSQNVKWDQSSV 2055

RESULT 15
 AAE24079
 ID AAE24079 standard; protein; 2053 AA.
 XX
 AC AAE24079;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human MDPK protein.
 XX
 KW Human; myotonic dystrophy type protein kinase; MDPK; 13245 protein;
 KW tumorigenesis; tumour growth; tumour metastasis; viral infection;
 KW skeletal muscle disorder; muscular dystrophy; myotonic dystrophy;
 KW immune disorder; neoplastic disorder; gene therapy.
 OS Homo sapiens.
 XX
 FH Key
 FT Domain
 FT /note="pkinase domain"
 FT Domain
 FT /note="pkinase domain"
 FT Region
 FT /note="Antigenic epitope"
 FT Region
 FT /note="Serine/Threonine protein kinase active site
 FT /note="signature"
 FT Region
 FT /note="Antigenic epitope"
 FT Domain
 FT /note="CNH domain"
 PN WO200234896-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 23-OCT-2001; 2001WO-US050636.
 XX
 PR 23-OCT-2000; 2000US-0242429P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.

XX Kapeller-Libermann R;
 XX WPI, 2002-479720/51.
 DR N-PSDB; AAD39191.
 XX
 XX Human myotonic dystrophy type protein kinase polypeptide and
 PT polynucleotide useful for prognosticating, diagnosing, preventing or
 PT inhibiting tumorigenesis, tumor growth, tumor metastasis and viral
 PT infection.
 XX
 XX Claim 8; Fig 3; 148pp; English.
 PS
 XX The invention relates to human myotonic dystrophy type protein kinase
 CC (MDPK) polypeptides designated as 13245 and nucleic acid molecules
 CC encoding such polypeptides. 13245 molecules are used to develop
 CC diagnostic and therapeutic agents for prognosticating, diagnosing,
 CC preventing, inhibiting, alleviating or curing MDPK-related disorders.
 CC Polypeptides of the invention are used to develop diagnostic and
 CC therapeutic agents for 13245-mediated or related disorders such as
 CC tumorigenesis, tumor growth, tumor metastasis, viral infection of a
 CC cell, skeletal muscle disorders (e.g. muscular and myotonic dystrophies),
 CC immune disorders and neoplastic disorders. The invention is also used in
 CC gene therapy. The present sequence is human MDPK protein
 XX
 SQ Sequence 2053 AA;

Query Match 95.5%; Score 10022.5; DB 5; Length 2053;
 Best Local Similarity 95.7%; Pred. No. 0;
 Matches 1979; Conservative 3; Mismatches 5; Indels 81; Gaps 3;

QY 1 MLKRYGARNPLDGAEPISASRLNLFQKRPMTQOQMSPLSEGLDALFVLE 60
 DB 1 MLKRYGARNPLDGAEPISASRLNLFQKRPMTQOQMSPLSEGLDALFVLE 60
 QY 61 ECSOPALMKIAGVSNFVRYKSDTIAIOELPSAKDFVRSIVCGGHFAEVOVREKATG 120
 DB 61 ECSOPALMKIAGVSNFVRYKSDTIAIOELPSAKDFVRSIVCGGHFAEVOVREKATG 120
 QY 121 DIYAMKWKKKALLAOEVSFFEEERNILSRSTPMIQLQYAFQDKNHLVMEYQPG 180
 DB 121 DIYAMKWKKKALLAOEVSFFEEERNILSRSTPMIQLQYAFQDKNHLVMEYQPG 180
 QY 181 DLISLRYEDQDENTIOFYLAELIAVSHVLMGVYHNDIKENILVDRTGHIKLVDF 240
 DB 181 DLISLRYEDQDENTIOFYLAELIAVSHVLMGVYHNDIKENILVDRTGHIKLVDF 240
 QY 241 GSAAKQNSNKNVNAKLPITGPDYMAPEVLTVMNGDGKTYGLDDCMWSVGVIAYEMIYGR 300
 DB 241 GSAAKQNSNKNVNAKLPITGPDYMAPEVLTVMNGDGKTYGLDDCMWSVGVIAYEMIYGR 300
 QY 301 SPFAEGTSARTFNINMFORFLKPPDPKVSDFLDLIQSLICQKRELKREGLCCHPFF 360
 DB 301 SPFAEGTSARTFNINMFORFLKPPDPKVSDFLDLIQSLICQKRELKREGLCCHPFF 360
 QY 361 SKIDMNNIRNSPPFVPTLKSDDDTSNFDEBEKNSWSSPCQLSPGSGSEELPFGFS 420
 DB 361 SKIDMNNIRNSPPFVPTLKSDDDTSNFDEBEKNSWSSPCQLSPGSGSEELPFGFS 420
 QY 421 YSKRALGILGRSESVVSLDPAKTSMSKELLISKELQSDQCHMEQMTLHRRVS 480
 DB 421 YSKRALGILGRSESVVSLDPAKTSMSKELLISKELQSDQCHMEQMTLHRRVS 480
 QY 481 EYAVAVLSQKEVELKASSETORSLEQDLATYITECSSLKRSLEQARMEVSQEDDALKL 540
 DB 481 EYAVAVLSQKEVELKASSETORSLEQDLATYITECSSLKRSLEQARMEVSQEDDALKL 540
 QY 541 DIFBQSRKLEIKQOEYQAOVEWRLMMNQLEEDLVARRSDLYESSELRESRLAAEFK 600
 DB 541 DIFBQSRKLEIKQOEYQAOVEWRLMMNQLEEDLVARRSDLYESSELRESRLAAEFK 600
 QY 601 RKATECHKLKADQKPEVGEYAKLEKINAEOQLKIOELQELGAVKASTATEATLLO 660
 DB 601 RKATECHKLKADQKPEVGEYAKLEKINAEOQLKIOELQELGAVKASTATEATLLO 660

DB 601 RKATECHKLKADQKPEVGEYAKLEKINAEOQLKIOELQELGAVKASTATEATLLO 648
 QY 661 NIROAKERARELEKQNRDESSSGIRKKLVAEERRSHLENKYRLTETMERENRLKDD 720
 DB 649 ----AKERARELEKQNRDESSSGIRKKLVAEERRSHLENKYRLTETMERENRLKDD 704
 QY 721 IQTSQOIQQWADKILIEEGHREAOVSQHLVHLKKEQHYEEKIVLDNQIKDLAD 780
 DB 705 IQTSQOIQQWADKILIEEGHREAOVSQHLVHLKKEQHYEEKIVLDNQIKDLAD 764
 QY 781 KETLENNMQRHEEHEKGLTSEOKAMINMDSKIRSLERIVELSPANKLAANSSTPT 840
 DB 765 KETLENNMQRHEEHEKGLTSEOKAMINMDSKIRSLERIVELSPANKLAANSSTPT 824
 QY 841 QRNKAQEMISELRQOKFYLETQAGKLEAQNRKLEOELEKISHQSDSKNRLLELETRL 900
 DB 825 QRNKAQEMISELRQOKFYLETQAGKLEAQNRKLEOELEKISHQSDSKNRLLELETRL 884
 QY 901 REVSLHEEOKLEIKROLTEILOSLQERESQITLQAARALLESQLRQAKTELETTAA 960
 DB 885 REVSLHEEOKLEIKROLTEILOSLQERESQITLQAARALLESQLRQAKTELETTAA 944
 QY 961 EEEIOALTARHDEIQRKPDALRNSCTVITDLEQNLQTEDNABLNQNFYLSQOLPAS 1020
 DB 945 EEEIOALTARHDEIQRKPDALRNSCTVITDLEQNLQTEDNABLNQNFYLSQOLPAS 1004
 QY 1021 GANDEIVQNSEVVDLREITEREMQTSQKQTEALKTCTMLEEQVMDLEALNDELLE 1080
 DB 1005 GANDEIVQNSEVVDLREITEREMQTSQKQTEALKTCTMLEEQVMDLEALNDELLE 1064
 QY 1081 KERQWEAMRSVLDGEKQFECRVEILOPMDTEKQSPARADQRTTESRQVVELAVKEKA 1140
 DB 1065 KERQWEAMRSVLDGEKQFECRVEILOPMDTEKQSPARADQRTTESRQVVELAVKEKA 1124
 QY 1141 EILALQALKEOKKKAESLSDKNDLEKKAMLEMMARSLQOKLETREILKORLLEBAK 1200
 DB 1125 EILALQALKEOKKKAESLSDKNDLEKKAMLEMMARSLQOKLETREILKORLLEBAK 1184
 QY 1201 LQQQMDLQKNHIFPLTQLOEALDRADLKTERSDLEVOLENIQVLSHEKYKMEGTSQ 1260
 DB 1185 LQQQMDLQKNHIFPLTQLOEALDRADLKTERSDLEVOLENIQVLSHEKYKMEGTSQ 1244
 QY 1261 QTKLIDFLQAKMDQPAKKK-----VPLQYNELKALKEKARCAELEEA 1305
 DB 1245 QTKLIDFLQAKMDQPAKKKGLFSRRKEDPALPTQVPLQYNELKALKEKARCAELEEA 1304
 QY 1306 LQKTRILRSAREBAARAKATDHPHSTPATARQOIMSAIVSRPEHQPSAMSLAPSS 1365
 DB 1305 LQKTRILRSAREBAARAKATDHPHSTPATARQOIMSAIVSRPEHQPSAMSLAPSS 1364
 QY 1366 RRKESSTPEEFSSRLKERMHNNIPHRFNVGLMRAATCAVCLDTVHGRQASKLECOVM 1425
 DB 1365 RRKESSTPEEFSSRLKERMHNNIPHRFNVGLMRAATCAVCLDTVHGRQASKLECOVM 1424
 QY 1426 CHPKCSTCLPATGCLPAEYATHTFEAFCRDKXNSPGLQTEBPSSSLHLEGMKVPRNNKR 1485
 DB 1425 CHPKCSTCLPATGCLPAEYATHTFEAFCRDKXNSPGLQTEBPSSSLHLEGMKVPRNNKR 1484
 QY 1486 GQGGMDRKYIVLBSKYLITDNEAREAGQRPVEFEELCPDGDVSIGAVGASLANTAK 1545
 DB 1485 GQGGMDRKYIVLBSKYLITDNEAREAGQRPVEFEELCPDGDVSIGAVGASLANTAK 1544
 QY 1546 ADVPYILKMSHPHTTQWPGRTLYLAPSPDQKRWYALBSVAGRVREKAEADAKL 1605
 DB 1545 A-----EKRAADAKL 1554
 QY 1606 LQNSLKLKEGDRLDMNCTLPFSDOVVLVGTBEGLYALANVLSLTHVPGIGAVFOIYII 1665
 DB 1555 LQNSLKLKEGDRLDMNCTLPFSDOVVLVGTBEGLYALANVLSLTHVPGIGAVFOIYII 1614
 QY 1666 KQLEKLMITGEBRALCLVDYKVKVKSLSQASHLPAPQDISPNIPEAVKGCHLFGAKTEN 1725
 DB 1615 KQLEKLMITGEBRALCLVDYKVKVKSLSQASHLPAPQDISPNIPEAVKGCHLFGAKTEN 1674

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Qy 1726 GLCICAMPBKVILRYNENLSKYCIKRIETSEPCSCIHFTNYSILIGTNKFEYIDMKQ 1785
Db 1675 GLCICAMPBKVILRYNENLSKYCIKRIETSEPCSCIHFTNYSILIGTNKFEYIDMKQ 1734
Qy 1786 YTLLEFLDKNDHSLAPAVFAASSNSFPVSIQVNSAQOREEYLLCFHEFGVFVDSYGRRS 1845
Db 1735 YTLLEFLDKNDHSLAPAVFAASSNSFPVSIQVNSAQOREEYLLCFHEFGVFVDSYGRRS 1794
Qy 1846 RTDDLKMSRLPLAFAYREPYLFTTHENSLEVIEIQARSSAGTPARAYLDIPNPRYLGPAL 1905
Db 1795 RTDDLKMSRLPLAFAYREPYLFTTHENSLEVIEIQARSSAGTPARAYLDIPNPRYLGPAL 1854
Qy 1906 SSGAIYLAASYQDKLRYICCKGNLVKESGTEHHRGPSSTRSSPNKRGPPTYNEHITKVA 1965
Db 1855 SSGAIYLAASYQDKLRYICCKGNLVKESGTEHHRGPSSTRSSPNKRGPPTYNEHITKVA 1914
Qy 1966 SSPAPPEGSPHREPSTPHRYREGRTELRDKSPGRPLEREKSPGRILSTRERESPAPLTF 2025
Db 1915 SSPAPPEGSPHREPSTPHRYREGRTELRDKSPGRPLEREKSPGRMLSTRERESPGRILF 1974
Qy 2026 EDSRGRPLPAGAVRTPLSQVNKXWDOSS 2053
Db 1975 EDSRGRPLPAGAVRTPLSQVNKXWDOSS 2002
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Search completed: May 11, 2005, 16:40:19
Job time : 239 secs